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(54) Title: METHODS OF DIAGNOSIS OF LUNG CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF LUNG CANCER

(57) Abstract: Described herein are methods and compositions that can be used for diagnosis and treatment of lung cancer and similar pathologies. Also described herein are methods that can be used to identify modulators of lung cancer and similar pathologies.

WO 02/086443 A2

METHODS OF DIAGNOSIS OF LUNG CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF LUNG CANCER

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CROSS-REFERENCES TO RELATED APPLICATIONS

This application is related to USSN 60/284,770, filed April 18, 2001; USSN 60/290,492, filed May 10, 2001; USSN 60/334,370, filed November 29, 2001; USSN 60/339,245, filed November 9, 2001; USSN 60/350,666, filed November 13, 2001; and
10 USSN 60/xxx,xxx, filed April 12, 2002 (Docket OMNI-002P); each of which is incorporated herein by reference in its entirety.

FIELD OF THE INVENTION

The invention relates to the identification of nucleic acid and protein expression
15 profiles and nucleic acids, products, and antibodies thereto that are involved in lung cancer; and to the use of such expression profiles and compositions in diagnosis and therapy of lung cancer. The invention further relates to methods for identifying and using agents and/or targets that inhibit lung cancer or related conditions.

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BACKGROUND OF THE INVENTION

Lung cancer is the second most commonly occurring cancer in the United States and is the leading cause of cancer-related death. It is estimated that there are over 160,000 new cases of lung cancer in the United States every year. Of those who are diagnosed with lung cancer, 86 percent will die within five years. Lung cancer is the most common visceral
25 cancer in men and accounts for nearly one third of all cancer deaths in both men and women. In fact, lung cancer accounts for 7% of all deaths, due to any cause, in both men and women.

Smoking is the primary cause of lung cancer, with more than 80% of lung cancers resulting from smoking. About 400 to 500 separate gaseous substances are present in the smoke of a non-filter cigarette. The most noteworthy substances include nitrogen oxides,
30 hydrogen cyanide, formaldehyde, benzene, and toluene. The particles present in cigarette smoke contain at least 3,500 individual compounds such as nicotine, tobacco alkaloids (nornicotine, anatabine, anabasine), polycyclic aromatic hydrocarbons (e.g., benzo(a)pyrene, B(a)P), naphthalenes, aromatic amines, phenols, and tobacco-specific nitrosamines.

Tobacco-specific nitrosamines are formed during tobacco curing and processing, and are suspected of causing lung cancer in humans. In rodent studies, regardless of the where or how it is applied, the tobacco-specific nitrosamine known as NNK produces lung adenomas and lung adenocarcinomas. The tobacco-specific nitrosamine known as NNAL also produces lung adenocarcinomas in rodents.

Many of the chemicals found in cigarette smoke also affect the nonsmoker inhaling "secondhand" or sidestream smoke. Indeed, the smoke inhaled by non-smokers has a chemical composition similar to the smoke inhaled by smokers, but, importantly, the concentrations of the carcinogenic tobacco-specific nitrosamines are present in higher concentrations in second hand smoke. For this and other reasons, "passive smoking" is an important cause of lung cancer, causing as many as 3,000 lung cancer deaths in nonsmokers each year.

In addition to smoking, other factors thought to be causes of lung cancer include on-the-job exposure to carcinogens such as asbestos and uranium, exposure to chemical hazards such as radon, polycyclic aromatic hydrocarbons, chromium, nickel, and inorganic arsenic, genetic factors, and diet.

Histological classification of various lung cancers define the types of cancer that begin in the lung. See, e.g., Travis, et al. (1999) Histological Typing of Lung and Pleural Tumours (International Histological Classification of Tumours, No 1. Four major cell types make up more than 88% of all primary lung neoplasms. These are: squamous or epidermoid carcinoma, small cell (also called oat cell) carcinoma, adenocarcinoma, and large cell (also called large cell anaplastic) carcinoma. The remainder include undifferentiated carcinomas, carcinoids, bronchial gland tumors, and other rarer types. The various cell types have different natural histories and responses to therapy, and, thus, a correct histologic diagnosis is the first step of effective treatment.

Small cell lung cancer (SCLC) accounts for 18-25% of all lung cancers, and occurs less frequently than non-small cell lung cancers, and generally spread to distant organs more rapidly than non-small cell lung cancer. In general, at the time of presentation small cell lung cancers have already spread beyond the bounds where surgery and curative intent can be undertaken. However, if identified early enough, these cancers are often responsive to chemotherapy and thoracic radiation treatment.

Non-small cell lung cancers (NSCLC) are the more frequently occurring form of lung cancer. They comprise squamous cell carcinoma, adenocarcinoma, and large cell carcinoma

The screening of asymptomatic persons at high risk for lung cancer has often proven ineffective. In general, only 5 to 15 percent of lung cancer patients have their disease detected while they are asymptomatic. Of course, early detection and treatment are critical factors in the fight against lung cancer. The average survival rate is 49% for those whose cancer is detected early, before the cancer has spread from the lung. Lung cancer often spreads outside of the lung, and it may have spread to the bones or brain by the time it is diagnosed. While the prognosis may be better for lung cancers that are detected early, because of the lack of effective curative treatments, early detection does not necessarily alter the total death rate from lung cancer.

Thus, methods for diagnosis and prognosis of lung cancer and effective treatment of lung cancer would be desirable. Accordingly, provided herein are methods that can be used in diagnosis and prognosis of lung cancer. Further provided are methods that can be used to screen candidate therapeutic agents for the ability to modulate, e.g., treat, lung cancer. Additionally, provided herein are molecular targets and compositions for therapeutic intervention in lung disease and other metastatic cancers.

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bronchiectasis. Other aspects of the invention will become apparent to the skilled artisan by the following description of the invention.

In one aspect, the present invention provides a method of detecting a lung cancer-associated transcript in a cell from a patient, the method comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16. Alternatively, the sample may be contacted with a specific binding reagent, e.g., antibody.

In one embodiment, the polynucleotide selectively hybridizes to a sequence at least 95% identical to a sequence as shown in Tables 1A-16. In another embodiment, the polynucleotide comprises a sequence as shown in Tables 1A-16.

In one embodiment, the biological sample is a tissue sample, or a body fluid. In another embodiment, the biological sample comprises isolated nucleic acids, e.g., mRNA.

In one embodiment, the polynucleotide is labeled, e.g., with a fluorescent label. In one embodiment, the polynucleotide is immobilized on a solid surface. In one embodiment, the patient is undergoing a therapeutic regimen to treat lung cancer. In another embodiment, the patient is suspected of having lung cancer. In one embodiment, the patient is a primate, e.g., a human.

In one embodiment, the method further comprises the step of amplifying nucleic acids before the step of contacting the biological sample with the polynucleotide.

In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of lung cancer, the method comprising the steps of: (i) providing a biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of a lung cancer-associated transcript in the biological sample by contacting the biological sample with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16, thereby monitoring the efficacy of the therapy. Or the sample may be evaluated for protein, e.g., contacting the sample with an antibody.

In one embodiment, the method further comprises the step of: (iii) comparing the level of the lung cancer-associated transcript to a level of the lung cancer-associated transcript in a biological sample from the patient prior to, or earlier in, the therapeutic treatment. Or the sample may be evaluated for comparison of protein.

In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of lung cancer, the method comprising the steps of: (i) providing a

biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of a lung cancer-associated antibody in the biological sample by contacting the biological sample with a polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16, wherein the polypeptide specifically binds to the lung cancer-associated antibody, thereby monitoring the efficacy of the therapy.

In one embodiment, the method further comprises the step of: (iii) comparing the level of the lung cancer-associated antibody to a level of the lung cancer-associated antibody in a biological sample from the patient prior to, or earlier in, the therapeutic treatment.

In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of lung cancer, the method comprising the steps of: (i) providing a biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of a lung cancer-associated polypeptide in the biological sample by contacting the biological sample with an antibody, wherein the antibody specifically binds to a polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16, thereby monitoring the efficacy of the therapy.

In one embodiment, the method further comprises the step of: (iii) comparing the level of the lung cancer-associated polypeptide to a level of the lung cancer-associated polypeptide in a biological sample from the patient prior to, or earlier in, the therapeutic treatment. In one aspect, the present invention provides an isolated nucleic acid molecule consisting of a polynucleotide sequence as shown in Tables 1A-16. In one embodiment, an expression vector or cell comprises the isolated nucleic acid. In one aspect, the present invention provides an isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1A-16.

In another aspect, the present invention provides an antibody that specifically binds to an isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1A-16. In one embodiment, the antibody is conjugated to an effector component, e.g., a fluorescent label, a radioisotope or a cytotoxic chemical. In one embodiment, the antibody is an antibody fragment. In another embodiment, the antibody is humanized.

In one aspect, the present invention provides a method of detecting lung cancer in a patient, the method comprising contacting a biological sample from the patient with an antibody or protein as described herein.

In another aspect, the present invention provides a method of detecting antibodies specific to a lung cancer gene in a patient, the method comprising contacting a biological sample from the patient with a polypeptide encoded by a nucleic acid comprises a sequence from Tables 1A-16.

5 In another aspect, the present invention provides a method for identifying a compound that modulates a lung cancer-associated polypeptide, the method comprising the steps of: (i) contacting the compound with a lung cancer-associated polypeptide, the polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16; and (ii) determining the functional effect of the
10 compound upon the polypeptide.

In one embodiment, the functional effect is a physical effect, an enzymatic effect, or a chemical effect. In one embodiment, the polypeptide is expressed in a eukaryotic host cell or cell membrane. In another embodiment, the polypeptide is recombinant. In one
15 embodiment, the functional effect is determined by measuring ligand binding to the polypeptide.

In another aspect, the present invention provides a method of inhibiting proliferation or another critical process of a lung cancer-associated cell to treat lung cancer in a patient, the method comprising the step of administering to the subject a therapeutically effective amount of a compound identified as described herein. In one embodiment, the compound is an
20 antibody.

In another aspect, the present invention provides a drug screening assay comprising the steps of: (i) administering a test compound to a mammal having lung cancer or a cell isolated therefrom; (ii) comparing the level of gene expression of a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables
25 1A-16 in a treated cell or mammal with the level of gene expression of the polynucleotide in a control cell or mammal, wherein a test compound that modulates the level of expression of the polynucleotide is a candidate for the treatment of lung cancer.

In one embodiment, the control is a mammal with lung cancer or a cell therefrom that has not been treated with the test compound. In another embodiment, the control is a normal
30 cell or mammal, or a non-malignant lung disease.

In another aspect, the present invention provides a method for treating a mammal having lung cancer comprising administering a compound identified by the assay described herein.

In another aspect, the present invention provides a pharmaceutical composition for treating a mammal having lung cancer, the composition comprising a compound identified by the assay described herein and a physiologically acceptable excipient.

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DETAILED DESCRIPTION OF THE INVENTION

In accordance with the objects outlined above, the present invention provides novel methods for diagnosis and treatment of lung disease or cancer, as well as methods for screening for compositions which modulate lung cancer. "Treatment, monitoring, detection or modulation of lung disease or cancer" includes treatment, monitoring, detection, or modulation of lung disease in those patients who have lung disease (whether malignant or non-malignant, e.g., emphysema, bronchitis, or fibrosis) as well as patients with lung cancers in which gene expression from a gene in Tables 1A-16 is increased or decreased, indicating that the subject is more likely to have disease. In particular, while these targets are identified primarily from lung cancer samples, these same targets are likely to be similarly found in analyses of other medical conditions. These other conditions may result from similar pathological processes which affect similar tissues, e.g., lung cancer, small cell lung carcinoma (oat cell carcinoma), non-small cell carcinomas (e.g., squamous cell carcinoma, adenocarcinoma, large cell lung carcinoma, carcinoid, granulomatous), fibrosis (idiopathic pulmonary fibrosis (IPF), hypersensitivity pneumonitis (HP), interstitial pneumonitis, nonspecific idiopathic pneumonitis (NSIP)), chronic obstructive pulmonary disease (COPD, e.g., emphysema, chronic bronchitis), asthma, bronchiectasis, and esophageal cancer. See, e.g., the NCI webpage and USSN 60/347,349 and USSN 60/xxx,xxx (docket LFBF-001-1P, filed March 29, 2002), each of which is incorporated herein by reference. The treatment may be of lung cancer or related condition itself, or treatment of metastasis.

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In particular, identification of markers selectively expressed on these cancers allows for use of that expression in diagnostic, prognostic, or therapeutic methods. As such, the invention defines various compositions, e.g., nucleic acids, polypeptides, antibodies, and small molecule agonists/antagonists, which will be useful to selectively identify those markers. For example, therapeutic methods may take the form of protein therapeutics which use the marker expression for selective localization or modulation of function (for those markers which have a causative disease effect), for vaccines, identification of binding partners, or antagonism, e.g., using antisense or RNAi. The markers may be useful for molecular characterization of subsets of lung diseases, which subsets may actually require

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very different treatments. Moreover, the markers may also be important in related diseases to the specific cancers, e.g., which affect similar tissues in non-malignant diseases, or have similar mechanisms of induction/maintenance. Metastatic processes or characteristics may also be targeted. Diagnostic and prognostic uses are made available, e.g., to subset related but distinct diseases, or to determine treatment strategy. The detection methods may be based upon nucleic acid, e.g., PCR or hybridization techniques, or protein, e.g., ELISA, imaging, IHC, etc. The diagnosis may be qualitative or quantitative, and may detect increases or decreases in expression levels.

Tables 1A-16 provide unigene cluster identification numbers for the nucleotide sequence of genes that exhibit increased or decreased expression in lung cancer samples. The tables also provide an exemplar accession number that provides a nucleotide sequence that is part of the unigene cluster. In Table 1A, genes marked as "target 1" or "target 2" are particularly useful as therapeutic targets. Genes marked as "target 3" are particularly useful as diagnostic markers. Genes marked as "chron" are upregulated in chronically diseased lung (e.g., emphysema, bronchitis, fibrosis) relative to lung tumors and normal tissue. In certain analyses, the ratio for the "chron" category was determined using the 70th percentile of chronically diseased lung samples divided by the 90th percentile of normal lung samples. The ratio for the targets was determined using the 70th percentile of lung tumor samples divided by the 90th percentile of normal lung samples.

Definitions

The term "lung cancer protein" or "lung cancer polynucleotide" or "lung cancer-associated transcript" refers to nucleic acid and polypeptide polymorphic variants, alleles, mutants, and interspecies homologs that: (1) have a nucleotide sequence that has greater than about 60% nucleotide sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% or greater nucleotide sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more nucleotides, to a nucleotide sequence of or associated with a unigene cluster of Tables 1A-16; (2) bind to antibodies, e.g., polyclonal antibodies, raised against an immunogen comprising an amino acid sequence encoded by a nucleotide sequence of or associated with a unigene cluster of Tables 1A-16, and conservatively modified variants thereof; (3) specifically hybridize under stringent hybridization conditions to a nucleic acid sequence, or the complement thereof of Tables 1A-16 and conservatively modified variants thereof; or (4)

have an amino acid sequence that has greater than about 60% amino acid sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% or greater amino sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more amino acid, to an amino acid sequence encoded by a nucleotide sequence of or associated with a unigene cluster of Tables 1A-16. A polynucleotide or polypeptide sequence is typically from a mammal including, but not limited to, primate, e.g., human; rodent, e.g., rat, mouse, hamster; cow, pig, horse, sheep, or other mammal. A "lung cancer polypeptide" and a "lung cancer polynucleotide," include both naturally occurring or recombinant forms.

A "full length" lung cancer protein or nucleic acid refers to a lung cancer polypeptide or polynucleotide sequence, or a variant thereof, that contains the elements normally contained in one or more naturally occurring, wild type lung cancer polynucleotide or polypeptide sequences. The "full length" may be prior to, or after, various stages of post-translational processing or splicing, including alternative splicing.

"Biological sample" as used herein is a sample of biological tissue or fluid that contains nucleic acids or polypeptides, e.g., of a lung cancer protein, polynucleotide, or transcript. Such samples include, but are not limited to, tissue isolated from primates, e.g., humans, or rodents, e.g., mice, and rats. Biological samples may also include sections of tissues such as biopsy and autopsy samples, frozen sections taken for histologic purposes, archival materials, blood, plasma, serum, sputum, stool, tears, mucus, hair, skin, etc.

Biological samples also include explants and primary and/or transformed cell cultures derived from patient tissues. A biological sample is typically obtained from a eukaryotic organism, most preferably a mammal such as a primate, e.g., chimpanzee or human; cow; dog; cat; a rodent, e.g., guinea pig, rat, mouse; rabbit; or other mammal; or a bird; reptile; fish. Livestock and domestic animals are of interest.

"Providing a biological sample" means to obtain a biological sample for use in methods described in this invention. Most often, this will be done by removing a sample of cells from an animal, but can also be accomplished by using previously isolated cells (e.g., isolated by another person, at another time, and/or for another purpose), or by performing the methods of the invention in vivo. Archival tissues or materials, having treatment or outcome history, will be particularly useful.

The terms "identical" or percent "identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the

same or have a specified percentage of amino acid residues or nucleotides that are the same (e.g., about 60% identity, preferably 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or higher identity over a specified region, when compared and aligned for maximum correspondence over a comparison window or designated region) as measured using, e.g., a BLAST or BLAST 2.0 sequence comparison algorithms with default parameters described below, or by manual alignment and visual inspection (see, e.g., NCBI web site <http://www.ncbi.nlm.nih.gov/BLAST/> or the like). Such sequences are then said to be “substantially identical.” This definition also refers to, or may be applied to, the complement of a test sequence. The definition also includes sequences that have deletions and/or insertions, substitutions, and naturally occurring, e.g., polymorphic or allelic variants, and man-made variants. As described below, the preferred algorithms can account for gaps and the like. Preferably, identity exists over a region that is at least about 25 amino acids or nucleotides in length, or more preferably over a region that is 50-100 amino acids or nucleotides in length.

For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Preferably, default program parameters can be used, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

A “comparison window”, as used herein, includes reference to a segment of contiguous positions selected from the group consisting typically of from 20 to 600, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well-known in the art. Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith and Waterman (1981) Adv. Appl. Math. 2:482, by the homology alignment algorithm of Needleman and Wunsch (1970) J. Mol. Biol. 48:443, by the search for similarity method of Pearson and Lipman (1988) Proc. Nat’l. Acad. Sci. USA 85:2444, by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer

Preferred examples of algorithms that are suitable for determining percent sequence identity and sequence similarity include the BLAST and BLAST 2.0 algorithms, which are described in Altschul, et al. (1977) Nuc. Acids Res. 25:3389-3402 and Altschul, et al. (1990) J. Mol. Biol. 215:403-410. BLAST and BLAST 2.0 are used, with the parameters described herein, to determine percent sequence identity for the nucleic acids and proteins of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul, et al., *supra*). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, e.g., for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff and Henikoff (1989) Proc. Natl. Acad. Sci. USA 89:10915) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

The BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, e.g., Karlin and Altschul (1993) Proc. Nat'l. Acad. Sci. USA 90:5873-5787). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between

two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, more preferably less than about 0.01, and most preferably less than about 0.001. Log values may be negative large numbers, e.g., 5, 10, 20, 30, 40, 40, 70, 90, 110, 150, 170, etc.

An indication that two nucleic acid sequences are substantially identical is that the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the antibodies raised against the polypeptide encoded by the second nucleic acid. Thus, a polypeptide is typically substantially identical to a second polypeptide, e.g., where the two peptides differ only by conservative substitutions. Another indication that two nucleic acid sequences are substantially identical is that the two molecules or their complements hybridize to each other under stringent conditions. Yet another indication that two nucleic acid sequences are substantially identical is that the same primers can be used to amplify the sequences.

A "host cell" is a naturally occurring cell or a transformed cell that contains an expression vector and supports the replication or expression of the expression vector. Host cells may be cultured cells, explants, cells *in vivo*, and the like. Host cells may be prokaryotic cells such as *E. coli*, or eukaryotic cells such as yeast, insect, amphibian, or mammalian cells such as CHO, HeLa, and the like (see, e.g., the American Type Culture Collection catalog or web site, www.atcc.org).

The terms "isolated," "purified," or "biologically pure" refer to material that is substantially or essentially free from components that normally accompany it as found in its native state. Purity and homogeneity are typically determined using analytical chemistry techniques such as polyacrylamide gel electrophoresis or high performance liquid chromatography. A protein or nucleic acid that is the predominant species present in a preparation is substantially purified. In particular, an isolated nucleic acid is separated from some open reading frames that naturally flank the gene and encode proteins other than protein encoded by the gene. The term "purified" in some embodiments denotes that a nucleic acid or protein gives rise to essentially one band in an electrophoretic gel. Preferably, it means that the nucleic acid or protein is at least about 85% pure, more preferably at least 95% pure, and most preferably at least 99% pure. "Purify" or "purification" in other embodiments means removing at least one contaminant or component from the composition to be purified.

In this sense, purification does not require that the purified compound be homogeneous, e.g., 100% pure.

The terms "polypeptide," "peptide" and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in which one or more amino acid residue is an artificial chemical mimetic of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers, those containing modified residues, and non-naturally occurring amino acid polymer.

The term "amino acid" refers to naturally occurring and synthetic amino acids, as well as amino acid analogs and amino acid mimetics that function similarly to the naturally occurring amino acids. Naturally occurring amino acids are those encoded by the genetic code, as well as those amino acids that are later modified, e.g., hydroxyproline, γ -carboxyglutamate, and O-phosphoserine. Amino acid analogs refer to compounds that have the same basic chemical structure as a naturally occurring amino acid, e.g., an α carbon that is bound to a hydrogen, a carboxyl group, an amino group, and an R group, e.g., homoserine, norleucine, methionine sulfoxide, methionine methyl sulfonium. Such analogs may have modified R groups (e.g., norleucine) or modified peptide backbones, but retain some basic chemical structure as a naturally occurring amino acid. Amino acid mimetics refer to chemical compounds that have a structure that is different from the general chemical structure of an amino acid, but that function similarly to another amino acid.

Amino acids may be referred to herein by either their commonly known three letter symbols or by the one-letter symbols recommended by the IUPAC-IUB Biochemical Nomenclature Commission. Nucleotides, likewise, may be referred to by their commonly accepted single-letter codes.

"Conservatively modified variants" applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences, conservatively modified variants refers to those nucleic acids which encode identical or essentially identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical or associated, e.g., naturally contiguous, sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode most proteins. For instance, the codons GCA, GCC, GCG, and GCU each encode the amino acid alanine. Thus, at each position where an alanine is specified by a codon, the codon can be altered to another of the corresponding codons described without altering the encoded polypeptide. Such nucleic acid variations are "silent variations," which are one species of

conservatively modified variations. Every nucleic acid sequence herein which encodes a polypeptide also describes silent variations of the nucleic acid. In certain contexts each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and TGG, which is ordinarily the only codon for tryptophan) can be modified to yield a functionally similar molecule. Accordingly, a silent variation of a nucleic acid which encodes a polypeptide is implicit in a described sequence with respect to the expression product, but not necessarily with respect to actual probe sequences.

As to amino acid sequences, one of skill will recognize that individual substitutions, deletions or additions to a nucleic acid, peptide, polypeptide, or protein sequence which alters, adds or deletes a single amino acid or a small percentage of amino acids in the encoded sequence is a "conservatively modified variant" where the alteration results in the substitution of an amino acid with a chemically similar amino acid. Conservative substitution tables providing functionally similar amino acids are well known in the art. Such conservatively modified variants are in addition to and do not exclude polymorphic variants, interspecies homologs, and alleles of the invention. Typically conservative substitutions include for one another: 1) Alanine (A), Glycine (G); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (K); 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); 7) Serine (S), Threonine (T); and 8) Cysteine (C), Methionine (M) (see, e.g., Creighton, Proteins (1984)).

Macromolecular structures such as polypeptide structures can be described in terms of various levels of organization. For a general discussion of this organization, see, e.g., Alberts, et al. (1994) Molecular Biology of the Cell (3rd ed.) and Cantor and Schimmel (1980) Biophysical Chemistry Part I: The Conformation of Biological Macromolecules. "Primary structure" refers to the amino acid sequence of a particular peptide. "Secondary structure" refers to locally ordered, three dimensional structures within a polypeptide. These structures are commonly known as domains. Domains are portions of a polypeptide that often form a compact unit of the polypeptide and are typically 25 to approximately 500 amino acids long. Typical domains are made up of sections of lesser organization such as stretches of β -sheet and α -helices. "Tertiary structure" refers to the complete three dimensional structure of a polypeptide monomer. "Quaternary structure" refers to the three dimensional structure formed, usually by the noncovalent association of independent tertiary units. Anisotropic terms are also known as energy terms.

"Nucleic acid" or "oligonucleotide" or "polynucleotide" or grammatical equivalents

used herein means at least two nucleotides covalently linked together. Oligonucleotides are typically from about 5, 6, 7, 8, 9, 10, 12, 15, 25, 30, 40, 50 or more nucleotides in length, up to about 100 nucleotides in length. Nucleic acids and polynucleotides are a polymers of any length, including longer lengths, e.g., 200, 300, 500, 1000, 2000, 3000, 5000, 7000, 10,000, etc. A nucleic acid of the present invention will generally contain phosphodiester bonds, although in some cases, nucleic acid analogs are included that may have at least one different linkage, e.g., phosphoramidate, phosphorothioate, phosphorodithioate, or O-methylphosphoroamidite linkages (see Eckstein (1992) Oligonucleotides and Analogues: A Practical Approach Oxford University Press); and peptide nucleic acid backbones and linkages. Other analog nucleic acids include those with positive backbones; non-ionic backbones, and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7, in Sanghui and Cook, eds. Carbohydrate Modifications in Antisense Research, ASC Symposium Series 580. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids. Modifications of the ribose-phosphate backbone may be done for a variety of reasons, e.g., to increase the stability and half-life of such molecules in physiological environments or as probes on a biochip. Mixtures of naturally occurring nucleic acids and analogs can be made; alternatively, mixtures of different nucleic acid analogs, and mixtures of naturally occurring nucleic acids and analogs may be made.

Particularly preferred are peptide nucleic acids (PNA) which includes peptide nucleic acid analogs. These backbones are substantially non-ionic under neutral conditions, in contrast to the highly charged phosphodiester backbone of naturally occurring nucleic acids. This results in two advantages. First, the PNA backbone exhibits improved hybridization kinetics. PNAs have larger changes in the melting temperature (T_m) for mismatched versus perfectly matched basepairs. DNA and RNA typically exhibit a 2-4° C drop in T_m for an internal mismatch. With the non-ionic PNA backbone, the drop is closer to 7-9° C. Similarly, due to their non-ionic nature, hybridization of the bases attached to these backbones is relatively insensitive to salt concentration. In addition, PNAs are not degraded by cellular enzymes, and thus can be more stable.

The nucleic acids may be single stranded or double stranded, as specified, or contain portions of both double stranded or single stranded sequence. As will be appreciated by those in the art, the depiction of a single strand also defines the sequence of the complementary

strand; thus the sequences described herein also provide the complement of the sequence.

The nucleic acid may be DNA, both genomic and cDNA, RNA, or a hybrid, where the nucleic acid may contain combinations of deoxyribo- and ribo-nucleotides, and combinations of bases, including uracil, adenine, thymine, cytosine, guanine, inosine, xanthine

5 hypoxanthine, isocytosine, isoguanine, etc. "Transcript" typically refers to a naturally occurring RNA, e.g., a pre-mRNA, hnRNA, or mRNA. As used herein, the term "nucleoside" includes nucleotides and nucleoside and nucleotide analogs, and modified nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occurring analog structures. Thus, e.g., the individual units of a peptide nucleic
10 acid, each containing a base, are referred to herein as a nucleoside.

A "label" or a "detectable moiety" is a composition detectable by spectroscopic, photochemical, biochemical, immunochemical, physiological, chemical, or other physical means. For example, useful labels include ^{32}P , fluorescent dyes, electron-dense reagents, enzymes (e.g., as commonly used in an ELISA), biotin, digoxigenin, or haptens and proteins
15 or other entities which can be made detectable, e.g., by incorporating a radiolabel into the peptide or used to detect antibodies specifically reactive with the peptide. The labels may be incorporated into the cancer nucleic acids, proteins, and antibodies. Many methods known in the art for conjugating the antibody to the label may be employed, including those methods described by Hunter, et al. (1962) Nature 144:945; David, et al. (1974) Biochemistry
20 13:1014-1021; Pain, et al. (1981) J. Immunol. Meth., 40:219-230; and Nygren (1982) J. Histochem. and Cytochem. 30:407-412.

An "effector" or "effector moiety" or "effector component" is a molecule that is bound (or linked, or conjugated), either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds, to an antibody.
25 The "effector" can be a variety of molecules including, e.g., detection moieties including radioactive compounds, fluorescent compounds, an enzyme or substrate, tags such as epitope tags, a toxin; activatable moieties, a chemotherapeutic agent; a lipase; an antibiotic; or a radioisotope emitting "hard" e.g., beta radiation.

A "labeled nucleic acid probe or oligonucleotide" is one that is bound, either
30 covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds to a label such that the presence of the probe may be detected by detecting the presence of the label bound to the probe. Alternatively, method

using high affinity interactions may achieve the same results where one of a pair of binding partners binds to the other, e.g., biotin, streptavidin.

As used herein a "nucleic acid probe or oligonucleotide" is a nucleic acid capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, e.g., through hydrogen bond formation. As used herein, a probe may include natural (i.e., A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in a probe may be joined by a linkage other than a phosphodiester bond, preferably one that does not functionally interfere with hybridization. Thus, e.g., probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages. Probes may bind target sequences lacking complete complementarity with the probe sequence depending upon the stringency of the hybridization conditions. The probes are preferably directly labeled, e.g., with isotopes, chromophores, lumiphores, chromogens, or indirectly labeled, e.g., with biotin to which a streptavidin complex may later bind. By assaying for the presence or absence of the probe, one can detect the presence or absence of the select sequence or subsequence. Diagnosis or prognosis may be based at the genomic level, or at the level of RNA or protein expression.

The term "recombinant" when used with reference, e.g., to a cell, or nucleic acid, protein, or vector, indicates that the cell, nucleic acid, protein or vector, has been modified by the introduction of a heterologous nucleic acid or protein or the alteration of a native nucleic acid or protein, or that the cell is derived from a cell so modified. Thus, e.g., recombinant cells express genes that are not found within the native (non-recombinant) form of the cell or express native genes that are otherwise abnormally expressed, under expressed or not expressed at all. By the term "recombinant nucleic acid" herein is meant nucleic acid, originally formed *in vitro*, in general, by the manipulation of nucleic acid, e.g., using polymerases and endonucleases, in a form not normally found in nature. In this manner, operably linkage of different sequences is achieved. Thus an isolated nucleic acid, in a linear form, or an expression vector formed *in vitro* by ligating DNA molecules that are not normally joined, are both considered recombinant for the purposes of this invention. It is understood that once a recombinant nucleic acid is made and reintroduced into a host cell or organism, it will replicate non-recombinantly, i.e., using the *in vivo* cellular machinery of the host cell rather than *in vitro* manipulations; however, such nucleic acids, once produced recombinantly, although subsequently replicated non-recombinantly, are still considered

recombinant for the purposes of the invention. Similarly, a “recombinant protein” is a protein made using recombinant techniques, i.e., through the expression of a recombinant nucleic acid as depicted above.

5 The term “heterologous” when used with reference to portions of a nucleic acid indicates that the nucleic acid comprises two or more subsequences that are not normally found in the same relationship to each other in nature. For instance, the nucleic acid is typically recombinantly produced, having two or more sequences, e.g., from unrelated genes arranged to make a new functional nucleic acid, e.g., a promoter from one source and a coding region from another source. Similarly, a heterologous protein will often refer to two
10 or more subsequences that are not found in the same relationship to each other in nature (e.g., a fusion protein).

A “promoter” is typically an array of nucleic acid control sequences that direct transcription of a nucleic acid. As used herein, a promoter includes necessary nucleic acid sequences near the start site of transcription, such as, in the case of a polymerase II type
15 promoter, a TATA element. A promoter also optionally includes distal enhancer or repressor elements, which can be located as much as several thousand base pairs from the start site of transcription. A “constitutive” promoter is a promoter that is active under most environmental and developmental conditions. An “inducible” promoter is a promoter that is active under environmental or developmental regulation. The term “operably linked” refers
20 to a functional linkage between a nucleic acid expression control sequence (such as a promoter, or array of transcription factor binding sites) and a second nucleic acid sequence, e.g., wherein the expression control sequence directs transcription of the nucleic acid corresponding to the second sequence.

An “expression vector” is a nucleic acid construct, generated recombinantly or
25 synthetically, with a series of specified nucleic acid elements that permit transcription of a particular nucleic acid in a host cell. The expression vector can be part of a plasmid, virus, or nucleic acid fragment. Typically, the expression vector includes a nucleic acid to be transcribed in operable linkage to a promoter.

The phrase “selectively (or specifically) hybridizes to” refers to the binding,
30 duplexing, or hybridizing of a molecule selectively to a particular nucleotide sequence under stringent hybridization conditions when that sequence is present in a complex mixture (e.g., total cellular or library DNA or RNA).

The phrase "stringent hybridization conditions" refers to conditions under which a probe will hybridize to its target subsequence, typically in a complex mixture of nucleic acids, but to essentially no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in "Overview of principles of hybridization and the strategy of nucleic acid assays" in Tijssen (1993) Techniques in Biochemistry and Molecular Biology--Hybridization with Nucleic Probes (vol. 24) Elsevier. Generally, stringent conditions are selected to be about 5-10° C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength pH. The T_m is the temperature (under defined ionic strength, pH, and nucleic concentration) at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at T_m , 50% of the probes are occupied at equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30° C for short probes (e.g., 10 to 50 nucleotides) and at least about 60° C for long probes (e.g., greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. For selective or specific hybridization, a positive signal is typically at least two times background, preferably 10 times background hybridization. Exemplary stringent hybridization conditions are often: 50% formamide, 5x SSC, and 1% SDS, incubating at 42° C, or, 5x SSC, 1% SDS, incubating at 65° C, with wash in 0.2x SSC, and 0.1% SDS at 65° C. For PCR, a temperature of about 36° C is typical for low stringency amplification, although annealing temperatures may vary between about 32° C and 48° C depending on primer length. For high stringency PCR amplification, a temperature of about 62° C is typical, although high stringency annealing temperatures can range from about 50° C to about 65° C, depending on the primer length and specificity. Typical cycle conditions for both high and low stringency amplifications include a denaturation phase of 90° C - 95° C for 0.5 - 2 min., an annealing phase lasting 0.5 - 2 min., and an extension phase of about 72° C for 1 - 2 min. Protocols and guidelines for low and high stringency amplification reactions are provided, e.g., in Innis, et al.(1990) PCR Protocols, A Guide to Methods and Applications.

Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides which they encode are substantially identical. This

occurs, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. In such cases, the nucleic acids typically hybridize under moderately stringent hybridization conditions. Exemplary “moderately stringent hybridization conditions” include a hybridization in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37° C, and a wash in 1X SSC at 45° C. A positive hybridization is at least twice background. Alternative hybridization and wash conditions can be utilized to provide conditions of similar stringency. Additional guidelines for determining hybridization parameters are provided in numerous reference, e.g., Ausubel, et al. (ed.) Current Protocols in Molecular Biology Lippincott.

The phrase “functional effects” in the context of assays for testing compounds that modulate activity of a lung cancer protein includes the determination of a parameter that is indirectly or directly under the influence of the lung cancer protein or nucleic acid, e.g., a physiological, enzymatic, functional, physical, or chemical effect, such as the ability to decrease lung cancer. It includes ligand binding activity; cell viability, cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis *in vivo*; mRNA and protein expression in cells undergoing metastasis, and other characteristics of lung cancer cells. “Functional effects” include *in vitro*, *in vivo*, and *ex vivo* activities.

By “determining the functional effect” is meant assaying for a compound that increases or decreases a parameter that is indirectly or directly under the influence of a lung cancer protein sequence, e.g., physiological, functional, enzymatic, physical, or chemical effects. Such functional effects can be measured by many means known to those skilled in the art, e.g., changes in spectroscopic characteristics (e.g., fluorescence, absorbance, refractive index), hydrodynamic (e.g., shape), chromatographic, or solubility properties for the protein, measuring inducible markers or transcriptional activation of the lung cancer protein; measuring binding activity or binding assays, e.g., binding to antibodies or other ligands, and measuring cellular proliferation. Determination of the functional effect of a compound on lung cancer can also be performed using lung cancer assays known to those of skill in the art such as an *in vitro* assays, e.g., cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis *in vivo*; mRNA and protein

expression in cells undergoing metastasis, and other characteristics of lung cancer cells. The functional effects can be evaluated by many means known to those skilled in the art, e.g., microscopy for quantitative or qualitative measures of alterations in morphological features, measurement of changes in RNA or protein levels for lung cancer-associated sequences, measurement of RNA stability, identification of downstream or reporter gene expression (CAT, luciferase, β -gal, GFP, and the like), e.g., via chemiluminescence, fluorescence, colorimetric reactions, antibody binding, inducible markers, and ligand binding assays.

"Inhibitors", "activators", and "modulators" of lung cancer polynucleotide and polypeptide sequences are used to refer to activating, inhibitory, or modulating molecules or compounds identified using *in vitro* and *in vivo* assays of lung cancer polynucleotide and polypeptide sequences. Inhibitors are compounds that, e.g., bind to, partially or totally block activity, decrease, prevent, delay activation, inactivate, desensitize, or down regulate the activity or expression of lung cancer proteins, e.g., antagonists. Antisense or inhibitory nucleic acids may seem to inhibit expression and subsequent function of the protein.

"Activators" are compounds that increase, open, activate, facilitate, enhance activation, sensitize, agonize, or up regulate lung cancer protein activity. Inhibitors, activators, or modulators also include genetically modified versions of lung cancer proteins, e.g., versions with altered activity, as well as naturally occurring and synthetic ligands, antagonists, agonists, antibodies, small chemical molecules and the like. Such assays for inhibitors and activators include, e.g., expressing the lung cancer protein *in vitro*, in cells, or cell membranes, applying putative modulator compounds, and then determining the functional effects on activity, as described above. Activators and inhibitors of lung cancer can also be identified by incubating lung cancer cells with the test compound and determining increases or decreases in the expression of 1 or more lung cancer proteins, e.g., 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 40, 50 or more lung cancer proteins, such as lung cancer proteins encoded by the sequences set out in Tables 1A-16.

Samples or assays comprising lung cancer proteins that are treated with a potential activator, inhibitor, or modulator are compared to control samples without the inhibitor, activator, or modulator to examine the extent of inhibition. Control samples (untreated with inhibitors) are assigned a relative protein activity value of 100%. Inhibition of a polypeptide is achieved when the activity value relative to the control is about 80%, preferably 50%, more preferably 25-0%. Activation of a lung cancer polypeptide is achieved when the activity value relative to the control (untreated with activators) is 110%, more preferably 150%, more

preferably 200-500% (i.e., two to five fold higher relative to the control), more preferably 1000-3000% higher.

The phrase "changes in cell growth" refers to any change in cell growth and proliferation characteristics *in vitro* or *in vivo*, such as cell viability, formation of foci, anchorage independence, semi-solid or soft agar growth, changes in contact inhibition and density limitation of growth, loss of growth factor or serum requirements, changes in cell morphology, gaining or losing immortalization, gaining or losing tumor specific markers, ability to form or suppress tumors when injected into suitable animal hosts, and/or immortalization of the cell. See, e.g., Freshney (1994) Culture of Animal Cells a Manual of Basic Technique pp. 231-241 (3rd ed.).

"Tumor cell" refers to precancerous, cancerous, and normal cells in a tumor.

"Cancer cells," "transformed" cells, or "transformation" in tissue culture, refers to spontaneous or induced phenotypic changes that do not necessarily involve the uptake of new genetic material. Although transformation can arise from infection with a transforming virus and incorporation of new genomic DNA, or uptake of exogenous DNA, it can also arise spontaneously or following exposure to a carcinogen, thereby mutating an endogenous gene. Transformation is associated with phenotypic changes, such as immortalization of cells, aberrant growth control, nonmorphological changes, and/or malignancy (see, Freshney (1994) Culture of Animal Cells a Manual of Basic Technique (3rd ed.)).

"Antibody" refers to a polypeptide comprising a framework region from an immunoglobulin gene or fragments thereof that specifically binds and recognizes an antigen. The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon, and mu constant region genes, as well as the myriad immunoglobulin variable region genes. Light chains are classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD, and IgE, respectively. Typically, the antigen-binding region of an antibody or its functional equivalent will be most critical in specificity and affinity of binding. See Paul, Fundamental Immunology.

An exemplary immunoglobulin (antibody) structural unit comprises a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one "light" (about 25 kD) and one "heavy" chain (about 50-70 kD). The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible

for antigen recognition. The terms variable light chain (V_L) and variable heavy chain (V_H) refer to these light and heavy chains respectively.

Antibodies exist, e.g., as intact immunoglobulins or as a number of well-characterized fragments produced by digestion with various peptidases. Thus, e.g., pepsin digests an antibody below the disulfide linkages in the hinge region to produce $F(ab)'_2$, a dimer of Fab which itself is a light chain joined to V_H - C_H1 by a disulfide bond. The $F(ab)'_2$ may be reduced under mild conditions to break the disulfide linkage in the hinge region, thereby converting the $F(ab)'_2$ dimer into an Fab' monomer. The Fab' monomer is essentially Fab with part of the hinge region (see Paul (ed. 1999) Fundamental Immunology (4th ed.). While various antibody fragments are defined in terms of the digestion of an intact antibody, one of skill will appreciate that such fragments may be synthesized *de novo* either chemically or by using recombinant DNA methodology. Thus, the term antibody, as used herein, also includes antibody fragments either produced by the modification of whole antibodies, or those synthesized *de novo* using recombinant DNA methodologies (e.g., single chain Fv) or those identified using phage display libraries (see, e.g., McCafferty, et al. (1990) Nature 348:552-554).

For preparation of antibodies, e.g., recombinant, monoclonal, or polyclonal antibodies, many technique known in the art can be used (see, e.g., Kohler and Milstein (1975) Nature 256:495-497; Kozbor, et al. (1983) Immunology Today 4:72; Cole, et al. (1985), pp. 77-96 in Monoclonal Antibodies and Cancer Therapy; Coligan (1991 and supplements) Current Protocols in Immunology; Harlow and Lane (1988) Antibodies, A Laboratory Manual; and Goding (1986) Monoclonal Antibodies: Principles and Practice (2d ed.)). Techniques for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce antibodies to polypeptides of this invention. Also, transgenic mice, or other organisms such as other mammals, may be used to express humanized antibodies. Alternatively, phage display technology can be used to identify antibodies and heteromeric Fab fragments that specifically bind to selected antigens (see, e.g., McCafferty, et al. (1990) Nature 348:552-554; Marks, et al. (1992) Biotechnology 10:779-783).

A "chimeric antibody" is an antibody molecule in which, e.g, (a) the constant region, or a portion thereof, is altered, replaced, or exchanged so that the antigen binding site (variable region) is linked to a constant region of a different or altered class, effector function, and/or species, or an entirely different molecule which confers new properties to the chimeric antibody, e.g., an enzyme, toxin, hormone, growth factor, drug, etc.; or (b) the

variable region, or a portion thereof, is altered, replaced, or exchanged with a variable region having a different or altered antigen specificity.

Identification of lung cancer-associated sequences

5 In one aspect, the expression levels of genes are determined in different patient samples for which diagnosis information is desired, to provide expression profiles. An expression profile of a particular sample is essentially a “fingerprint” of the state of the sample; while two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is
10 characteristic of the state of the cell. That is, normal tissue may be distinguished from cancerous or metastatic cancerous tissue, or metastatic cancerous tissue can be compared with tissue from surviving cancer patients. By comparing expression profiles of tissue in known different lung cancer states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained.
15 Molecular profiling may distinguish subtypes of a currently collective disease designation, e.g., different forms of lung cancer (chronic disease, adenocarcinoma, etc.)

 The identification of sequences that are differentially expressed in lung cancer versus non-lung cancer tissue allows the use of this information in a number of ways. For example, a particular treatment regime may be evaluated: does a chemotherapeutic drug act to down-
20 regulate lung cancer, and thus tumor growth or recurrence, in a particular patient. Alternatively, a treatment step may induce other markers which may be used as targets to destroy tumor cells. Similarly, diagnosis and treatment outcomes may be done or confirmed by comparing patient samples with the known expression profiles. Malignant disease may be compared to non-malignant conditions. Metastatic tissue can also be analyzed to determine
25 the stage of lung cancer in the tissue, or origin of primary tumor, e.g., metastasis from a remote primary site. Furthermore, these gene expression profiles (or individual genes) allow screening of drug candidates with an eye to mimicking or altering a particular expression profile; e.g., screening can be done for drugs that suppress the lung cancer expression profile. This may be done by making biochips comprising sets of the important lung cancer genes,
30 which can then be used in these screens. PCR methods may be applied with selected primer pairs, and analysis may be of RNA or of genomic sequences. These methods can also be done on the protein basis; that is, protein expression levels of the lung cancer proteins can be evaluated for diagnostic purposes or to screen candidate agents. In addition, the lung cancer

nucleic acid sequences can be administered for gene therapy purposes, including the administration of antisense nucleic acids, or the lung cancer proteins (including antibodies and other modulators thereof) administered as therapeutic drugs or as protein or DNA vaccines.

5 Thus the present invention provides nucleic acid and protein sequences that are differentially expressed in lung cancer relative to normal tissues and/or non-malignant lung disease, or in different types of lung disease, herein termed "lung cancer sequences." As outlined below, lung cancer sequences include those that are up-regulated (i.e., expressed at a higher level) in lung cancer, as well as those that are down-regulated (i.e., expressed at a lower level). In a preferred embodiment, the lung cancer sequences are from humans;
10 however, as will be appreciated by those in the art, lung cancer sequences from other organisms may be useful in animal models of disease and drug evaluation; thus, other lung cancer sequences are provided, from vertebrates, including mammals, including rodents (rats, mice, hamsters, guinea pigs, etc.), primates, farm animals (including sheep, goats, pigs, cows, horses, etc.) and pets (dogs, cats, etc.). Lung cancer sequences from other organisms may be
15 obtained using the techniques outlined below.

 Lung cancer sequences can include both nucleic acid and amino acid sequences. As will be appreciated by those in the art and is more fully outlined below, lung cancer nucleic acid sequences are useful in a variety of applications, including diagnostic applications,
20 which will detect naturally occurring nucleic acids, as well as screening applications; e.g., biochips comprising nucleic acid probes or PCR microtiter plates with selected probes to the lung cancer sequences can be generated.

 A lung cancer sequence can be initially identified by substantial nucleic acid and/or amino acid sequence homology to the lung cancer sequences outlined herein. Such
25 homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, e.g., using homology programs or hybridization conditions.

 For identifying lung cancer-associated sequences, the lung cancer screen typically includes comparing genes identified in different tissues, e.g., normal and cancerous tissues, cancer and non-malignant conditions, non-malignant conditions and normal tissues, or tumor
30 tissue samples from patients who have metastatic disease vs. non metastatic tissue. Other suitable tissue comparisons include comparing lung cancer samples with metastatic cancer samples from other cancers, such as, breast, other gastrointestinal cancers, prostate, ovarian,

etc. Samples of, non metastatic disease tissue and tissue undergoing metastasis are applied to biochips comprising nucleic acid probes. The samples are first microdissected, if applicable, and treated as is known in the art for the preparation of mRNA. Suitable biochips are commercially available, e.g., from Affymetrix, Santa Clara, CA. Gene expression profiles as described herein are generated and the data analyzed.

In one embodiment, the genes showing changes in expression as between normal and disease states are compared to genes expressed in other normal tissues, preferably normal lung, but also including, and not limited to colon, heart, brain, liver, breast, kidney, muscle, prostate, small intestine, large intestine, spleen, bone, and/or placenta. In a preferred embodiment, those genes identified during the lung cancer screen that are expressed in significant amounts in other tissues (e.g., essential organs) are removed from the profile, although in some embodiments, this is not necessary (e.g., where organs may be dispensable at a later stage of life). That is, when screening for drugs, it is usually preferable that the target expression be disease specific, to minimize possible side effects on other organs.

In a preferred embodiment, lung cancer sequences are those that are up-regulated in lung cancer; that is, the expression of these genes is higher in cancerous tissue than in normal lung or other tissue. "Up-regulation" as used herein means, when the ratio is presented as a number greater than one, that the ratio is greater than one, preferably 1.5 or greater, more preferably 2.0 or greater. Another embodiment is directed to sequences up-regulated in non-malignant conditions relative to normal. Unigene cluster identification numbers and accession numbers herein are for the GenBank sequence database and the sequences of the accession numbers are hereby expressly incorporated by reference. GenBank is known in the art, see, e.g., Benson, DA, et al (1998) *Nucleic Acids Research* 26:1-7 and <http://www.ncbi.nlm.nih.gov/>. Sequences are also available in other databases, e.g., European Molecular Biology Laboratory (EMBL) and DNA Database of Japan (DDBJ). Another embodiment is directed to sequences up-regulated in non-malignant conditions relative to normal. In some situations, the sequences may be derived from assembly of available sequences or be predicted from genomic DNA using exon prediction algorithms, such as FGENESH (Salamov and Solovyev (2000) *Genome Res.* 10:516-522). In other situations, sequences have been derived from cloning and sequencing of isolated nucleic acids.

In another preferred embodiment, lung cancer sequences are those that are down-regulated in the lung cancer; that is, the expression of these genes is lower in cancerous tissue

or normal lung or other tissue. "Down-regulation" as used herein means, when the ratio is presented as a number greater than one, that the ratio is greater than one, preferably 1.5 or greater, more preferably 2.0 or greater, or, when the ratio is presented as a number less than one, that the ratio is less than one, preferably 0.5 or less, more preferably 0.25 or less.

5

Informatics

The ability to identify genes that are over or under expressed in lung cancer can additionally provide high-resolution, high-sensitivity datasets which can be used in the areas of diagnostics, therapeutics, drug development, pharmacogenetics, protein structure,
10 biosensor development, and other related areas. For example, the expression profiles can be used in diagnostic or prognostic evaluation of patients with lung cancer. Or as another example, subcellular toxicological information can be generated to better direct drug structure and activity correlation (see Anderson (1998) Pharmaceutical Proteomics: Targets, Mechanism, and Function, paper presented at the IBC Proteomics conference, Coronado, CA
15 (June 11-12, 1998)). Subcellular toxicological information can also be utilized in a biological sensor device to predict the likely toxicological effect of chemical exposures and likely tolerable exposure thresholds (see U.S. Patent No. 5,811,231). Similar advantages accrue from datasets relevant to other biomolecules and bioactive agents (e.g., nucleic acids, saccharides, lipids, drugs, and the like).

20 Thus, in another embodiment, the present invention provides a database that includes at least one set of assay data. The data contained in the database is acquired, e.g., using array analysis either singly or in a library format. The database can be in a form in which data can be maintained and transmitted, but is preferably an electronic database. The electronic database of the invention can be maintained on any electronic device allowing for the storage
25 of and access to the database, such as a personal computer, but is preferably distributed on a wide area network, such as the World Wide Web.

The focus of the present section on databases that include peptide sequence data is for clarity of illustration only. It will be apparent to those of skill in the art that similar databases can be assembled for assay data acquired using an assay of the invention.

30 The compositions and methods for identifying and/or quantitating the relative and/or absolute abundance of a variety of molecular and macromolecular species from a biological sample representing lung cancer, i.e., the identification of lung cancer-associated sequences described herein, provide an abundance of information, which can be correlated with

pathological conditions, predisposition to disease, drug testing, therapeutic monitoring, gene-disease causal linkages, identification of correlates of immunity and physiological status, among others. Although the data generated from the assays of the invention is suited for manual review and analysis, in a preferred embodiment, data processing using high-speed computers is utilized.

An array of methods for indexing and retrieving biomolecular information is known in the art. For example, U.S. Patents 6,023,659 and 5,966,712 disclose a relational database system for storing biomolecular sequence information in a manner that allows sequences to be catalogued and searched according to one or more protein function hierarchies. U.S.

Patent 5,953,727 discloses a relational database having sequence records containing information in a format that allows a collection of partial-length DNA sequences to be catalogued and searched according to association with one or more sequencing projects for obtaining full-length sequences from the collection of partial length sequences. U.S. Patent 5,706,498 discloses a gene database retrieval system for making a retrieval of a gene sequence similar to a sequence data item in a gene database based on the degree of similarity between a key sequence and a target sequence. U.S. Patent 5,538,897 discloses a method using mass spectroscopy fragmentation patterns of peptides to identify amino acid sequences in computer databases by comparison of predicted mass spectra with experimentally-derived mass spectra using a closeness-of-fit measure. U.S. Patent 5,926,818 discloses a multi-dimensional database comprising a functionality for multi-dimensional data analysis described as on-line analytical processing (OLAP), which entails the consolidation of projected and actual data according to more than one consolidation path or dimension. U.S. Patent 5,295,261 reports a hybrid database structure in which the fields of each database record are divided into two classes, navigational and informational data, with navigational fields stored in a hierarchical topological map which can be viewed as a tree structure or as the merger of two or more such tree structures.

See also Mount, et al. (2001) Bioinformatics; Durbin, et al. (eds., 1999) Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids (; Baxevanis and Ouellette (eds., 1998) Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins); Rashidi and Buehler (1999) Bioinformatics: Basic Applications in Biological Science and Medicine; Setubal, et al. (eds 1997) Introduction to Computational Molecular Biology; Misener and Krawetz (eds, 2000) Bioinformatics: Methods and Protocols; Higgins and Taylor (eds., 2000) Bioinformatics: Sequence, Structure, and Databanks: A Practical

Approach; Brown (2001) Bioinformatics: A Biologist's Guide to Biocomputing and the Internet; Han and Kamber (2000) Data Mining: Concepts and Techniques (2000); and Waterman (1995) Introduction to Computational Biology: Maps, Sequences, and Genomes.

The present invention provides a computer database comprising a computer and
5 software for storing in computer-retrievable form assay data records cross-tabulated, e.g., with data specifying the source of the target-containing sample from which each sequence specificity record was obtained.

In an exemplary embodiment, at least one of the sources of target-containing sample is from a control tissue sample known to be free of pathological disorders. In a variation, at
10 least one of the sources is a known pathological tissue specimen, e.g., a neoplastic lesion or another tissue specimen to be analyzed for lung cancer. In another variation, the assay records cross-tabulate one or more of the following parameters for each target species in a sample: (1) a unique identification code, which can include, e.g., a target molecular structure and/or characteristic separation coordinate (e.g., electrophoretic coordinates); (2) sample
15 source; and (3) absolute and/or relative quantity of the target species present in the sample.

The invention also provides for the storage and retrieval of a collection of target data in a computer data storage apparatus, which can include magnetic disks, optical disks, magneto-optical disks, DRAM, SRAM, SGRAM, SDRAM, RDRAM, DDR RAM, magnetic
20 bubble memory devices, and other data storage devices, including CPU registers and on-CPU data storage arrays. Typically, the target data records are stored as a bit pattern in an array of magnetic domains on a magnetizable medium or as an array of charge states or transistor gate states, such as an array of cells in a DRAM device (e.g., each cell comprised of a transistor and a charge storage area, which may be on the transistor). In one embodiment, the invention provides such storage devices, and computer systems built therewith, comprising a bit pattern
25 encoding a protein expression fingerprint record comprising unique identifiers for at least 10 target data records cross-tabulated with target source.

When the target is a peptide or nucleic acid, the invention preferably provides a method for identifying related peptide or nucleic acid sequences, comprising performing a computerized comparison between a peptide or nucleic acid sequence assay record stored in
30 or retrieved from a computer storage device or database and at least one other sequence. The comparison can include a sequence analysis or comparison algorithm or computer program embodiment thereof (e.g., FASTA, TFASTA, GAP, BESTFIT) and/or the comparison may

be of the relative amount of a peptide or nucleic acid sequence in a pool of sequences determined from a polypeptide or nucleic acid sample of a specimen.

The invention also preferably provides a magnetic disk, such as an IBM-compatible (DOS, Windows, Windows95/98/2000, Windows NT, OS/2) or other format (e.g., Linux,
5 SunOS, Solaris, AIX, SCO Unix, VMS, MV, Macintosh, etc.) floppy diskette or hard (fixed, Winchester) disk drive, comprising a bit pattern encoding data from an assay of the invention in a file format suitable for retrieval and processing in a computerized sequence analysis, comparison, or relative quantitation method.

The invention also provides a network, comprising a plurality of computing devices
10 linked via a data link, such as an Ethernet cable (coax or 10BaseT), telephone line, ISDN line, wireless network, optical fiber, or other suitable signal transmission medium, whereby at least one network device (e.g., computer, disk array, etc.) comprises a pattern of magnetic domains (e.g., magnetic disk) and/or charge domains (e.g., an array of DRAM cells) composing a bit pattern encoding data acquired from an assay of the invention.

15 The invention also provides a method for transmitting assay data that includes generating an electronic signal on an electronic communications device, such as a modem, ISDN terminal adapter, DSL, cable modem, ATM switch, or the like, wherein the signal includes (in native or encrypted format) a bit pattern encoding data from an assay or a database comprising a plurality of assay results obtained by the method of the invention.

20 In a preferred embodiment, the invention provides a computer system for comparing a query target to a database containing an array of data structures, such as an assay result obtained by the method of the invention, and ranking database targets based on the degree of identity and gap weight to the target data. A central processor is preferably initialized to load and execute the computer program for alignment and/or comparison of the assay results.

25 Data for a query target is entered into the central processor via an I/O device. Execution of the computer program results in the central processor retrieving the assay data from the data file, which comprises a binary description of an assay result.

The target data or record and the computer program can be transferred to secondary
30 memory, which is typically random access memory (e.g., DRAM, SRAM, SGRAM, or SDRAM). Targets are ranked according to the degree of correspondence between a selected assay characteristic (e.g., binding to a selected affinity moiety) and the same characteristic of the query target and results are output via an I/O device. For example, a central processor can be a conventional computer (e.g., Intel Pentium, PowerPC, Alpha, PA-8000, SPARC,

MIPS 4400, MIPS 10000, VAX, etc.); a program can be a commercial or public domain molecular biology software package (e.g., UWGCG Sequence Analysis Software, Darwin); a data file can be an optical or magnetic disk, a data server, a memory device (e.g., DRAM, SRAM, SGRAM, SDRAM, EPROM, bubble memory, flash memory, etc.); an I/O device can be a terminal comprising a video display and a keyboard, a modem, an ISDN terminal adapter, an Ethernet port, a punched card reader, a magnetic strip reader, or other suitable I/O device.

The invention also preferably provides the use of a computer system, such as that described above, which comprises: (1) a computer; (2) a stored bit pattern encoding a collection of peptide sequence specificity records obtained by the methods of the invention, which may be stored in the computer; (3) a comparison target, such as a query target; and (4) a program for alignment and comparison, typically with rank-ordering of comparison results on the basis of computed similarity values.

Characteristics of lung cancer-associated proteins

Lung cancer proteins of the present invention may be classified as secreted proteins, transmembrane proteins or intracellular proteins. In one embodiment, the lung cancer protein is an intracellular protein. Intracellular proteins may be found in the cytoplasm and/or in the nucleus. Intracellular proteins are involved in all aspects of cellular function and replication (including, e.g., signaling pathways); aberrant expression of such proteins often results in unregulated or dysregulated cellular processes (see, e.g., Alberts (ed. 1994) Molecular Biology of the Cell (3d ed.)). For example, many intracellular proteins have enzymatic activity such as protein kinase activity, protein phosphatase activity, protease activity, nucleotide cyclase activity, polymerase activity and the like. Intracellular proteins also serve as docking proteins that are involved in organizing complexes of proteins, or targeting proteins to various subcellular localizations, and are involved in maintaining the structural integrity of organelles.

An increasingly appreciated concept in characterizing proteins is the presence in the proteins of one or more structural motifs for which defined functions have been attributed. In addition to the highly conserved sequences found in the enzymatic domain of proteins, highly conserved sequences have been identified in proteins that are involved in protein-protein interaction. For example, Src-homology-2 (SH2) domains bind tyrosine-phosphorylated targets in a sequence dependent manner. PTB domains, which are distinct from SH2

domains, also bind tyrosine phosphorylated targets. SH3 domains bind to proline-rich targets. In addition, PH domains, tetratricopeptide repeats and WD domains to name only a few, have been shown to mediate protein-protein interactions. Some of these may also be involved in binding to phospholipids or other second messengers. As will be appreciated by one of ordinary skill in the art, these motifs can be identified on the basis of amino acid sequence; thus, an analysis of the sequence of proteins may provide insight into both the enzymatic potential of the molecule and/or molecules with which the protein may associate. One useful database is Pfam (protein families), which is a large collection of multiple sequence alignments and hidden Markov models covering many common protein domains.

Versions are available via the internet from Washington University in St. Louis, the Sanger Center in England, and the Karolinska Institute in Sweden (see, e.g., Bateman, et al (2000) *Nuc. Acids Res.* 28:263-266; Sonnhammer, et al. (1997) *Proteins* 28:405-420; Bateman, et al. (1999) *Nuc. Acids Res.* 27:260-262; and Sonnhammer, et al. (1998) *Nuc. Acids Res.* 26:320-322).

In another embodiment, the lung cancer sequences are transmembrane proteins. Transmembrane proteins are molecules that span a phospholipid bilayer of a cell. They may have an intracellular domain, an extracellular domain, or both. The intracellular domains of such proteins may have a number of functions including those already described for intracellular proteins. For example, the intracellular domain may have enzymatic activity and/or may serve as a binding site for additional proteins. Frequently the intracellular domain of transmembrane proteins serves both roles. For example certain receptor tyrosine kinases have both protein kinase activity and SH2 domains. In addition, autophosphorylation of tyrosines on the receptor molecule itself, creates binding sites for additional SH2 domain containing proteins.

Transmembrane proteins may contain from one to many transmembrane domains. For example, receptor tyrosine kinases, certain cytokine receptors, receptor guanylyl cyclases and receptor serine/threonine protein kinases contain a single transmembrane domain. However, various other proteins including channels, pumps, and adenylyl cyclases contain numerous transmembrane domains. Many important cell surface receptors such as G protein coupled receptors (GPCRs) are classified as "seven transmembrane domain" proteins, as they contain 7 membrane spanning regions. Characteristics of transmembrane domains include approximately 17 consecutive hydrophobic amino acids that may be followed by charged amino acids. Therefore, upon analysis of the amino acid sequence of a particular protein, the

localization and number of transmembrane domains within the protein may be predicted (see, e.g., PSORT web site <http://psort.nibb.ac.jp/>).

The extracellular domains of transmembrane proteins are diverse; however, conserved motifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. Many extracellular domains are involved in binding to other molecules. In one aspect, extracellular domains are found on receptors. Factors that bind the receptor domain include circulating ligands, which may be peptides, proteins, or small molecules such as adenosine and the like. For example, growth factors such as EGF, FGF, and PDGF are circulating growth factors that bind to their cognate receptors to initiate a variety of cellular responses. Other factors include cytokines, mitogenic factors, hormones, neurotrophic factors and the like. Extracellular domains also bind to cell-associated molecules. In this respect, they may mediate cell-cell interactions. Cell-associated ligands can be tethered to the cell, e.g., via a glycosylphosphatidylinositol (GPI) anchor, or may themselves be transmembrane proteins. Extracellular domains may also associate with the extracellular matrix and contribute to the maintenance of the cell structure.

Lung cancer proteins that are transmembrane are particularly preferred in the present invention as they are readily accessible targets for extracellular immunotherapeutics, as are described herein. In addition, as outlined below, transmembrane proteins can be also useful in imaging modalities. Antibodies may be used to label such readily accessible proteins *in situ* or in histological analysis. Alternatively, antibodies can also label intracellular proteins, in which case analytical samples are typically permeablized to provide access to intracellular proteins. In addition, some membrane proteins can be processed to release a soluble protein, or to expose a residual fragment. Released soluble proteins may be useful diagnostic markers, processed residual protein fragments may be useful lung markers of disease.

It will also be appreciated by those in the art that a transmembrane protein can be made soluble by removing transmembrane sequences, e.g., through recombinant methods. Furthermore, transmembrane proteins that have been made soluble can be made to be secreted through recombinant means by adding an appropriate signal sequence.

In another embodiment, the lung cancer proteins are secreted proteins; the secretion of which can be either constitutive or regulated. These proteins may have a signal peptide or signal sequence that targets the molecule to the secretory pathway. Secreted proteins are involved in numerous physiological events; e.g., if circulating, they often serve to transmit

signals to various other cell types. The secreted protein may function in an autocrine manner (acting on the cell that secreted the factor), a paracrine manner (acting on cells in close proximity to the cell that secreted the factor), an endocrine manner (acting on cells at a distance, e.g., secretion into the blood stream), or exocrine (secretion, e.g., through a duct or to adjacent epithelial surface as sweat glands, sebaceous glands, pancreatic ducts, lacrimal glands, mammary glands, wax producing glands of the ear, etc.). Thus secreted molecules often find use in modulating or altering numerous aspects of physiology. Lung cancer proteins that are secreted proteins are particularly preferred in the present invention as they serve as good targets for diagnostic markers, e.g., for blood, plasma, serum, or stool tests. Those which are enzymes may be antibody or small molecule targets. Others may be useful as vaccine targets, e.g., via CTL mechanisms.

Use of lung cancer nucleic acids

As described above, lung cancer sequence is initially identified by substantial nucleic acid and/or amino acid sequence homology or linkage to the lung cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions. Typically, linked sequences on a mRNA are found on the same molecule.

The lung cancer nucleic acid sequences of the invention, e.g., the sequences in Tables 1A-16, can be fragments of larger genes, i.e., they are nucleic acid segments. "Genes" in this context includes coding regions, non-coding regions, and mixtures of coding and non-coding regions. Accordingly, as will be appreciated by those in the art, using the sequences provided herein, extended sequences, in either direction, of the lung cancer genes can be obtained, using techniques well known in the art for cloning either longer sequences or the full length sequences; see Ausubel, et al., *supra*. Much can be done by informatics and many sequences can be clustered to include multiple sequences corresponding to a single gene, e.g., systems such as UniGene (see, <http://www.ncbi.nlm.nih.gov/UniGene/>).

Once a lung cancer nucleic acid is identified, it can be cloned and, if necessary, its constituent parts recombined to form the entire lung cancer nucleic acid coding regions or the entire mRNA sequence. Once isolated from its natural source, e.g., contained within a plasmid or other vector or excised therefrom as a linear nucleic acid segment, the recombinant lung cancer nucleic acid can be further-used as a probe to identify and isolate

other lung cancer nucleic acids, e.g., extended coding regions. It can also be used as a “precursor” nucleic acid to make modified or variant lung cancer nucleic acids and proteins.

The lung cancer nucleic acids of the present invention are used in several ways. In a first embodiment, nucleic acid probes to the lung cancer nucleic acids are made and attached to biochips to be used in screening and diagnostic methods, as outlined below, or for administration, e.g., for gene therapy, RNAi, vaccine, and/or antisense applications. Alternatively, the lung cancer nucleic acids that include coding regions of lung cancer proteins can be put into expression vectors for the expression of lung cancer proteins, again for screening purposes or for administration to a patient.

In a preferred embodiment, nucleic acid probes to lung cancer nucleic acids (both the nucleic acid sequences outlined in the figures and/or the complements thereof) are made. The nucleic acid probes attached to the biochip are designed to be substantially complementary to the lung cancer nucleic acids, i.e., the target sequence (either the target sequence of the sample or to other probe sequences, e.g., in sandwich assays), such that hybridization of the target sequence and the probes of the present invention occurs. As outlined below, this complementarity need not be perfect; there may be any number of base pair mismatches which will interfere with hybridization between the target sequence and the single stranded nucleic acids of the present invention. However, if the number of mutations is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary target sequence. Thus, by “substantially complementary” herein is meant that the probes are sufficiently complementary to the target sequences to hybridize under appropriate reaction conditions, particularly high stringency conditions, as outlined herein.

A nucleic acid probe is generally single stranded but can be partially single and partially double stranded. The strandedness of the probe is dictated by the structure, composition, and properties of the target sequence. In general, the nucleic acid probes range from about 8 to about 100 bases long, with from about 10 to about 80 bases being preferred, and from about 30 to about 50 bases being particularly preferred. That is, generally complements of ORFs or whole genes are not used. In some embodiments, nucleic acids of lengths up to hundreds of bases can be used.

In a preferred embodiment, more than one probe per sequence is used, with either overlapping probes or probes to different sections of the target being used. That is, two, three, four or more probes, with three being preferred, are used to build in a redundancy for a

particular target. The probes can be overlapping (i.e., have some sequence in common), or separate. In some cases, PCR primers may be used to amplify signal for higher sensitivity.

As will be appreciated by those in the art, nucleic acids can be attached or immobilized to a solid support in a wide variety of ways. By “immobilized” and grammatical equivalents herein is meant the association or binding between the nucleic acid probe and the solid support is sufficient to be stable under the conditions of binding, washing, analysis, and removal as outlined below. The binding can typically be covalent or non-covalent. By “non-covalent binding” and grammatical equivalents herein is typically meant one or more of electrostatic, hydrophilic, and hydrophobic interactions. Included in non-covalent binding is the covalent attachment of a molecule, such as, streptavidin to the support and the non-covalent binding of the biotinylated probe to the streptavidin. By “covalent binding” and grammatical equivalents herein is meant that the two moieties, the solid support and the probe, are attached by at least one bond, including sigma bonds, pi bonds and coordination bonds. Covalent bonds can be formed directly between the probe and the solid support or can be formed by a cross linker or by inclusion of a specific reactive group on either the solid support or the probe or both molecules. Immobilization may also involve a combination of covalent and non-covalent interactions.

In general, the probes are attached to a biochip in a wide variety of ways, as will be appreciated by those in the art. As described herein, the nucleic acids can either be synthesized first, with subsequent attachment to the biochip, or can be directly synthesized on the biochip.

The biochip comprises a suitable solid substrate. By “substrate” or “solid support” or other grammatical equivalents herein is meant a material that can be modified for the attachment or association of the nucleic acid probes and is amenable to at least one detection method. Often the substrate may contain discrete individual sites appropriate for individual partitioning and identification. As will be appreciated by those in the art, the number of possible substrates are very large, and include, but are not limited to, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, Teflon, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silica-based materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, etc. In general, the substrates allow optical detection and do not appreciably fluoresce. A preferred substrate is described in US application entitled Reusable Low Fluorescent Plastic Biochip, U.S.

Application Serial No. 09/270,214, filed March 15, 1999, herein incorporated by reference in its entirety.

Generally the substrate is planar, although as will be appreciated by those in the art, other configurations of substrates may be used as well. For example, the probes may be placed on the inside surface of a tube, for flow-through sample analysis to minimize sample volume. Similarly, the substrate may be flexible, such as a flexible foam, including closed cell foams made of particular plastics.

In a preferred embodiment, the surface of the biochip and the probe may be derivatized with chemical functional groups for subsequent attachment of the two. Thus, e.g., the biochip is derivatized with a chemical functional group including, but not limited to, amino groups, carboxy groups, oxo groups and thiol groups, with amino groups being particularly preferred. Using these functional groups, the probes can be attached using functional groups on the probes. For example, nucleic acids containing amino groups can be attached to surfaces comprising amino groups, e.g., using linkers as are known in the art; e.g., homo-or hetero-bifunctional linkers as are well known (see 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200). In addition, in some cases, additional linkers, such as alkyl groups (including substituted and heteroalkyl groups) may be used.

In this embodiment, oligonucleotides are synthesized, and then attached to the surface of the solid support. Either the 5' or 3' terminus may be attached to the solid support, or attachment may be via linkage to an internal nucleoside.

In another embodiment, the immobilization to the solid support may be very strong, yet non-covalent. For example, biotinylated oligonucleotides can be made, which bind to surfaces covalently coated with streptavidin, resulting in attachment.

Alternatively, the oligonucleotides may be synthesized on the surface, as is known in the art. For example, photoactivation techniques utilizing photopolymerization compounds and techniques are used. In a preferred embodiment, the nucleic acids can be synthesized *in situ*, using known photolithographic techniques, such as those described in WO 95/25116; WO 95/35505; U.S. Patent Nos. 5,700,637 and 5,445,934; and references cited within, all of which are expressly incorporated by reference; these methods of attachment form the basis of the Affymetrix GeneChip™ technology.

Often, amplification-based assays are performed to measure the expression level of lung cancer-associated sequences. These assays are typically performed in conjunction with

reverse transcription. In such assays, a lung cancer-associated nucleic acid sequence acts as a template in an amplification reaction (e.g., Polymerase Chain Reaction, or PCR). In a quantitative amplification, the amount of amplification product will be proportional to the amount of template in the original sample. Comparison to appropriate controls provides a measure of the amount of lung cancer-associated RNA. Methods of quantitative amplification are well known to those of skill in the art. Detailed protocols for quantitative PCR are provided, e.g., in Innis, et al. (1990) PCR Protocols, A Guide to Methods and Applications.

In some embodiments, a TaqMan based assay is used to measure expression.

TaqMan based assays use a fluorogenic oligonucleotide probe that contains a 5' fluorescent dye and a 3' quenching agent. The probe hybridizes to a PCR product, but cannot itself be extended due to a blocking agent at the 3' end. When the PCR product is amplified in subsequent cycles, the 5' nuclease activity of the polymerase, e.g., AmpliTaq, results in the cleavage of the TaqMan probe. This cleavage separates the 5' fluorescent dye and the 3' quenching agent, thereby resulting in an increase in fluorescence as a function of amplification (see, e.g., literature provided by Perkin-Elmer, e.g., www2.perkin-elmer.com).

Other suitable amplification methods include, but are not limited to, ligase chain reaction (LCR) (see Wu and Wallace (1989) Genomics 4:560, Landegren, et al. (1988) Science 241:1077, and Barringer, et al. (1990) Gene 89:117), transcription amplification (Kwoh, et al. (1989) Proc. Natl. Acad. Sci. USA 86:1173), self-sustained sequence replication (Guatelli, et al. (1990) Proc. Nat. Acad. Sci. USA 87:1874), dot PCR, and linker adapter PCR, etc.

Expression of lung cancer proteins from nucleic acids

In a preferred embodiment, lung cancer nucleic acids, e.g., encoding lung cancer proteins, are used to make a variety of expression vectors to express lung cancer proteins which can then be used in screening assays, as described below. Expression vectors and recombinant DNA technology are well known to those of skill in the art (see, e.g., Ausubel, *supra*, and Fernandez and Hoeffler (eds 1999) Gene Expression Systems) and are used to express proteins. The expression vectors may be either self-replicating extrachromosomal vectors or vectors which integrate into a host genome. Generally, these expression vectors include transcriptional and translational regulatory nucleic acid operably linked to the nucleic acid encoding the lung cancer protein. The term "control sequences" refers to DNA

sequences used for the expression of an operably linked coding sequence in a particular host organism. Control sequences that are suitable for prokaryotes, e.g., include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

5 Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding
10 sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is typically accomplished by ligation at convenient restriction sites. If such sites do not exist, synthetic oligonucleotide adaptors or linkers are used in
15 accordance with conventional practice. Transcriptional and translational regulatory nucleic acid will generally be appropriate to the host cell used to express the lung cancer protein. Numerous types of appropriate expression vectors, and suitable regulatory sequences are known in the art for a variety of host cells.

In general, transcriptional and translational regulatory sequences may include, but are
20 not limited to, promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, and enhancer or activator sequences. In a preferred embodiment, the regulatory sequences include a promoter and transcriptional start and stop sequences.

Promoter sequences may be either constitutive or inducible promoters. The promoters
25 may be either naturally occurring promoters or hybrid promoters. Hybrid promoters, which combine elements of more than one promoter, are also known in the art, and are useful in the present invention.

In addition, an expression vector may comprise additional elements. For example, the expression vector may have two replication systems, thus allowing it to be maintained in two
30 organisms, e.g., in mammalian or insect cells for expression and in a prokaryotic host for cloning and amplification. Furthermore, for integrating expression vectors, the expression vector often contains at least one sequence homologous to the host cell genome, and preferably two homologous sequences which flank the expression construct. The integrating

vector may be directed to a specific locus in the host cell by selecting the appropriate homologous sequence for inclusion in the vector. Constructs for integrating vectors are well known in the art (e.g., Fernandez and Hoeffler, *supra*).

In addition, in a preferred embodiment, the expression vector contains a selectable
5 marker gene to allow the selection of transformed host cells. Selection genes are well known in the art and will vary with the host cell used.

The lung cancer proteins of the present invention are usually produced by culturing a host cell transformed with an expression vector containing nucleic acid encoding a lung cancer protein, under the appropriate conditions to induce or cause expression of the lung
10 cancer protein. Conditions appropriate for lung cancer protein expression will vary with the choice of the expression vector and the host cell, and will be easily ascertained by one skilled in the art through routine experimentation or optimization. For example, the use of constitutive promoters in the expression vector will require optimizing the growth and proliferation of the host cell, while the use of an inducible promoter requires the appropriate
15 growth conditions for induction. In addition, in some embodiments, the timing of the harvest is important. For example, the baculoviral systems used in insect cell expression are lytic viruses, and thus harvest time selection can be crucial for product yield.

Appropriate host cells include yeast, bacteria, archaebacteria, fungi, and insect and animal cells, including mammalian cells. Of particular interest are *Saccharomyces cerevisiae*
20 and other yeasts, *E. coli*, *Bacillus subtilis*, Sf9 cells, C129 cells, 293 cells, *Neurospora*, BHK, CHO, COS, HeLa cells, HUVEC (human umbilical vein endothelial cells), THP1 cells (a macrophage cell line) and various other human cells and cell lines.

In a preferred embodiment, the lung cancer proteins are expressed in mammalian cells. Mammalian expression systems are also known in the art, and include retroviral and
25 adenoviral systems. Of particular use as mammalian promoters are the promoters from mammalian viral genes, since the viral genes are often highly expressed and have a broad host range. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter, herpes simplex virus promoter, and the CMV promoter (see, e.g., Fernandez and Hoeffler, *supra*). Typically, transcription termination and
30 polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. Examples of transcription terminator and polyadenylation signals include those derived from SV40.

The methods of introducing exogenous nucleic acid into mammalian hosts, as well as other hosts, is well known in the art, and will vary with the host cell used. Techniques include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, viral infection, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

In a preferred embodiment, lung cancer proteins are expressed in bacterial systems. Promoters from bacteriophage may also be used and are known in the art. In addition, synthetic promoters and hybrid promoters are also useful; e.g., the tac promoter is a hybrid of the trp and lac promoter sequences. Furthermore, a bacterial promoter can include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. In addition to a functioning promoter sequence, an efficient ribosome binding site is desirable. The expression vector may also include a signal peptide sequence that provides for secretion of the lung cancer protein in bacteria. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). The bacterial expression vector may also include a selectable marker gene to allow for the selection of bacterial strains that have been transformed. Suitable selection genes include genes which render the bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin, neomycin and tetracycline. Selectable markers also include biosynthetic genes, such as those in the histidine, tryptophan and leucine biosynthetic pathways. These components are assembled into expression vectors. Expression vectors for bacteria are well known in the art, and include vectors for *Bacillus subtilis*, *E. coli*, *Streptococcus cremoris*, and *Streptococcus lividans*, among others (e.g., Fernandez and Hoeffler, *supra*). The bacterial expression vectors are transformed into bacterial host cells using techniques well known in the art, such as calcium chloride treatment, electroporation, and others.

In one embodiment, lung cancer proteins are produced in insect cells. Expression vectors for the transformation of insect cells, and in particular, baculovirus-based expression vectors, are well known in the art.

In a preferred embodiment, lung cancer protein is produced in yeast cells. Yeast expression systems are well known in the art, and include expression vectors for *Saccharomyces cerevisiae*, *Candida albicans* and *C. maltosa*, *Hansenula polymorpha*,

Khuyveromyces fragilis and *K. lactis*, *Pichia guillermondii*, and *P. pastoris*, *Schizosaccharomyces pombe*, and *Yarrowia lipolytica*.

The lung cancer protein may also be made as a fusion protein, using techniques well known in the art. Thus, e.g., for the creation of monoclonal antibodies, if the desired epitope is small, the lung cancer protein may be fused to a carrier protein to form an immunogen. Alternatively, the lung cancer protein may be made as a fusion protein to increase expression for affinity purification purposes, or for other reasons. For example, when the lung cancer protein is a lung cancer peptide, the nucleic acid encoding the peptide may be linked to other nucleic acid for expression purposes.

In a preferred embodiment, the lung cancer protein is purified or isolated after expression. Lung cancer proteins may be isolated or purified in a variety of appropriate ways. Standard purification methods include electrophoretic, molecular, immunological and chromatographic techniques, including ion exchange, hydrophobic, affinity, and reverse-phase HPLC chromatography, and chromatofocusing. For example, the lung cancer protein may be purified using a standard anti-lung cancer protein antibody column. Ultrafiltration and diafiltration techniques, in conjunction with protein concentration, are also useful. For general guidance in suitable purification techniques, see Scopes (1982) Protein Purification. The degree of purification necessary will vary depending on the use of the lung cancer protein. In some instances no purification will be necessary.

Once expressed and purified if necessary, the lung cancer proteins and nucleic acids are useful in a number of applications. They may be used as immunoselection reagents, as vaccine reagents, as screening agents, therapeutic entities, for production of antibodies, as transcription or translation inhibitors, etc.

Variants of lung cancer proteins

In one embodiment, the lung cancer proteins are derivative or variant lung cancer proteins as compared to the wild-type sequence. That is, as outlined more fully below, the derivative lung cancer peptide will often contain at least one amino acid substitution, deletion or insertion, with amino acid substitutions being particularly preferred. The amino acid substitution, insertion or deletion may occur at a particular residue within the lung cancer peptide.

Also included within one embodiment of lung cancer proteins of the present invention are amino acid sequence variants. These variants typically fall into one or more of three

classes: substitutional, insertional or deletional variants. These variants ordinarily are prepared by site specific mutagenesis of nucleotides in the DNA encoding the lung cancer protein, using cassette or PCR mutagenesis or other techniques, to produce DNA encoding the variant, and thereafter expressing the DNA in recombinant cell culture as outlined above.

- 5 However, variant lung cancer protein fragments having up to about 100-150 residues may be prepared by *in vitro* synthesis. Amino acid sequence variants are characterized by the predetermined nature of the variation, a feature that sets them apart from naturally occurring allelic or interspecies variation of the lung cancer protein amino acid sequence. The variants typically exhibit a similar qualitative biological activity as the naturally occurring analogue,
10 although variants can also be selected which have modified characteristics as will be more fully outlined below.

- While the site or region for introducing an amino acid sequence variation is often predetermined, the mutation per se need not be predetermined. For example, in order to optimize the performance of a mutation at a given site, random mutagenesis may be
15 conducted at the target codon or region and the expressed lung cancer variants screened for the optimal combination of desired activity. Techniques exist for making substitution mutations at predetermined sites in DNA having a known sequence, e.g., M13 primer mutagenesis and PCR mutagenesis. Screening of mutants is often done using assays of lung cancer protein activities.

- 20 Amino acid substitutions are typically of single residues; insertions usually will be on the order of from about 1 to 20 amino acids, although considerably larger insertions may be occasionally tolerated. Deletions generally range from about 1 to about 20 residues, although in some cases deletions may be much larger.

- Substitutions, deletions, insertions or any combination thereof may be used to arrive
25 at a final derivative. Generally these changes are done on a few amino acids to minimize the alteration of the molecule. Larger changes may be tolerated in certain circumstances. When small alterations in the characteristics of a lung cancer protein are desired, substitutions are generally made in accordance with the amino acid substitution chart provided in the definition section.

- 30 Variants typically exhibit essentially the same qualitative biological activity and will elicit the same immune response as a naturally-occurring analog, although variants also are selected to modify the characteristics of lung cancer proteins as needed. Alternatively, the

variant may be designed or reorganized such that a biological activity of the lung cancer protein is altered. For example, glycosylation sites may be added, altered, or removed.

Covalent modifications of lung cancer polypeptides are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of a lung cancer polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N-or C-terminal residues of a lung cancer polypeptide. Derivatization with bifunctional agents is useful, for instance, for crosslinking lung cancer polypeptides to a water-insoluble support matrix or surface for use in a method for purifying anti-lung cancer polypeptide antibodies or screening assays, as is more fully described below. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, e.g., esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-((p-azidophenyl)dithio)propionimide.

Other modifications include deamidation of glutamyl and asparagyl residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of serinyl, threonyl or tyrosyl residues, methylation of the γ -amino groups of lysine, arginine, and histidine side chains (Creighton (1983) Proteins: Structure and Molecular Properties, pp. 79-86), acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

Another type of covalent modification of the lung cancer polypeptide encompassed by this invention is an altered native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended herein to mean adding to or deleting one or more carbohydrate moieties of a native sequence lung cancer polypeptide. Glycosylation patterns can be altered in many ways. For example the use of different cell types to express lung cancer-associated sequences can result in different glycosylation patterns.

Addition of glycosylation sites to lung cancer polypeptides may also be accomplished by altering the amino acid sequence thereof. The alteration may be made, e.g., by the addition of, or substitution by, one or more serine or threonine residues to the native sequence lung cancer polypeptide (for O-linked glycosylation sites). The lung cancer amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the lung cancer polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the lung cancer polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. Such methods are described in the art, e.g., in WO 87/05330, and in Aplin and Wriston (1981) CRC Crit. Rev. Biochem., pp. 259-306.

Removal of carbohydrate moieties present on the lung cancer polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art and described, for instance, by Hakimuddin, et al. (1987) Arch. Biochem. Biophys., 259:52 and by Edge, et al. (1981) Anal. Biochem., 118:131.

Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo-and exo-glycosidases as described by Thotakura, et al. (1987) Meth. Enzymol., 138:350.

Another type of covalent modification of lung cancer comprises linking the lung cancer polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol, polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192, or 4,179,337.

Lung cancer polypeptides of the present invention may also be modified in a way to form chimeric molecules comprising a lung cancer polypeptide fused to another, heterologous polypeptide or amino acid sequence. In one embodiment, such a chimeric molecule comprises a fusion of a lung cancer polypeptide with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino-or carboxyl-terminus of the lung cancer polypeptide. The presence of such epitope-tagged forms of a lung cancer polypeptide can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the lung cancer polypeptide to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. In an alternative embodiment, the chimeric molecule may comprise a fusion of a lung cancer polypeptide with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule, such a fusion could be to the Fc region of an IgG molecule.

Various tag polypeptides and their respective antibodies are well known and examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; HIS6 and metal chelation tags, the flu HA tag polypeptide and its antibody 12CA5 (Field, et al. (1988) Mol. Cell. Biol. 8:2159-2165); the c-myc tag and the 8F9, 3C7, 6E10, G4, B7 and 9E10 antibodies

thereto (Evan, et al. (1985) Molecular and Cellular Biology 5:3610-3616); and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody (Paborsky, et al. (1990) Protein Engineering 3(6):547-553). Other tag polypeptides include the Flag-peptide (Hopp, et al. (1988) BioTechnology 6:1204-1210); the KT3 epitope peptide (Martin, et al. (1992) Science 255:192-194); tubulin epitope peptide (Skinner, et al. (1991) J. Biol. Chem. 266:15163-15166); and the T7 gene 10 protein peptide tag (Lutz-Freyermuth, et al. (1990) Proc. Nat'l Acad. Sci. USA 87:6393-6397).

Also included are other lung cancer proteins of the lung cancer family, and lung cancer proteins from other organisms, which are cloned and expressed as outlined below.

Thus, probe or degenerate polymerase chain reaction (PCR) primer sequences may be used to find other related lung cancer proteins from primates or other organisms. As will be appreciated by those in the art, particularly useful probe and/or PCR primer sequences include unique areas of the lung cancer nucleic acid sequence. As is generally known in the art, preferred PCR primers are from about 15 to about 35 nucleotides in length, with from about 20 to about 30 being preferred, and may contain inosine as needed. PCR reaction conditions are well known in the art (e.g., Innis, PCR Protocols, *supra*).

Antibodies to lung cancer proteins

In a preferred embodiment, when a lung cancer protein is to be used to generate antibodies, e.g., for immunotherapy or immunodiagnosis, the lung cancer protein should share at least one epitope or determinant with the full length protein. By "epitope" or "determinant" herein is typically meant a portion of a protein which will generate and/or bind an antibody or T-cell receptor in the context of MHC. Thus, in most instances, antibodies made to a smaller lung cancer protein will be able to bind to the full-length protein, particularly linear epitopes. In a preferred embodiment, the epitope is unique; that is, antibodies generated to a unique epitope show little or no cross-reactivity.

Methods of preparing polyclonal antibodies are well known (e.g., Coligan, *supra*; and Harlow and Lane, *supra*). Polyclonal antibodies can be raised in a mammal, e.g., by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include a protein encoded by a nucleic acid of Tables 1A-16 or fragment thereof or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal

being immunized. Immunogenic proteins include, e.g., keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Adjuvants include, e.g., Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected by one skilled in the art.

The antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein (1975) Nature 256:495. In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized *in vitro*. The immunizing agent will typically include a polypeptide encoded by a nucleic acid of the tables, or fragment thereof, or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding (1986) Monoclonal Antibodies: Principles and Practice, pp. 59-103). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovin, or primate origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

In one embodiment, the antibodies are bispecific antibodies. Bispecific antibodies are typically monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens or that have binding specificities for two epitopes on the same antigen. In one embodiment, one of the binding specificities is for a protein encoded by a nucleic acid of the tables or a fragment thereof, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit, preferably one that is tumor specific. Alternatively, tetramer-type technology may create multivalent reagents.

In a preferred embodiment, the antibodies to lung cancer protein are capable of reducing or eliminating a biological function of a lung cancer protein, in a naked form or conjugated to an effector moiety. That is, the addition of anti-lung cancer protein antibodies (either polyclonal or preferably monoclonal) to lung cancer tissue (or cells containing lung cancer) may reduce or eliminate the lung cancer. Generally, at least a 25% decrease in activity, growth, size or the like is preferred, with at least about 50% being particularly preferred and about a 95-100% decrease being especially preferred.

In a preferred embodiment the antibodies to the lung cancer proteins are humanized antibodies (e.g., Xenerex Biosciences, Medarex, Inc., Abgenix, Inc., Protein Design Labs, Inc.) Humanized forms of non-human (e.g., murine) antibodies are chimeric molecules of immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of a human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, a humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework (FR) regions are those of a human immunoglobulin consensus sequence. A humanized antibody optimally also will typically comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-329; and Presta (1992) Curr. Op. Struct. Biol. 2:593-596). Humanization can be performed following the method of Winter and co-workers (Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-327; Verhoeyen, et al. (1988) Science 239:1534-1536), by substituting rodent CDRs or CDR sequences for corresponding sequences of a human antibody. Accordingly, such humanized antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by corresponding sequence from a non-human species.

Human-like antibodies can also be produced using various techniques known in the art, including phage display libraries (Hoogenboom and Winter (1991) J. Mol. Biol. 227:381; Marks, et al. (1991) J. Mol. Biol. 222:581). The techniques of Cole, et al. and Boerner, et al. are also available for the preparation of human monoclonal antibodies (Cole, et al. (1985) Monoclonal Antibodies and Cancer Therapy, p. 77 and Boerner, et al. (1991) J. Immunol. 147(1):86-95). Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in nearly all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, e.g., in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the following scientific publications: Marks, et al. (1992) Bio/Technology 10:779-783; Lonberg, et al. (1994) Nature 368:856-859; Morrison (1994) Nature 368:812-13; Fishwild, et al. (1996) Nature Biotechnology 14:845-51; Neuberger (1996) Nature Biotechnology 14:826; and Lonberg and Huszar (1995) Intern. Rev. Immunol. 13:65-93.

By immunotherapy is meant treatment of lung cancer with an antibody raised against a lung cancer proteins. As used herein, immunotherapy can be passive or active. Passive immunotherapy as defined herein is the passive transfer of antibody to a recipient (patient). Active immunization is the induction of antibody and/or T-cell responses in a recipient (patient). Induction of an immune response is the result of providing the recipient with an antigen to which antibodies are raised. The antigen may be provided by injecting a polypeptide against which antibodies are desired to be raised into a recipient, or contacting the recipient with a nucleic acid capable of expressing the antigen and under conditions for expression of the antigen, leading to an immune response.

In a preferred embodiment the lung cancer proteins against which antibodies are raised are secreted proteins as described above. Without being bound by theory, antibodies used for treatment, may bind and prevent the secreted protein from binding to its receptor, thereby inactivating the secreted lung cancer protein.

In another preferred embodiment, the lung cancer protein to which antibodies are raised is a transmembrane protein. Without being bound by theory, antibodies used for treatment may bind the extracellular domain of the lung cancer protein and prevent it from binding to other proteins, such as circulating ligands or cell-associated molecules. The

antibody may cause down-regulation of the transmembrane lung cancer protein. The antibody may be a competitive, non-competitive or uncompetitive inhibitor of protein binding to the extracellular domain of the lung cancer protein. The antibody may be an antagonist of the lung cancer protein or may prevent activation of a transmembrane lung cancer protein, or may induce or suppress a particular cellular pathway. In some embodiments, when the antibody prevents the binding of other molecules to the lung cancer protein, the antibody prevents growth of the cell. The antibody may also be used to target or sensitize the cell to cytotoxic agents, including, but not limited to TNF- α , TNF- β , IL-1, INF- γ , and IL-2, or chemotherapeutic agents including 5FU, vinblastine, actinomycin D, cisplatin, methotrexate, and the like. In some instances the antibody may belong to a sub-type that activates serum complement when complexed with the transmembrane protein thereby mediating cytotoxicity or antigen-dependent cytotoxicity (ADCC). Thus, lung cancer may be treated by administering to a patient antibodies directed against the transmembrane lung cancer protein. Antibody-labeling may activate a co-toxin, localize a toxin payload, or otherwise provide means to locally ablate cells.

In another preferred embodiment, the antibody is conjugated to an effector moiety. The effector moiety can be various molecules, including labeling moieties such as radioactive labels or fluorescent labels, or can be a therapeutic moiety. In one aspect the therapeutic moiety is a small molecule that modulates the activity of a lung cancer protein. In another aspect the therapeutic moiety may modulate an activity of molecules associated with or in close proximity to a lung cancer protein. The therapeutic moiety may inhibit enzymatic or signaling activity such as protease or collagenase activity associated with lung cancer.

In a preferred embodiment, the therapeutic moiety can also be a cytotoxic agent. In this method, targeting the cytotoxic agent to lung cancer tissue or cells results in a reduction in the number of afflicted cells, thereby reducing symptoms associated with lung cancer. Cytotoxic agents are numerous and varied and include, but are not limited to, cytotoxic drugs or toxins or active fragments of such toxins. Suitable toxins and their corresponding fragments include diphtheria A chain, exotoxin A chain, ricin A chain, abrin A chain, curcin, crotin, phenomycin, enomycin, saporin, auristatin, and the like. Cytotoxic agents also include radiochemicals made by conjugating radioisotopes to antibodies raised against lung cancer proteins, or binding of a radionuclide to a chelating agent that has been covalently attached to the antibody. Targeting the therapeutic moiety to transmembrane lung cancer proteins not only serves to increase the local concentration of therapeutic moiety in the lung cancer

afflicted area, but also serves to reduce deleterious side effects that may be associated with the untargeted therapeutic moiety.

In another preferred embodiment, the lung cancer protein against which the antibodies are raised is an intracellular protein. In this case, the antibody may be conjugated to a protein or other entity which facilitates entry into the cell. In one case, the antibody enters the cell by endocytosis. In another embodiment, a nucleic acid encoding the antibody is administered to the individual or cell. Moreover, wherein the lung cancer protein can be targeted within a cell, i.e., the nucleus, an antibody theretomay contain a signal for that target localization, i.e., a nuclear localization signal.

The lung cancer antibodies of the invention specifically bind to lung cancer proteins. By "specifically bind" herein is meant that the antibodies bind to the protein with a K_d of at least about 0.1 mM, more usually at least about 1 μ M, preferably at least about 0.1 μ M or better, and most preferably, 0.01 μ M or better. Selectivity of binding to the specific target and not to related other sequences is also important.

Detection of lung cancer sequence for diagnostic and therapeutic applications

In one aspect, the RNA expression levels of genes are determined for different cellular states in the lung cancer phenotype. Expression levels of genes in normal tissue (e.g., not undergoing lung cancer), in lung cancer tissue (and in some cases, for varying severities of lung cancer that relate to prognosis, as outlined below), or in non-malignant disease are evaluated to provide expression profiles. A gene expression profile of a particular cell state or point of development is essentially a "fingerprint" of the state of the cell. While two states may have a particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is reflective of the state of the cell. By comparing expression profiles of cells in different states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Then, diagnosis may be performed or confirmed to determine whether a tissue sample has the gene expression profile of normal or cancerous tissue. This will provide for molecular diagnosis of related conditions.

"Differential expression," or grammatical equivalents as used herein, refers to qualitative or quantitative differences in the temporal and/or cellular gene expression patterns within and among cells and tissue. Thus, a differentially expressed gene can qualitatively have its expression altered, including an activation or inactivation, in, e.g.,

normal versus lung cancer tissue. Genes may be turned on or turned off in a particular state, relative to another state thus permitting comparison of two or more states. A qualitatively regulated gene will exhibit an expression pattern within a state or cell type which is detectable by standard techniques. Some genes will be expressed in one state or cell type, but not in both. Alternatively, the difference in expression may be quantitative, e.g., in that expression is increased or decreased; i.e., gene expression is either upregulated, resulting in an increased amount of transcript, or downregulated, resulting in a decreased amount of transcript. The degree to which expression differs need only be large enough to quantify via standard characterization techniques as outlined below, such as by use of Affymetrix GeneChip™ expression arrays, Lockhart (1996) Nature Biotechnology 14:1675-1680, hereby expressly incorporated by reference. Other techniques include, but are not limited to, quantitative reverse transcriptase PCR, northern analysis and RNase protection. As outlined above, preferably the change in expression (i.e., upregulation or downregulation) is typically at least about 50%, more preferably at least about 100%, more preferably at least about 150%, more preferably at least about 200%, with from 300 to at least 1000% being especially preferred.

Evaluation may be at the gene transcript or the protein level. The amount of gene expression may be monitored using nucleic acid probes to the RNA or DNA equivalent of the gene transcript, and the quantification of gene expression levels, or, alternatively, the final gene product itself (protein) can be monitored, e.g., with antibodies to the lung cancer protein and standard immunoassays (ELISAs, etc.) or other techniques, including mass spectroscopy assays, 2D gel electrophoresis assays, etc. Proteins corresponding to lung cancer genes, e.g., those identified as being important in a lung cancer or disease phenotype, can be evaluated in a lung cancer diagnostic test. In a preferred embodiment, gene expression monitoring is performed simultaneously on a number of genes.

The lung cancer nucleic acid probes may be attached to biochips as outlined herein for the detection and quantification of lung cancer sequences in a particular cell. The assays are further described below in the example. PCR techniques can be used to provide greater sensitivity. Multiple protein expression monitoring can be performed as well. Similarly, these assays may be performed on an individual basis as well.

In a preferred embodiment nucleic acids encoding the lung cancer protein are detected. Although DNA or RNA encoding the lung cancer protein may be detected, of particular interest are methods wherein an mRNA encoding a lung cancer protein is detected.

Probes to detect mRNA can be a nucleotide/deoxynucleotide probe that is complementary to and hybridizes with the mRNA and includes, but is not limited to, oligonucleotides, cDNA or RNA. Probes also should contain a detectable label, as defined herein. In one method the mRNA is detected after immobilizing the nucleic acid to be examined on a solid support such as nylon membranes and hybridizing the probe with the sample. Following washing to remove the non-specifically bound probe, the label is detected. In another method detection of the mRNA is performed *in situ*. In this method permeabilized cells or tissue samples are contacted with a detectably labeled nucleic acid probe for sufficient time to allow the probe to hybridize with the target mRNA. Following washing to remove the non-specifically bound probe, the label is detected. For example a digoxigenin labeled riboprobe (RNA probe) that is complementary to the mRNA encoding a lung cancer protein is detected by binding the digoxigenin with an anti-digoxigenin secondary antibody and developed with nitro blue tetrazolium and 5-bromo-4-chloro-3-indoyl phosphate.

In a preferred embodiment, various proteins from the three classes of proteins as described herein (secreted, transmembrane or intracellular proteins) are used in diagnostic assays. The lung cancer proteins, antibodies, nucleic acids, modified proteins and cells containing lung cancer sequences are used in diagnostic assays. This can be performed on an individual gene or corresponding polypeptide level. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes and/or corresponding polypeptides.

As described and defined herein, lung cancer proteins, including intracellular, transmembrane, or secreted proteins, find use as markers of lung cancer, e.g., for prognostic or diagnostic purposes. Detection of these proteins in putative lung cancer tissue allows for detection, prognosis, or diagnosis of lung cancer or similar disease, and perhaps for selection of therapeutic strategy. In one embodiment, antibodies are used to detect lung cancer proteins. A preferred method separates proteins from a sample by electrophoresis on a gel (typically a denaturing and reducing protein gel, but may be another type of gel, including isoelectric focusing gels and the like). Following separation of proteins, the lung cancer protein is detected, e.g., by immunoblotting with antibodies raised against the lung cancer protein. Methods of immunoblotting are well known to those of ordinary skill in the art.

In another preferred method, antibodies to the lung cancer protein find use in *in situ* imaging techniques, e.g., in histology (e.g., Asai (ed. 1993) Methods in Cell Biology:

Antibodies in Cell Biology, volume 37. In this method cells are contacted with from one to

many antibodies to the lung cancer protein(s). Following washing to remove non-specific antibody binding, the presence of the antibody or antibodies is detected. In one embodiment the antibody is detected by incubating with a secondary antibody that contains a detectable
5 label, e.g., multicolor fluorescence or confocal imaging. In another method the primary antibody to the lung cancer protein(s) contains a detectable label, e.g., an enzyme marker that can act on a substrate. In another preferred embodiment each one of multiple primary antibodies contains a distinct and detectable label. This method finds particular use in simultaneous screening for a plurality of lung cancer proteins. Many other histological
10 imaging techniques are also provided by the invention.

In a preferred embodiment the label is detected in a fluorometer which has the ability to detect and distinguish emissions of different wavelengths. In addition, a fluorescence activated cell sorter (FACS) can be used in the method.

In another preferred embodiment, antibodies find use in diagnosing lung cancer from
15 blood, serum, plasma, stool, and other samples. Such samples, therefore, are useful as samples to be probed or tested for the presence of lung cancer proteins. Antibodies can be used to detect a lung cancer protein by previously described immunoassay techniques including ELISA, immunoblotting (western blotting), immunoprecipitation, BIACORE technology and the like. Conversely, the presence of antibodies may indicate an immune
20 response against an endogenous lung cancer protein or vaccine.

In a preferred embodiment, *in situ* hybridization of labeled lung cancer nucleic acid probes to tissue arrays is done. For example, arrays of tissue samples, including lung cancer tissue and/or normal tissue, are made. *In situ* hybridization (see, e.g., Ausubel, *supra*) is then performed. When comparing the fingerprints between an individual and a standard, the
25 skilled artisan can make a diagnosis, a prognosis, or a prediction based on the findings. It is further understood that the genes which indicate the diagnosis may differ from those which indicate the prognosis and molecular profiling of the condition of the cells may lead to distinctions between responsive or refractory conditions or may be predictive of outcomes.

In a preferred embodiment, the lung cancer proteins, antibodies, nucleic acids,
30 modified proteins and cells containing lung cancer sequences are used in prognosis assays. As above, gene expression profiles can be generated that correlate to lung cancer, clinical, pathological, or other information, in terms of long term prognosis. Again, this may be done on either a protein or gene level, with the use of genes being preferred. Single or multiple

genes may be useful in various combinations. As above, lung cancer probes may be attached to biochips for the detection and quantification of lung cancer sequences in a tissue or patient. The assays proceed as outlined above for diagnosis. PCR method may provide more sensitive and accurate quantification.

5

Assays for therapeutic compounds

In a preferred embodiment, the proteins, nucleic acids, and antibodies as described herein are used in drug screening assays. The lung cancer proteins, antibodies, nucleic acids, modified proteins and cells containing lung cancer sequences are used in drug screening
10 assays or by evaluating the effect of drug candidates on a “gene expression profile” or expression profile of polypeptides. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent (e.g., Zlokarnik, et al. (1998) Science 279:84-8; Heid (1996) Genome Res. 6:986-94.

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In a preferred embodiment, the lung cancer proteins, antibodies, nucleic acids, modified proteins and cells containing the native or modified lung cancer proteins are used in screening assays. That is, the present invention provides novel methods for screening for compositions which modulate the lung cancer phenotype or an identified physiological function of a lung cancer protein. As above, this can be done on an individual gene level or
20 by evaluating the effect of drug candidates on a “gene expression profile”. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent, see Zlokarnik, *supra*.

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Having identified differentially expressed genes herein, a variety of assays may be performed. In a preferred embodiment, assays may be run on an individual gene or protein level. That is, having identified a particular gene with altered regulation in lung cancer, test compounds can be screened for the ability to modulate gene expression or for binding to the lung cancer protein. “Modulation” thus includes an increase or a decrease in gene expression. The preferred amount of modulation will depend on the original change of the
30 gene expression in normal versus tissue undergoing lung cancer, with changes of at least 10%, preferably 50%, more preferably 100-300%, and in some embodiments 300-1000% or greater. Thus, if a gene exhibits a 4-fold increase in lung cancer tissue compared to normal tissue, a decrease of about four-fold is often desired; similarly, a 10-fold decrease in lung

cancer tissue compared to normal tissue often provides a target value of a 10-fold increase in expression to be induced by the test compound.

The amount of gene expression may be monitored using nucleic acid probes and the quantification of gene expression levels, or, alternatively, the gene product itself can be monitored, e.g., through the use of antibodies to the lung cancer protein and standard immunoassays. Proteomics and separation techniques may also allow quantification of expression.

In a preferred embodiment, gene or protein expression monitoring of a number of entities, i.e., an expression profile, is monitored simultaneously. Such profiles will typically involve a plurality of those entities described herein.

In this embodiment, the lung cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of lung cancer sequences in a particular cell. Alternatively, PCR may be used. Thus, a series, e.g., of microtiter plate, may be used with dispensed primers in desired wells. A PCR reaction can then be performed and analyzed for each well.

Expression monitoring can be performed to identify compounds that modify the expression of one or more lung cancer-associated sequences, e.g., a polynucleotide sequence set out in the tables. Generally, in a preferred embodiment, a test compound is added to the cells prior to analysis. Moreover, screens are also provided to identify agents that modulate lung cancer, modulate lung cancer proteins, bind to a lung cancer protein, or interfere with the binding of a lung cancer protein and an antibody, substrate, or other binding partner.

The term "test compound" or "drug candidate" or "modulator" or grammatical equivalents as used herein describes a molecule, e.g., protein, oligopeptide, small organic molecule, polysaccharide, polynucleotide, etc., to be tested for the capacity to directly or indirectly alter the lung cancer phenotype or the expression of a lung cancer sequence, e.g., a nucleic acid or protein sequence. In preferred embodiments, modulators alter expression profiles of nucleic acids or proteins provided herein. In one embodiment, the modulator suppresses a lung cancer phenotype, e.g., to a normal or non-malignant tissue fingerprint. In another embodiment, a modulator induces a lung cancer phenotype. Generally, a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, i.e., at zero concentration or below the level of detection.

In one aspect, a modulator will neutralize the effect of a lung cancer protein. By “neutralize” is meant that activity of a protein and the consequent effect on the cell is inhibited or blocked.

In certain embodiments, combinatorial libraries of potential modulators will be screened for an ability to bind to a lung cancer polypeptide or to modulate activity. Conventionally, new chemical entities with useful properties are generated by identifying a chemical compound (called a “lead compound”) with some desirable property or activity, e.g., inhibiting activity, creating variants of the lead compound, and evaluating the property and activity of those variant compounds. Often, high throughput screening (HTS) methods are employed for such an analysis.

In one preferred embodiment, high throughput screening methods involve providing a library containing a large number of potential therapeutic compounds (candidate compounds). Such “combinatorial chemical libraries” are then screened in one or more assays to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as conventional “lead compounds” or can themselves be used as potential or actual therapeutics.

A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis by combining a number of chemical “building blocks” such as reagents. For example, a linear combinatorial chemical library, such as a polypeptide (e.g., mutein) library, is formed by combining a set of chemical building blocks called amino acids in every possible way for a given compound length (i.e., the number of amino acids in a polypeptide compound). Millions of chemical compounds can be synthesized through such combinatorial mixing of chemical building blocks (Gallop, et al. (1994) J. Med. Chem. 37(9):1233-1251).

Preparation and screening of combinatorial chemical libraries is well known to those of skill in the art. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (see, e.g., U.S. Patent No. 5,010,175, Furka (1991) Pept. Prot. Res. 37:487-493, Houghton, et al. (1991) Nature, 354:84-88), peptoids (PCT Publication No WO 91/19735), encoded peptides (PCT Publication WO 93/20242), random bio-oligomers (PCT Publication WO 92/00091), benzodiazepines (U.S. Pat. No. 5,288,514), diversomers such as hydantoins, benzodiazepines and dipeptides (Hobbs, et al. (1993) Proc. Nat. Acad. Sci. USA 90:6909-6913), vinylogous polypeptides (Hagihara, et al. (1992) J. Amer. Chem. Soc. 114:6568), nonpeptidal peptidomimetics with a Beta-D-Glucose scaffolding (Hirschmann, et

al. (1992) J. Amer. Chem. Soc. 114:9217-9218), analogous organic syntheses of small compound libraries (Chen, et al. (1994) J. Amer. Chem. Soc. 116:2661), oligocarbamates (Cho, et al. (1993) Science 261:1303), and/or peptidyl phosphonates (Campbell, et al. (1994) J. Org. Chem. 59:658). See, generally, Gordon, et al. (1994) J. Med. Chem. 37:1385, nucleic acid libraries (see, e.g., Stratagene, Corp.), peptide nucleic acid libraries (see, e.g., U.S. Patent 5,539,083), antibody libraries (see, e.g., Vaughn, et al. (1996) Nature Biotechnology 14(3):309-314, and PCT/US96/10287), carbohydrate libraries (see, e.g., Liang, et al. (1996) Science 274:1520-1522, and U.S. Patent No. 5,593,853), and small organic molecule libraries (see, e.g., benzodiazepines, Baum (1993) C&EN, Jan 18, page 33; isoprenoids, U.S. Patent No. 5,569,588; thiazolidinones and metathiazanones, U.S. Patent No. 5,549,974; pyrrolidines, U.S. Patent Nos. 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent No. 5,506,337; benzodiazepines, U.S. Patent No. 5,288,514; and the like).

Devices for the preparation of combinatorial libraries are commercially available (see, e.g., 357 MPS, 390 MPS, Advanced Chem Tech, Louisville KY, Symphony, Rainin, Woburn, MA, 433A Applied Biosystems, Foster City, CA, 9050 Plus, Millipore, Bedford, MA).

A number of well known robotic systems have also been developed for solution phase chemistries. These systems include automated workstations like the automated synthesis apparatus developed by Takeda Chemical Industries, LTD. (Osaka, Japan) and many robotic systems utilizing robotic arms (Zymate II, Zymark Corporation, Hopkinton, Mass.; Orca, Hewlett-Packard, Palo Alto, Calif.), which mimic the manual synthetic operations performed by a chemist. The above devices, with appropriate modification, are suitable for use with the present invention. In addition, numerous combinatorial libraries are themselves commercially available (see, e.g., ComGenex, Princeton, N.J., Asinex, Moscow, Ru, Tripos, Inc., St. Louis, MO, ChemStar, Ltd, Moscow, RU, 3D Pharmaceuticals, Exton, PA, Martek Biosciences, Columbia, MD, etc.).

The assays to identify modulators are amenable to high throughput screening. Preferred assays thus detect modulation of lung cancer gene transcription, polypeptide expression, and polypeptide activity.

High throughput assays for evaluating the presence, absence, quantification, or other properties of particular nucleic acids or protein products are well known to those of skill in the art. Similarly, binding assays and reporter gene assays are similarly well known. Thus, e.g., U.S. Patent No. 5,559,410 discloses high throughput screening methods for proteins,

U.S. Patent No. 5,585,639 discloses high throughput screening methods for nucleic acid binding (i.e., in arrays), while U.S. Patent Nos. 5,576,220 and 5,541,061 disclose high throughput methods of screening for ligand/antibody binding.

In addition, high throughput screening systems are commercially available (see, e.g.,
5 Zymark Corp., Hopkinton, MA; Air Technical Industries, Mentor, OH; Beckman
Instruments, Inc. Fullerton, CA; Precision Systems, Inc., Natick, MA, etc.). These systems
typically automate procedures, including sample and reagent pipetting, liquid dispensing,
timed incubations, and final readings of the microplate in detector(s) appropriate for the
assay. These configurable systems provide high throughput and rapid start up as well as a
10 high degree of flexibility and customization. The manufacturers of such systems provide
detailed protocols for various high throughput systems. Thus, e.g., Zymark Corp. provides
technical bulletins describing screening systems for detecting the modulation of gene
transcription, ligand binding, and the like.

In one embodiment, modulators are proteins, often naturally occurring proteins or
15 fragments of naturally occurring proteins. Thus, e.g., cellular extracts containing proteins, or
random or directed digests of proteinaceous cellular extracts, may be used. In this way
libraries of proteins may be made for screening in the methods of the invention. Particularly
preferred in this embodiment are libraries of bacterial, fungal, viral, and mammalian proteins,
with the latter being preferred, and human proteins being especially preferred. Particularly
20 useful test compound will be directed to the class of proteins to which the target belongs, e.g.,
substrates for enzymes or ligands and receptors.

In a preferred embodiment, modulators are peptides of from about 5 to about 30
amino acids, with from about 5 to about 20 amino acids being preferred, and from about 7 to
about 15 being particularly preferred. The peptides may be digests of naturally occurring
25 proteins, random peptides, or "biased" random peptides. By "randomized" or grammatical
equivalents herein is meant that the nucleic acid or peptide consists of essentially random
sequences of nucleotides and amino acids, respectively. Since these random peptides (or
nucleic acids, discussed below) are often chemically synthesized, they may incorporate a
nucleotide or amino acid at any position. The synthetic process can be designed to generate
30 randomized proteins or nucleic acids, to allow the formation of all or most of the possible
combinations over the length of the sequence, thus forming a library of randomized candidate
bioactive proteinaceous agents.

In one embodiment, the library is fully randomized, with no sequence preferences or constants at any position. In a preferred embodiment, the library is biased. That is, some positions within the sequence are either held constant, or are selected from a limited number of possibilities. In a preferred embodiment, the nucleotides or amino acid residues are
5 randomized within a defined class, e.g., of hydrophobic amino acids, hydrophilic residues, sterically biased (either small or large) residues, towards the creation of nucleic acid binding domains, the creation of cysteines, for cross-linking, prolines for SH-3 domains, serines, threonines, tyrosines or histidines for phosphorylation sites, etc.

Modulators of lung cancer can also be nucleic acids, as defined above.

10 As described above generally for proteins, nucleic acid modulating agents may be naturally occurring nucleic acids, random nucleic acids, or "biased" random nucleic acids. Digests of procaryotic or eucaryotic genomes may be used as is outlined above for proteins.

In a preferred embodiment, the candidate compounds are organic chemical moieties, a wide variety of which are available in the literature.

15 After a candidate agent has been added and the cells allowed to incubate for some period of time, the sample containing a target sequence is analyzed. If required, the target sequence is prepared using known techniques. For example, the sample may be treated to lyse the cells, using known lysis buffers, electroporation, etc., with purification and/or amplification such as PCR performed as appropriate. For example, an *in vitro* transcription
20 with labels covalently attached to the nucleotides is performed. Generally, the nucleic acids are labeled with biotin-FITC or PE, or with cy3 or cy5.

In a preferred embodiment, the target sequence is labeled with, e.g., a fluorescent, a chemiluminescent, a chemical, or a radioactive signal, to provide a means of detecting the target sequence's specific binding to a probe. The label also can be an enzyme, such as,
25 alkaline phosphatase or horseradish peroxidase, which when provided with an appropriate substrate produces a product that can be detected. Alternatively, the label can be a labeled compound or small molecule, such as an enzyme inhibitor, that binds but is not catalyzed or altered by the enzyme. The label also can be a moiety or compound, such as, an epitope tag or biotin which specifically binds to streptavidin. For the example of biotin, the streptavidin
30 is labeled as described above, thereby, providing a detectable signal for the bound target sequence. Unbound labeled streptavidin is typically removed prior to analysis.

Nucleic acid assays can be direct hybridization assays or can comprise "sandwich assays", which include the use of multiple probes, as is generally outlined in U.S. Patent Nos.

5,681,702, 5,597,909, 5,545,730, 5,594,117, 5,591,584, 5,571,670, 5,580,731, 5,571,670, 5,591,584, 5,624,802, 5,635,352, 5,594,118, 5,359,100, 5,124,246 and 5,681,697, all of which are hereby incorporated by reference. In this embodiment, in general, the target nucleic acid is prepared as outlined above, and then added to the biochip comprising a plurality of nucleic acid probes, under conditions that allow the formation of a hybridization complex.

A variety of hybridization conditions may be used in the present invention, including high, moderate and low stringency conditions as outlined above. The assays are generally run under stringency conditions which allow formation of the label probe hybridization complex only in the presence of target. Stringency can be controlled by altering a step parameter that is a thermodynamic variable, including, but not limited to, temperature, formamide concentration, salt concentration, chaotropic salt concentration, pH, organic solvent concentration, etc.

These parameters may also be used to control non-specific binding, as is generally outlined in U.S. Patent No. 5,681,697. Thus it may be desirable to perform certain steps at higher stringency conditions to reduce non-specific binding.

The reactions outlined herein may be accomplished in a variety of ways. Components of the reaction may be added simultaneously, or sequentially, in different orders, with preferred embodiments outlined below. In addition, the reaction may include a variety of other reagents. These include salts, buffers, neutral proteins, e.g., albumin, detergents, etc. which may be used to facilitate optimal hybridization and detection, and/or reduce non-specific or background interactions. Reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may also be used as appropriate, depending on the sample preparation methods and purity of the target.

The assay data are analyzed to determine the expression levels, and changes in expression levels as between states, of individual genes, forming a gene expression profile.

Screens are performed to identify modulators of the lung cancer phenotype. In one embodiment, screening is performed to identify modulators that can induce or suppress a particular expression profile, thus preferably generating the associated phenotype. In another embodiment, e.g., for diagnostic applications, having identified differentially expressed genes important in a particular state, screens can be performed to identify modulators that alter expression of individual genes. In an another embodiment, screening is performed to identify modulators that alter a biological function of the expression product of a differentially expressed gene. Again, having identified the importance of a gene in a particular state,

screens are performed to identify agents that bind and/or modulate the biological activity of the gene product, or evaluate genetic polymorphisms.

Genes can be screened for those that are induced in response to a candidate agent. After identifying a modulator based upon its ability to suppress a lung cancer expression pattern leading to a normal expression pattern, or to modulate a single lung cancer gene expression profile so as to mimic the expression of the gene from normal tissue, a screen as described above can be performed to identify genes that are specifically modulated in response to the agent. Comparing expression profiles between normal tissue and agent treated lung cancer tissue reveals genes that are not expressed in normal tissue or lung cancer tissue, but are expressed in agent treated tissue. These agent-specific sequences can be identified and used by methods described herein for lung cancer genes or proteins. In particular these sequences and the proteins they encode find use in marking or identifying agent treated cells. In addition, antibodies can be raised against the agent induced proteins and used to target novel therapeutics to the treated lung cancer tissue sample.

Thus, in one embodiment, a test compound is administered to a population of lung cancer cells, that have an associated lung cancer expression profile. By "administration" or "contacting" herein is meant that the candidate agent is added to the cells in such a manner as to allow the agent to act upon the cell, whether by uptake and intracellular action, or by action at the cell surface. In some embodiments, nucleic acid encoding a proteinaceous candidate agent (i.e., a peptide) may be put into a viral construct such as an adenoviral or retroviral construct, and added to the cell, such that expression of the peptide agent is accomplished, e.g., PCT US97/01019. Regulatable gene therapy systems can also be used.

Once a test compound has been administered to the cells, the cells can be washed if desired and are allowed to incubate under preferably physiological conditions for some period of time. The cells are then harvested and a new gene expression profile is generated, as outlined herein.

Thus, e.g., lung cancer or non-malignant tissue may be screened for agents that modulate, e.g., induce or suppress a lung cancer phenotype. A change in at least one gene, preferably many, of the expression profile indicates that the agent has an effect on lung cancer activity. By defining such a signature for the lung cancer phenotype, screens for new drugs that alter the phenotype can be devised. With this approach, the drug target need not be known and need not be represented in the original expression screening platform, nor does the level of transcript for the target protein need to change.

Measure of lung cancer polypeptide activity, or of lung cancer or the lung cancer

phenotype can be performed using a variety of assays. For example, the effects of the test compounds upon the function of the metastatic polypeptides can be measured by examining parameters described above. A suitable physiological change that affects activity can be used to assess the influence of a test compound on the polypeptides of this invention. When the functional consequences are determined using intact cells or animals, one can also measure a variety of effects such as, in the case of lung cancer associated with tumors, tumor growth, tumor metastasis, neovascularization, hormone release, transcriptional changes to both known and uncharacterized genetic markers (e.g., northern blots), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second messengers such as cGMP. In the assays of the invention, mammalian lung cancer polypeptide is typically used, e.g., mouse, preferably human.

Assays to identify compounds with modulating activity can be performed *in vitro*. For example, a lung cancer polypeptide is first contacted with a potential modulator and incubated for a suitable amount of time, e.g., from 0.5 to 48 hours. In one embodiment, the lung cancer polypeptide levels are determined *in vitro* by measuring the level of protein or mRNA. The level of protein is typically measured using immunoassays such as western blotting, ELISA and the like with an antibody that selectively binds to the lung cancer polypeptide or a fragment thereof. For measurement of mRNA, amplification, e.g., using PCR, LCR, or hybridization assays, e.g., northern hybridization, RNase protection, dot blotting, are preferred. The level of protein or mRNA is typically detected using directly or indirectly labeled detection agents, e.g., fluorescently or radioactively labeled nucleic acids, radioactively or enzymatically labeled antibodies, and the like, as described herein.

Alternatively, a reporter gene system can be devised using a lung cancer protein promoter operably linked to a reporter gene such as luciferase, green fluorescent protein, CAT, or β -gal. The reporter construct is typically transfected into a cell. After treatment with a potential modulator, the amount of reporter gene transcription, translation, or activity is measured according to standard techniques known to those of skill in the art.

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of the expression of the gene or the gene product itself can be done. The gene products of differentially expressed

genes are sometimes referred to herein as "lung cancer proteins." The lung cancer protein may be a fragment, or alternatively, be the full length protein to a fragment shown herein.

In one embodiment, screening for modulators of expression of specific genes is performed. Typically, the expression of only one or a few genes are evaluated. In another
5 embodiment, screens are designed to first find compounds that bind to differentially expressed proteins. These compounds are then evaluated for the ability to modulate differentially expressed activity. Moreover, once initial candidate compounds are identified, variants can be further screened to better evaluate structure activity relationships.

In a preferred embodiment, binding assays are done. In general, purified or isolated
10 gene product is used; that is, the gene products of one or more differentially expressed nucleic acids are made. For example, antibodies are generated to the protein gene products, and standard immunoassays are run to determine the amount of protein present. Alternatively, cells comprising the lung cancer proteins can be used in the assays.

Thus, in a preferred embodiment, the methods comprise combining a lung cancer
15 protein and a candidate compound, and determining the binding of the compound to the lung cancer protein. Preferred embodiments utilize the human lung cancer protein, although other mammalian proteins may also be used, e.g., for the development of animal models of human disease. In some embodiments, as outlined herein, variant or derivative lung cancer proteins may be used.

20 Generally, in a preferred embodiment of the methods herein, the lung cancer protein or the candidate agent is non-diffusably bound to an insoluble support, preferably having isolated sample receiving areas (e.g., a microtiter plate, an array, etc.). The insoluble supports may be made of a composition to which the compositions can be bound, is readily separated from soluble material, and is otherwise compatible with the overall method of
25 screening. The surface of such supports may be solid or porous and of a convenient shape. Examples of suitable insoluble supports include microtiter plates, arrays, membranes and beads. These are typically made of glass, plastic (e.g., polystyrene), polysaccharides, nylon or nitrocellulose, teflon™, etc. Microtiter plates and arrays are especially convenient because a large number of assays can be carried out simultaneously, using small amounts of reagents
30 and samples. The particular manner of binding of the composition is typically not crucial so long as it is compatible with the reagents and overall methods of the invention, maintains the activity of the composition, and is nondiffusable. Preferred methods of binding include the use of antibodies (which do not sterically block either the ligand binding site or activation

sequence when the protein is bound to the support), direct binding to "sticky" or ionic supports, chemical crosslinking, the synthesis of the protein or agent on the surface, etc. Following binding of the protein or agent, excess unbound material is removed by washing. The sample receiving areas may then be blocked through incubation with bovine serum albumin (BSA), casein or other innocuous protein or other moiety.

In a preferred embodiment, the lung cancer protein is bound to the support, and a test compound is added to the assay. Alternatively, the candidate agent is bound to the support and the lung cancer protein is added. Novel binding agents include specific antibodies, non-natural binding agents identified in screens of chemical libraries, peptide analogs, etc. Of particular interest are screening assays for agents that have a low toxicity for human cells. A wide variety of assays may be used for this purpose, including labeled *in vitro* protein-protein binding assays, electrophoretic mobility shift assays, immunoassays for protein binding, functional assays (phosphorylation assays, etc.) and the like.

The determination of the binding of the test modulating compound to the lung cancer protein may be done in a number of ways. In a preferred embodiment, the compound is labeled, and binding determined directly, e.g., by attaching all or a portion of the lung cancer protein to a solid support, adding a labeled candidate agent (e.g., a fluorescent label), washing off excess reagent, and determining whether the label is present on the solid support. Various blocking and washing steps may be utilized as appropriate.

In some embodiments, only one of the components is labeled, e.g., the proteins (or proteinaceous candidate compounds) can be labeled. Alternatively, more than one component can be labeled with different labels, e.g., ^{125}I for the proteins and a fluorophor for the compound. Proximity reagents, e.g., quenching or energy transfer reagents are also useful.

In one embodiment, the binding of the test compound is determined by competitive binding assay. The competitor may be a binding moiety known to bind to the target molecule (i.e., a lung cancer protein), such as an antibody, peptide, binding partner, ligand, etc. Under certain circumstances, there may be competitive binding between the compound and the binding moiety, with the binding moiety displacing the compound. In one embodiment, the test compound is labeled. Either the compound, or the competitor, or both, is added first to the protein for a time sufficient to allow binding, if present. Incubations may be performed at a temperature which facilitates optimal activity, typically between 4 and 40° C. Incubation periods are typically optimized, e.g., to facilitate rapid high throughput screening. Typically

between 0.1 and 1 hour will be sufficient. Excess reagent is generally removed or washed away. The second component is then added, and the presence or absence of the labeled component is followed, to indicate binding.

In a preferred embodiment, the competitor is added first, followed by a test compound. Displacement of the competitor is an indication that the test compound is binding to the lung cancer protein and thus is capable of binding to, and potentially modulating, the activity of the lung cancer protein. In this embodiment, either component can be labeled. Thus, e.g., if the competitor is labeled, the presence of label in the wash solution indicates displacement by the agent. Alternatively, if the test compound is labeled, the presence of the label on the support indicates displacement.

In an alternative embodiment, the test compound is added first, with incubation and washing, followed by the competitor. The absence of binding by the competitor may indicate that the test compound is bound to the lung cancer protein with a higher affinity. Thus, if the test compound is labeled, the presence of the label on the support, coupled with a lack of competitor binding, may indicate that the test compound is capable of binding to the lung cancer protein.

In a preferred embodiment, the methods comprise differential screening to identify agents that are capable of modulating the activity of the lung cancer proteins. In one embodiment, the methods comprise combining a lung cancer protein and a competitor in a first sample. A second sample comprises a test compound, a lung cancer protein, and a competitor. The binding of the competitor is determined for both samples, and a change, or difference in binding between the two samples indicates the presence of an agent capable of binding to the lung cancer protein and potentially modulating its activity. That is, if the binding of the competitor is different in the second sample relative to the first sample, the agent is capable of binding to the lung cancer protein.

Alternatively, differential screening is used to identify drug candidates that bind to the native lung cancer protein, but cannot bind to modified lung cancer proteins. The structure of the lung cancer protein may be modeled, and used in rational drug design to synthesize agents that interact with that site. Drug candidates that affect the activity of a lung cancer protein are also identified by screening drugs for the ability to either enhance or reduce the activity of the protein.

Positive controls and negative controls may be used in the assays. Preferably control and test samples are performed in at least triplicate to obtain statistically significant results.

Incubation of all samples is for a time sufficient for the binding of the agent to the protein. Following incubation, samples are washed free of non-specifically bound material and the amount of bound, generally labeled agent determined. For example, where a radiolabel is employed, the samples may be counted in a scintillation counter to determine the amount of bound compound.

A variety of other reagents may be included in the screening assays. These include reagents like salts, neutral proteins, e.g., albumin, detergents, etc. which may be used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used. The mixture of components may be added in an order that provides for the requisite binding.

In a preferred embodiment, the invention provides methods for screening for a compound capable of modulating the activity of a lung cancer protein. The methods comprise adding a test compound, as defined above, to a cell comprising lung cancer proteins. Preferred cell types include almost any cell. The cells contain a recombinant nucleic acid that encodes a lung cancer protein. In a preferred embodiment, a library of candidate agents are tested on a plurality of cells.

In one aspect, the assays are evaluated in the presence or absence or previous or subsequent exposure of physiological signals, e.g., hormones, antibodies, peptides, antigens, cytokines, growth factors, action potentials, pharmacological agents including chemotherapeutics, radiation, carcinogenics, or other cells (e.g., cell-cell contacts). In another example, the determinations are determined at different stages of the cell cycle process.

In this way, compounds that modulate lung cancer agents are identified. Compounds with pharmacological activity are able to enhance or interfere with the activity of the lung cancer protein. Once identified, similar structures are evaluated to identify critical structural feature of the compound.

In one embodiment, a method of inhibiting lung cancer cell division is provided. The method comprises administration of a lung cancer inhibitor. In another embodiment, a method of inhibiting lung cancer is provided. The method may comprise administration of a lung cancer inhibitor. In a further embodiment, methods of treating cells or individuals with lung cancer are provided, e.g., comprising administration of a lung cancer inhibitor.

In one embodiment, a lung cancer inhibitor is an antibody as discussed above. In another embodiment, the lung cancer inhibitor is an antisense molecule.

A variety of cell growth, proliferation, viability, and metastasis assays are known to those of skill in the art, as described below.

Soft agar growth or colony formation in suspension

5 Normal cells require a solid substrate to attach and grow. When the cells are transformed, they lose this phenotype and grow detached from the substrate. For example, transformed cells can grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft agar. The transformed cells, when transfected with tumor suppressor genes, regenerate normal phenotype and require a solid substrate to attach and
10 grow. Soft agar growth or colony formation in suspension assays can be used to identify modulators of lung cancer sequences, which when expressed in host cells, inhibit abnormal cellular proliferation and transformation. A therapeutic compound would reduce or eliminate the host cells' ability to grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft.

15 Techniques for soft agar growth or colony formation in suspension assays are described in Freshney (1994) Culture of Animal Cells a Manual of Basic Technique (3rd ed.), herein incorporated by reference. See also, the methods section of Garkavtsev, et al. (1996), *supra*, herein incorporated by reference.

20 *Contact inhibition and density limitation of growth*

 Normal cells typically grow in a flat and organized pattern in a petri dish until they touch other cells. When the cells touch one another, they are contact inhibited and stop growing. When cells are transformed, however, the cells are not contact inhibited and continue to grow to high densities in disorganized foci. Thus, the transformed cells grow to a
25 higher saturation density than normal cells. This can be detected morphologically by the formation of a disoriented monolayer of cells or rounded cells in foci within the regular pattern of normal surrounding cells. Alternatively, labeling index with (³H)-thymidine at saturation density can be used to measure density limitation of growth. See Freshney (1994), *supra*. The transformed cells, when transfected with tumor suppressor genes, regenerate a
30 normal phenotype and become contact inhibited and would grow to a lower density.

 In this assay, labeling index with (³H)-thymidine at saturation density is a preferred method of measuring density limitation of growth. Transformed host cells are transfected with a lung cancer-associated sequence and are grown for 24 hours at saturation density in

non-limiting medium conditions. The percentage of cells labeling with (^3H)-thymidine is determined autoradiographically. See, Freshney (1994), *supra*.

Growth factor or serum dependence

5 Transformed cells typically have a lower serum dependence than their normal counterparts (see, e.g., Temin (1966) J. Natl. Cancer Inst. 37:167-175; Eagle, et al. (1970) J. Exp. Med. 131:836-879); Freshney, *supra*. This is in part due to release of various growth factors by the transformed cells. Growth factor or serum dependence of transformed host cells can be compared with that of control.

Tumor specific markers levels

Tumor cells release an increased amount of certain factors (hereinafter "tumor specific markers") than their normal counterparts. For example, plasminogen activator (PA) is released from human glioma at a higher level than from normal brain cells (see, e.g.,
15 Gullino, "Angiogenesis, tumor vascularization, and potential interference with tumor growth" in Mihich (ed. 1985) Biological Responses in Cancer, pp. 178-184). Similarly, Tumor angiogenesis factor (TAF) is released at a higher level in tumor cells than their normal counterparts. See, e.g., Folkman (1992) "Angiogenesis and Cancer" in Sem Cancer Biol.).

Various techniques which measure the release of these factors are described in
20 Freshney (1994), *supra*. Also, see, Unkeless, et al. (1974) J. Biol. Chem. 249:4295-4305; Strickland and Beers (1976) J. Biol. Chem. 251:5694-5702; Whur, et al. (1980) Br. J. Cancer 42:305-312; Gullino, "Angiogenesis, tumor vascularization, and potential interference with tumor growth" in Mihich (ed. 1985) Biological Responses in Cancer, pp. 178-184; Freshney Anticancer Res. 5:111-130 (1985).

Invasiveness into Matrigel

The degree of invasiveness into Matrigel or some other extracellular matrix constituent can be used as an assay to identify compounds that modulate lung cancer-associated sequences. Tumor cells exhibit a good correlation between malignancy and
30 invasiveness of cells into Matrigel or some other extracellular matrix constituent. In this assay, tumorigenic cells are typically used as host cells. Expression of a tumor suppressor gene in these host cells would decrease invasiveness of the host cells.

Techniques described in Freshney (1994), *supra*, can be used. Briefly, the level of invasion of host cells can be measured by using filters coated with Matrigel or some other extracellular matrix constituent. Penetration into the gel, or through to the distal side of the filter, is rated as invasiveness, and rated histologically by number of cells and distance moved, or by prelabeling the cells with ^{125}I and counting the radioactivity on the distal side of the filter or bottom of the dish. See, e.g., Freshney (1984), *supra*.

Tumor growth in vivo

Effects of lung cancer-associated sequences on cell growth can be tested in transgenic or immune-suppressed mice. Knock-out transgenic mice can be made, in which the lung cancer gene is disrupted or in which a lung cancer gene is inserted. Knock-out transgenic mice can be made by insertion of a marker gene or other heterologous gene into the endogenous lung cancer gene site in the mouse genome via homologous recombination. Such mice can also be made by substituting the endogenous lung cancer gene with a mutated version of the lung cancer gene, or by mutating the endogenous lung cancer gene, e.g., by exposure to carcinogens.

A DNA construct is introduced into the nuclei of embryonic stem cells. Cells containing the newly engineered genetic lesion are injected into a host mouse embryo, which is re-implanted into a recipient female. Some of these embryos develop into chimeric mice that possess germ cells partially derived from the mutant cell line. Therefore, by breeding the chimeric mice it is possible to obtain a new line of mice containing the introduced genetic lesion (see, e.g., Capecchi, et al. (1989) Science 244:1288). Chimeric targeted mice can be derived according to Hogan, et al. (1988) Manipulating the Mouse Embryo: A Laboratory Manual, Cold Spring Harbor Laboratory and Robertson (ed. 1987) Teratocarcinomas and Embryonic Stem Cells: A Practical Approach, IRL Press, Washington, D.C.

Alternatively, various immune-suppressed or immune-deficient host animals can be used. For example, genetically athymic "nude" mouse (see, e.g., Giovanella, et al. (1974) J. Natl. Cancer Inst. 52:921), a SCID mouse, a thymectomized mouse, or an irradiated mouse (see, e.g., Bradley, et al. (1978) Br. J. Cancer 38:263; Selby, et al. (1980) Br. J. Cancer 41:52) can be used as a host. Transplantable tumor cells (typically about 10^6 cells) injected into isogenic hosts will produce invasive tumors in a high proportions of cases, while normal cells of similar origin will not. In hosts which developed invasive tumors, cells expressing a lung cancer-associated sequences are injected subcutaneously. After a suitable length of time,

preferably 4-8 weeks, tumor growth is measured (e.g., by volume or by its two largest dimensions) and compared to the control. Tumors that have statistically significant reduction (using, e.g., Student's T test) are said to have inhibited growth.

5 Polynucleotide modulators of lung cancer

Antisense and RNAi Polynucleotides

In certain embodiments, the activity of a lung cancer-associated protein is downregulated, or entirely inhibited, by the use of antisense or an inhibitory polynucleotide, i.e., a nucleic acid complementary to, and which can preferably hybridize specifically to, a
10 coding mRNA nucleic acid sequence, e.g., a lung cancer protein mRNA, or a subsequence thereof. Binding of the antisense polynucleotide to the mRNA reduces the translation and/or stability of the mRNA.

In the context of this invention, antisense polynucleotides can comprise naturally-occurring nucleotides, or synthetic species formed from naturally-occurring subunits or their
15 close homologs. Antisense polynucleotides may also have altered sugar moieties or inter-sugar linkages. Exemplary among these are the phosphorothioate and other sulfur containing species which are known for use in the art. Analogs are comprehended by this invention so long as they function effectively to hybridize with the lung cancer protein mRNA. See, e.g., Isis Pharmaceuticals, Carlsbad, CA; Sequitor, Inc., Natick, MA.

20 Such antisense polynucleotides can readily be synthesized using recombinant means, or can be synthesized *in vitro*. Equipment for such synthesis is sold by several vendors, including Applied Biosystems. The preparation of other oligonucleotides such as phosphorothioates and alkylated derivatives is also well known to those of skill in the art.

Antisense molecules as used herein include antisense or sense oligonucleotides.
25 Sense oligonucleotides can, e.g., be employed to block transcription by binding to the antisense strand. The antisense and sense oligonucleotide comprise a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA (sense) or DNA (antisense) sequences for lung cancer molecules. A preferred antisense molecule is for a lung cancer sequence in the tables, or for a ligand or activator thereof. Antisense or sense
30 oligonucleotides, according to the present invention, comprise a fragment generally at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein

is described in, e.g., Stein and Cohen (1988) Cancer Res. 48:2659 and van der Krol, et al. (1988) BioTechniques 6:958).

RNA interference is a mechanism to suppress gene expression in a sequence specific manner. See, e.g., Brumelkamp, et al. (2002) Scienceexpress (21March2002); Sharp (1999) Genes Dev. 13:139-141; and Cathew (2001) Curr. Op. Cell Biol. 13:244-248. In mammalian cells, short, e.g., 21 nt, double stranded small interfering RNAs (siRNA) have been shown to be effective at inducing an RNAi response. See, e.g., Elbashir, et al. (2001) Nature 411:494-498. The mechanism may be used to downregulate expression levels of identified genes, e.g., treatment of, or validation of relevance to disease.

Ribozymes

In addition to antisense polynucleotides, ribozymes can be used to target and inhibit transcription of lung cancer-associated nucleotide sequences. A ribozyme is an RNA molecule that catalytically cleaves other RNA molecules. Different kinds of ribozymes have been described, including group I ribozymes, hammerhead ribozymes, hairpin ribozymes, RNase P, and axhead ribozymes (see, e.g., Castanotto, et al. (1994) Adv. in Pharmacology 25: 289-317 for a general review of the properties of different ribozymes).

The general features of hairpin ribozymes are described, e.g., in Hampel, et al. (1990) Nucl. Acids Res. 18:299-304; European Patent Publication No. 0 360 257; U.S. Patent No. 5,254,678. Methods of preparing are well known to those of skill in the art (see, e.g., WO 94/26877; Ojwang, et al. (1993) Proc. Natl. Acad. Sci. USA 90:6340-6344; Yamada, et al. (1994) Human Gene Therapy 1:39-45; Leavitt, et al. (1995) Proc. Natl. Acad. Sci. USA 92:699-703; Leavitt, et al. (19994) Human Gene Therapy 5:1151-120; and Yamada, et al. (1994) Virology 205: 121-126).

Polynucleotide modulators of lung cancer may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell. Alternatively, a polynucleotide modulator of lung cancer may be introduced into a cell containing the target nucleic acid sequence, e.g., by

formation of an polynucleotide-lipid complex, as described in WO 90/10448. It is understood that the use of antisense molecules or knock out and knock in models may also be used in screening assays as discussed above, in addition to methods of treatment.

Thus, in one embodiment, methods of modulating lung cancer in cells or organisms are provided. In one embodiment, the methods comprise administering to a cell an anti-lung cancer antibody that reduces or eliminates the biological activity of an endogenous lung cancer protein. Alternatively, the methods comprise administering to a cell or organism a recombinant nucleic acid encoding a lung cancer protein. This may be accomplished in any number of ways. In a preferred embodiment, e.g., when the lung cancer sequence is down-regulated in lung cancer, such state may be reversed by increasing the amount of lung cancer gene product in the cell. This can be accomplished, e.g., by overexpressing the endogenous lung cancer gene or administering a gene encoding the lung cancer sequence, using known gene-therapy techniques. In a preferred embodiment, the gene therapy techniques include the incorporation of the exogenous gene using enhanced homologous recombination (EHR), e.g., as described in PCT/US93/03868, hereby incorporated by reference in its entirety. Alternatively, e.g., when the lung cancer sequence is up-regulated in lung cancer, the activity of the endogenous lung cancer gene is decreased, e.g., by the administration of a lung cancer antisense or RNAi nucleic acid.

In one embodiment, the lung cancer proteins of the present invention may be used to generate polyclonal and monoclonal antibodies to lung cancer proteins. Similarly, the lung cancer proteins can be coupled, using standard technology, to affinity chromatography columns. These columns may then be used to purify lung cancer antibodies useful for production, diagnostic, or therapeutic purposes. In a preferred embodiment, the antibodies are generated to epitopes unique to a lung cancer protein; that is, the antibodies show little or no cross-reactivity to other proteins. The lung cancer antibodies may be coupled to standard affinity chromatography columns and used to purify lung cancer proteins. The antibodies may also be used as blocking polypeptides, as outlined above, since they will specifically bind to the lung cancer protein.

30 **Methods of identifying variant lung cancer-associated sequences**

Without being bound by theory, expression of various lung cancer sequences is correlated with lung cancer. Accordingly, disorders based on mutant or variant lung cancer genes may be determined. In one embodiment, the invention provides methods for

identifying cells containing variant lung cancer genes, e.g., determining all or part of the sequence of at least one endogenous lung cancer genes in a cell. In a preferred embodiment, the invention provides methods of identifying the lung cancer genotype of an individual, e.g., determining all or part of the sequence of at least one lung cancer gene of the individual.

- 5 This is generally done in at least one tissue of the individual, and may include the evaluation of a number of tissues or different samples of the same tissue. The method may include comparing the sequence of the sequenced lung cancer gene to a known lung cancer gene, i.e., a wild-type gene.

10 The sequence of all or part of the lung cancer gene can then be compared to the sequence of a known lung cancer gene to determine if any differences exist. This can be done using known homology programs, such as Bestfit, etc. In a preferred embodiment, the presence of a difference in the sequence between the lung cancer gene of the patient and the known lung cancer gene correlates with a disease state or a propensity for a disease state, as outlined herein.

- 15 In a preferred embodiment, the lung cancer genes are used as probes to determine the number of copies of the lung cancer gene in the genome.

In another preferred embodiment, the lung cancer genes are used as probes to determine the chromosomal localization of the lung cancer genes. Information such as chromosomal localization finds use in providing a diagnosis or prognosis in particular when
20 chromosomal abnormalities such as translocations, and the like are identified in the lung cancer gene locus.

Administration of pharmaceutical and vaccine compositions

- 25 In one embodiment, a therapeutically effective dose of a lung cancer protein or modulator thereof, is administered to a patient. By "therapeutically effective dose" herein is meant a dose that produces effects for which it is administered. The exact dose will depend on the purpose of the treatment, and will be ascertainable by one skilled in the art using known techniques (e.g., Ansel, et al. (1992) Pharmaceutical Dosage Forms and Drug Delivery; Lieberman, Pharmaceutical Dosage Forms (vols. 1-3), Dekker, ISBN 0824770846,
30 082476918X, 0824712692, 0824716981; Lloyd (1999) The Art, Science and Technology of Pharmaceutical Compounding; and Pickar (1999) Dosage Calculations). Adjustments for lung cancer degradation, systemic versus localized delivery, and rate of new protease synthesis, as well as the age, body weight, general health, sex, diet, time of administration,

drug interaction and the severity of the condition may be necessary, and will be ascertainable with routine experimentation by those skilled in the art.

A "patient" for the purposes of the present invention includes both humans and other animals, particularly mammals. Thus the methods are applicable to both human therapy and veterinary applications. In the preferred embodiment the patient is a mammal, preferably a primate, and in the most preferred embodiment the patient is human.

The administration of the lung cancer proteins and modulators thereof of the present invention can be done in a variety of ways, including, but not limited to, orally, subcutaneously, intravenously, intranasally, transdermally, intraperitoneally, intramuscularly, intrapulmonary, vaginally, rectally, or intraocularly. In some instances, e.g., in the treatment of wounds and inflammation, the lung cancer proteins and modulators may be directly applied as a solution or spray.

The pharmaceutical compositions of the present invention comprise a lung cancer protein in a form suitable for administration to a patient. In the preferred embodiment, the pharmaceutical compositions are in a water soluble form, such as being present as pharmaceutically acceptable salts, which is meant to include both acid and base addition salts. "Pharmaceutically acceptable acid addition salt" refers to those salts that retain the biological effectiveness of the free bases and that are not biologically or otherwise undesirable, formed with inorganic acids such as hydrochloric acid, hydrobromic acid, sulfuric acid, nitric acid, phosphoric acid and the like, and organic acids such as acetic acid, propionic acid, glycolic acid, pyruvic acid, oxalic acid, maleic acid, malonic acid, succinic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, methanesulfonic acid, ethanesulfonic acid, p-toluenesulfonic acid, salicylic acid and the like. "Pharmaceutically acceptable base addition salts" include those derived from inorganic bases such as sodium, potassium, lithium, ammonium, calcium, magnesium, iron, zinc, copper, manganese, aluminum salts and the like. Particularly preferred are the ammonium, potassium, sodium, calcium, and magnesium salts. Salts derived from pharmaceutically acceptable organic non-toxic bases include salts of primary, secondary, and tertiary amines, substituted amines including naturally occurring substituted amines, cyclic amines and basic ion exchange resins, such as isopropylamine, trimethylamine, diethylamine, triethylamine, tripropylamine, and ethanolamine.

The pharmaceutical compositions may also include one or more of the following: carrier proteins such as serum albumin; buffers; fillers such as microcrystalline cellulose,

lactose, corn and other starches; binding agents; sweeteners and other flavoring agents; coloring agents; and polyethylene glycol.

The pharmaceutical compositions can be administered in a variety of unit dosage forms depending upon the method of administration. For example, unit dosage forms suitable for oral administration include, but are not limited to, powder, tablets, pills, capsules and lozenges. It is recognized that lung cancer protein modulators (e.g., antibodies, antisense constructs, ribozymes, small organic molecules, etc.) when administered orally, should be protected from digestion. This is typically accomplished either by complexing the molecule(s) with a composition to render it resistant to acidic and enzymatic hydrolysis, or by packaging the molecule(s) in an appropriately resistant carrier, such as a liposome or a protection barrier. Means of protecting agents from digestion are well known in the art.

The compositions for administration will commonly comprise a lung cancer protein modulator dissolved in a pharmaceutically acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers can be used, e.g., buffered saline and the like. These solutions are sterile and generally free of undesirable matter. These compositions may be sterilized by conventional, well known sterilization techniques. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions such as pH adjusting and buffering agents, toxicity adjusting agents and the like, e.g., sodium acetate, sodium chloride, potassium chloride, calcium chloride, sodium lactate and the like. The concentration of active agent in these formulations can vary widely, and will be selected primarily based on fluid volumes, viscosities, body weight and the like in accordance with the particular mode of administration selected and the patient's needs (e.g., Remington's Pharmaceutical Science (15th ed., 1980) and Hardman, et al. (eds. 1996) Goodman and Gilman: The Pharmacological Basis of Therapeutics).

Thus, a typical pharmaceutical composition for intravenous administration would be about 0.1 to 10 mg per patient per day. Dosages from 0.1 up to about 100 mg per patient per day may be used, particularly when the drug is administered to a secluded site and not into the blood stream, such as into a body cavity or into a lumen of an organ. Substantially higher dosages are possible in topical administration. Actual methods for preparing parenterally administrable compositions will be known or apparent to those skilled in the art, e.g., Remington's Pharmaceutical Science and Goodman and Gilman, The Pharmacological Basis of Therapeutics, *supra*.

The compositions containing modulators of lung cancer proteins can be administered for therapeutic or prophylactic treatments. In therapeutic applications, compositions are administered to a patient suffering from a disease (e.g., a cancer) in an amount sufficient to cure or at least partially arrest the disease and its complications. An amount adequate to accomplish this is defined as a "therapeutically effective dose." Amounts effective for this use will depend upon the severity of the disease and the general state of the patient's health. Single or multiple administrations of the compositions may be administered depending on the dosage and frequency as required and tolerated by the patient. In any event, the composition should provide a sufficient quantity of the agents of this invention to effectively treat the patient. An amount of modulator that is capable of preventing or slowing the development of cancer in a mammal is referred to as a "prophylactically effective dose." The particular dose required for a prophylactic treatment will depend upon the medical condition and history of the mammal, the particular cancer being prevented, as well as other factors such as age, weight, gender, administration route, efficiency, etc. Such prophylactic treatments may be used, e.g., in a mammal who has previously had cancer to prevent a recurrence of the cancer, or in a mammal who is suspected of having a significant likelihood of developing cancer based, at least in part, upon gene expression profiles. Vaccine strategies may be used, in either a DNA vaccine form, or protein vaccine.

It will be appreciated that the present lung cancer protein-modulating compounds can be administered alone or in combination with additional lung cancer modulating compounds or with other therapeutic agent, e.g., other anti-cancer agents or treatments.

In numerous embodiments, one or more nucleic acids, e.g., polynucleotides comprising nucleic acid sequences set forth in the tables, such as antisense or RNAi polynucleotides or ribozymes, will be introduced into cells, *in vitro* or *in vivo*. The present invention provides methods, reagents, vectors, and cells useful for expression of lung cancer-associated polypeptides and nucleic acids using *in vitro* (cell-free), *ex vivo*, or *in vivo* (cell or organism-based) recombinant expression systems.

The particular procedure used to introduce the nucleic acids into a host cell for expression of a protein or nucleic acid is application specific. Many procedures for introducing foreign nucleotide sequences into host cells may be used. These include the use of calcium phosphate transfection, spheroplasts, electroporation, liposomes, microinjection, plasma vectors, viral vectors and other well known methods for introducing cloned genomic DNA, cDNA, synthetic DNA or other foreign genetic material into a host cell (see, e.g.,

Berger and Kimmel, Guide to Molecular Cloning Techniques, Methods in Enzymology volume 152 (Berger), Ausubel, et al. (eds. 1999) Current Protocols (supplemented through 1999), and Sambrook, et al. (1989) Molecular Cloning - A Laboratory Manual (2nd ed., Vol. 1-3).

5 In a preferred embodiment, lung cancer proteins and modulators are administered as therapeutic agents, and can be formulated as outlined above. Similarly, lung cancer genes (including both the full-length sequence, partial sequences, or regulatory sequences of the lung cancer coding regions) can be administered in a gene therapy application. These lung cancer genes can include antisense or inhibitory applications, e.g., as inhibitory RNA or gene
10 therapy (e.g., for incorporation into the genome) or as antisense compositions.

Lung cancer polypeptides and polynucleotides can also be administered as vaccine compositions to stimulate HTL, CTL, and antibody responses.. Such vaccine compositions can include, e.g., lipidated peptides (see, e.g., Vitiello, et al. (1995) J. Clin. Invest. 95:341), peptide compositions encapsulated in poly(DL-lactide-co-glycolide) ("PLG") microspheres
15 (see, e.g., Eldridge, et al. (1991) Molec. Immunol. 28:287-294; Alonso, et al. (1994) Vaccine 12:299-306; Jones, et al. (1995) Vaccine 13:675-681), peptide compositions contained in immune stimulating complexes (ISCOMS) (see, e.g., Takahashi, et al. (1990) Nature 344:873-875; Hu, et al. (1998) Clin Exp Immunol. 113:235-243), multiple antigen peptide systems (MAPs) (see, e.g., Tam (1988) Proc. Natl. Acad. Sci. U.S.A. 85:5409-5413; Tam
20 (1996) J. Immunol. Methods 196:17-32), peptides formulated as multivalent peptides; peptides for use in ballistic delivery systems, typically crystallized peptides, viral delivery vectors (Perkus, et al., p. 379 In: Kaufmann (ed. 1996) Concepts in vaccine development; Chakrabarti, et al. (1986) Nature 320:535; Hu, et al. (1986) Nature 320:537; Kieny, et al. (1986) AIDS Bio/Technology 4:790; Top, et al. (1971) J. Infect. Dis. 124:148; Chanda, et al.
25 (1990) Virology 175:535), particles of viral or synthetic origin (see, e.g., Kofler, et al. (1996) J. Immunol. Methods 192:25; Eldridge, et al. (1993) Sem. Hematol. 30:16; Falo, et al. (1995) Nature Med. 7:649), adjuvants (Warren, et al. (1986) Annu. Rev. Immunol. 4:369; Gupta, et al. (1993) Vaccine 11:293), liposomes (Reddy, et al. (1992) J. Immunol. 148:1585; Rock (1996) Immunol. Today 17:131), or, naked or particle absorbed cDNA (Ulmer, et al. (1993) Science 259:1745; Robinson, et al. (1993) Vaccine 11:957; Shiver, et al., p. 423 In:
30 Kaufmann (ed. 1996) Concepts in vaccine development; Cease and Berzofsky (1994) Annu. Rev. Immunol. 12:923 and Eldridge, et al. (1993) Sem. Hematol. 30:16). Toxin-targeted

delivery technologies, also known as receptor mediated targeting, such as those of Avant Immunotherapeutics, Inc. (Needham, Massachusetts) may also be used.

Vaccine compositions often include adjuvants. Many adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, *Bordetella pertussis* or *Mycobacterium tuberculosis* derived proteins. Certain adjuvants are commercially available as, e.g., Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham, Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF, interleukin-2, -7, -12, and other like growth factors, may also be used as adjuvants.

Vaccines can be administered as nucleic acid compositions wherein DNA or RNA encoding one or more of the polypeptides, or a fragment thereof, is administered to a patient. This approach is described, for instance, in Wolff, et. al. (1990) Science 247:1465 as well as U.S. Patent Nos. 5,580,859; 5,589,466; 5,804,566; 5,739,118; 5,736,524; 5,679,647; WO 98/04720; and in more detail below. Examples of DNA-based delivery technologies include "naked DNA", facilitated (bupivacaine, polymers, peptide-mediated) delivery, cationic lipid complexes, and particle-mediated ("gene gun") or pressure-mediated delivery (see, e.g., U.S. Patent No. 5,922,687).

For therapeutic or prophylactic immunization purposes, the peptides of the invention can be expressed by viral or bacterial vectors. Examples of expression vectors include attenuated viral hosts, such as vaccinia or fowlpox. This approach involves the use of vaccinia virus, e.g., as a vector to express nucleotide sequences that encode lung cancer polypeptides or polypeptide fragments. Upon introduction into a host, the recombinant vaccinia virus expresses the immunogenic peptide, and thereby elicits an immune response. Vaccinia vectors and methods useful in immunization protocols are described in, e.g., U.S. Patent No. 4,722,848. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are described in Stover, et al. (1991) Nature 351:456-460. A wide variety of other vectors useful for therapeutic administration or immunization e.g., adeno and adeno-associated virus vectors, retroviral vectors, *Salmonella typhi* vectors, detoxified anthrax toxin vectors, and the

like, will be apparent to those skilled in the art from the description herein (see, e.g., Shata, et al. (2000) Mol Med Today 6:66-71; Shedlock, et al. (2000) J. Leukoc. Biol. 68:793-806; Hipp, et al. (2000) In Vivo 14:571-85).

Methods for the use of genes as DNA vaccines are well known, and include placing a lung cancer gene or portion of a lung cancer gene under the control of a regulatable promoter or a tissue-specific promoter for expression in a lung cancer patient. The lung cancer gene used for DNA vaccines can encode full-length lung cancer proteins, but more preferably encodes portions of the lung cancer proteins including peptides derived from the lung cancer protein. In one embodiment, a patient is immunized with a DNA vaccine comprising a plurality of nucleotide sequences derived from a lung cancer gene. For example, lung cancer-associated genes or sequence encoding subfragments of a lung cancer protein are introduced into expression vectors and tested for their immunogenicity in the context of Class I MHC and an ability to generate cytotoxic T cell responses. This procedure provides for production of cytotoxic T cell responses against cells which present antigen, including intracellular epitopes.

In a preferred embodiment, DNA vaccines include a gene encoding an adjuvant molecule with the DNA vaccine. Such adjuvant molecules include cytokines that increase the immunogenic response to the lung cancer polypeptide encoded by the DNA vaccine. Additional or alternative adjuvants are available.

In another preferred embodiment lung cancer genes find use in generating animal models of lung cancer. When the lung cancer gene identified is repressed or diminished in metastatic tissue, gene therapy technology, e.g., wherein antisense or inhibitory RNA directed to the lung cancer gene will also diminish or repress expression of the gene. Animal models of lung cancer find use in screening for modulators of a lung cancer-associated sequence or modulators of lung cancer. Similarly, transgenic animal technology including gene knockout technology, e.g., as a result of homologous recombination with an appropriate gene targeting vector, will result in the absence or increased expression of the lung cancer protein. When desired, tissue-specific expression or knockout of the lung cancer protein may be necessary.

It is also possible that the lung cancer protein is overexpressed in lung cancer. As such, transgenic animals can be generated that overexpress the lung cancer protein. Depending on the desired expression level, promoters of various strengths can be employed to express the transgene. Also, the number of copies of the integrated transgene can be determined and compared for a determination of the expression level of the transgene.

Animals generated by such methods will find use as animal models of lung cancer and are additionally useful in screening for modulators to treat lung cancer.

Kits for Use in Diagnostic and/or Prognostic Applications

5 For use in diagnostic, research, and therapeutic applications suggested above, kits are also provided by the invention. In diagnostic and research applications such kits may include at least one of the following: assay reagents, buffers, lung cancer-specific nucleic acids or antibodies, hybridization probes and/or primers, antisense polynucleotides, ribozymes, RNAi, dominant negative lung cancer polypeptides or polynucleotides, small molecule inhibitors of
10 lung cancer-associated sequences, etc. A therapeutic product may include sterile saline or another pharmaceutically acceptable emulsion and suspension base.

 In addition, the kits may include instructional materials containing instructions (e.g., protocols) for the practice of the methods of this invention. While the instructional materials typically comprise written or printed materials they are not limited to such. A medium
15 capable of storing such instructions and communicating them to an end user is contemplated by this invention. Such media include, but are not limited to electronic storage media (e.g., magnetic discs, tapes, cartridges, chips), optical media (e.g., CD ROM), and the like. Such media may include addresses to internet sites that provide such instructional materials.

 The present invention also provides for kits for screening for modulators of lung
20 cancer-associated sequences. Such kits can be prepared from readily available materials and reagents. For example, such kits can comprise one or more of the following materials: a lung cancer-associated polypeptide or polynucleotide, reaction tubes, and instructions for testing lung cancer-associated activity. Optionally, the kit contains biologically active lung cancer protein. A wide variety of kits and components can be prepared according to the present
25 invention, depending upon the intended user of the kit and the particular needs of the user. Diagnosis would typically involve evaluation of a plurality of genes or products. The genes typically will be selected based on correlations with important parameters in disease which may be identified in historical or outcome data.

EXAMPLES

Example 1: Gene Chip Analysis

5 Molecular profiles of various normal and cancerous tissues were determined and analyzed using gene chips. RNA was isolated and gene chip analysis was performed as described (Glynne, et al. (2000) Nature 403:672-676; Zhao, et al. (2000) Genes Dev. 14:981-993).

Tables 1A and 1B were previously filed on April 18, 2001 in USSN 60/284,770 (18501-001500US) and on November 29, 2001 in USSN 60/334,370 (18501-001520US)

5	Table 1A					
	Pkey	ExAccn	UnigenelD	Unigene Title	70% chron/90% NL	70% SQUAD/90% NL
	100134	D13264	Hs.49	macrophage scavenger receptor 1	1.61	0.74
	100780	HG3731-HT4001		***Immunoglobulin Heavy Chain, VdJrc Reg	2.68	3.28
	100971	J02874	Hs.83213	fatty acid binding protein 4; adipocyte	1.96	0.14
10	101088	L05568	Hs.553	solute carrier family 6 (neurotransmitter)	0.79	0.07
	101102	L07594	Hs.79059	transforming growth factor; beta receptor	2.55	1
	101168	L15388	Hs.211569	G protein-coupled receptor kinase 5	0.88	0.27
	101277	L38486	Hs.118223	microfibrillar-associated protein 4	0.89	0.26
	101330	L43821	Hs.80261	enhancer of filamentation 1 (cas-like do	0.59	0.29
15	101336	L49169	Hs.75678	FBJ murine osteosarcoma viral oncogene h	1.15	0.41
	101345	L76380	Hs.152175	calcitonin receptor-like	0.81	0.31
	101678	M62505	Hs.2161	complement component 5 receptor 1 (C5a1	1.31	0.77
	101764	M80563	Hs.81256	S100 calcium-binding protein A4 (calcium	1.44	0.82
	101771	M81750	Hs.153837	myeloid cell nuclear differentiation ant	0.96	0.45
20	101842	M93221	Hs.75182	mannose receptor; C type 1	1.27	0.37
	102283	U31384	Hs.83381	guanine nucleotide binding protein 11	1.04	0.3
	102363	U39447	Hs.198241	amine oxidase; copper containing 3 (vasc	0.96	0.26
	102507	U52154	Hs.193044	potassium inwardly-rectifying channel; s	2.81	3.45
	102698	U75272	Hs.1867	progastricsin (pepsinogen C)	0.95	0.23
25	103025	X54131	Hs.123641	protein tyrosine phosphatase; receptor t	1.62	0.21
	103280	X79981	Hs.76206	cadherin 5; VE-cadherin (vascular epithe	0.9	0.41
	103496	Y09267	Hs.132821	flavin containing monooxygenase 2	1.27	0.49
	103541	Z11697	Hs.79197	CD83 antigen (activated B lymphocytes; l	1.86	1
	103554	Z18951	Hs.74034	caveolin 1; caveolae protein; 22kD	1.27	0.47
30	104212	AB002298	Hs.173035	KIAA0300 protein	1.17	0.16
	104691	AA011176	Hs.37744	ESTs	1.08	0.35
	104825	AA035613	Hs.141883	ESTs	0.75	0.27
	104857	AA043219	Hs.19058	ESTs	2.6	3.3
	104865	AA045136	Hs.22575	ESTs	1.23	0.49
35	104989	AA102098	Hs.118615	ESTs	0.63	0.32
	105729	AA292694	Hs.3807	ESTs; Weakly similar to PHOSPHOLEMMAN PR	0.86	0.34
	105847	AA398606	Hs.32241	ESTs	1.32	0.4
	105894	AA400979	Hs.25691	calcitonin receptor-like receptor activi	0.78	0.28
	106490	AA451861	Hs.115537	ESTs; Weakly similar to dipeptidase prec	1.2	0.47
40	106536	AA453997	Hs.23804	ESTs	0.82	0.15
	106605	AA457718	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (fr	0.99	0.07
	106667	AA461086	Hs.16578	ESTs	1.17	0.4
	106773	AA478109	Hs.188833	ESTs	1.46	0.43
	106797	AA478962	Hs.169943	ESTs	1.18	0.32
45	106844	AA485055	Hs.158213	sperm associated antigen 6	0.98	0.51
	106870	AA487576	Hs.26530	serum deprivation response (phosphatidyl)	1.05	0.14
	106954	AA496980	Hs.204038	ESTs	1.25	0.33
	107054	AA600150	Hs.14366	ESTs	1.11	0.4
	107292	T30407	Hs.4789	ESTs; Weakly similar to oxidative-stress	1.07	2.58
50	107994	AA036811	Hs.165030	ESTs	0.7	0.21
	107997	AA037388	Hs.82223	Human DNA sequence from clone 141H5 on c	1.02	0.48
	108041	AA041552	Hs.61957	ESTs	1.44	0.51
	108087	AA045709	Hs.40545	ESTs	1.98	1
	108382	AA074885	Hs.67726	macrophage receptor with collagenous str	1.52	0.72
55	108435	AA078787	Hs.194101	ESTs	2.53	1.53
	108480	AA081093	Hs.68055	ESTs	1.56	0.48
	109252	AA194830	Hs.85944	ESTs	2.69	3.18
	109550	F01534	Hs.26981	ESTs	1.19	0.65
	109613	F03031	Hs.27519	ESTs	1.01	0.29
60	109837	H00656	Hs.29792	ESTs	0.81	0.15
	109893	H04768	Hs.30484	ESTs	1.44	0.32
	109984	H09594	Hs.10299	ESTs	0.62	0.14
	110099	H16568	Hs.23748	ESTs	1.01	0.28
	110837	N30796	Hs.17424	ESTs; Weakly similar to semaphorin F [H.	1.1	0.22
65	111247	N69825	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	1.26	0.26
	111341	N80935	Hs.22483	ESTs	1.57	0.52
	111510	R07856	Hs.16355	ESTs	3.96	1
	111737	R25410	Hs.9218	ESTs	0.97	0.24
	113195	T57112		***yc20g11.s1 Stratagene lung (#937210)	1.22	0.35
70	113238	T62979	Hs.189813	ESTs	2.27	0.45
	113540	T90496	Hs.16757	ESTs	1.06	0.22
	113552	T90889	Hs.16026	ESTs	1.16	0.42
	113606	T93093	Hs.17125	ESTs	1.48	0.7
	113695	T96965	Hs.17948	ESTs	1.54	0.28
75	113946	W84753	Hs.37896	ESTs	1.79	0.72
	114251	Z39898	Hs.21948	ESTs	1.95	0.25
	114359	Z41589	Hs.153483	ESTs; Moderately similar to H1 chloride	1.42	0.13
	115230	AA278300	Hs.182980	ESTs	2.62	0.42
	115279	AA279760	Hs.63671	ESTs	1.79	0.91
80	115566	AA398083	Hs.43977	ESTs	0.86	0.2
	115965	AA446661	Hs.173233	ESTs	0.79	0.04
	116166	AA461556	Hs.202949	KIAA1102 protein	2.29	0.68
	116279	AA486073	Hs.57362	ESTs	2.27	0.78
	117023	H88157	Hs.41105	ESTs	1.36	0.16

	117209	H99959	Hs.42768	ESTs	1.46	0.48
	118901	N90719	Hs.94445	ESTs	1.51	1
	118981	N93839	Hs.39288	ESTs	1.34	0.48
5	119073	R32894	Hs.45514	v-ets avian erythroblastosis virus E26 o	1.14	0.27
	119221	R98105		***yr30g11.s1 Soares fetal liver spleen	1.32	0.53
	119824	W74536	Hs.184	advanced glycosylation end product-speci	1	0.19
	119861	W80715		ESTs; Moderately similar to !!!! ALU SUB	1.83	0.45
	120041	W92775	Hs.59368	ESTs	1.23	0.55
10	120132	Z38839	Hs.125019	ESTs; Highly similar to KIAA0886 protein	0.91	0.37
	120467	AA251579	Hs.187628	ESTs	1.87	1.91
	121314	AA402799	Hs.182538	ESTs	1.3	0.31
	121643	AA417078	Hs.193767	ESTs	2.31	0.68
	121690	AA418074	Hs.110286	ESTs	1.47	0.51
15	122633	AA454080	Hs.34853	inhibitor of DNA binding 4; dominant neg	1.31	0.63
	123978	C20653	Hs.170278	ESTs	1.52	0.32
	124214	H58608	Hs.151323	ESTs	0.93	0.35
	124357	N22401		***yw37g07.s1 Morton Fetal Cochlea Homo	1.29	1
	124438	N40188	Hs.102550	ESTs	1.36	0.7
20	125167	W45560	Hs.102541	ESTs	1.46	0.69
	125174	W51835	Hs.231082	EST	3.07	3.76
	125422	AA903229	Hs.153717	ESTs	1.34	0.3
	125561	AJ417667	Hs.22978	ESTs	1.89	0.63
	125831	D60988		***HUM145B09B Clontech human fetal brain	0.94	0.36
25	127002	R35380	Hs.24979	ESTs	3.02	4.06
	127307	AA369367	Hs.126712	ESTs; Weakly similar to pL2 hypothetica	1.01	0.69
	127609	AA622559	Hs.150318	ESTs	1.21	0.32
	127959	AJ302471	Hs.124292	ESTs	2.5	1
	128458	D52193	Hs.56340	ESTs	1.13	0.33
30	128624	AA479209	Hs.102647	ESTs	1.45	0.58
	128789	AA486567	Hs.105695	ESTs	1.1	0.34
	128798	AF014958	Hs.105938	chemokine (C-C motif) receptor-like 2	1.16	0.55
	128952	R51076	Hs.107361	ESTs; Highly similar to Rap2 interacting	2.04	2.4
	129057	X62466	Hs.214742	CDW52 antigen (CAMPATH-1 antigen)	1.77	0.73
35	129210	AA401654	Hs.202949	KIAA1102 protein	1.11	0.36
	129240	W24360	Hs.237868	Interleukin 7 receptor	0.91	0.41
	129402	T63781		***yc21g01.s1 Stratagene lung (#937210)	1.36	0.43
	129565	X77777	Hs.198726	vasoactive intestinal peptide receptor 1	0.67	0.08
	129593	AA487015	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (f	1.3	0.42
40	129626	AA447410	Hs.11712	ESTs; Weakly similar to !!!! ALU SUBFAM	1.28	0.46
	129699	AA458578	Hs.12017	KIAA0439 protein; homolog of yeast ublqu	1.58	1
	129898	N48595	Hs.13256	ESTs	1.13	0.53
	129958	L20591	Hs.1378	annexin A3	0.81	0.31
45	130273	U59914	Hs.153863	MAD (mothers against decapentaplegic; Dr	0.59	0.22
	130655	N92934	Hs.17409	cysteine-rich protein 1 (Intestinal)	1.44	0.76
	130657	T94452	Hs.201591	ESTs	0.96	0.42
	131061	N64328	Hs.22567	ESTs; Moderately similar to HYPOTHETICAL	1.51	0.45
	131066	F09006	Hs.22588	ESTs	0.97	0.37
	131263	R38334	Hs.24950	regulator of G-protein signalling 5	2.34	2.82
50	131589	U52100	Hs.29191	epithelial membrane protein 2	1.2	0.62
	131686	AA157428	Hs.30687	Grb2-associated binder 2	0.95	0.38
	131751	H18335	Hs.31562	ESTs	1.47	0.52
	132430	T23630	Hs.258675	EST	1.86	2.09
	132476	N67192	Hs.49476	Homo sapiens clone TUA8 Cri-du-chat regi	1.73	0.58
55	132836	F09557	Hs.57929	slit (Drosophila) homolog 3	0.91	0.29
	133120	X64559	Hs.65424	tetranectin (plasminogen-binding protein	0.82	0.2
	133488	D45370	Hs.74120	adipose specific 2	1.29	0.48
	133565	H57056	Hs.204831	ESTs	2.25	0.57
	133651	U97105	Hs.173381	dihydropyrimidinase-like 2	1.65	0.62
60	133835	AA059489	Hs.76640	ESTs; Highly similar to RGC-32 [R.norveg	1.16	0.34
	133978	W73859	Hs.78061	transcription factor 21	0.79	0.27
	133985	L34657	Hs.78146	platelet/endothelial cell adhesion molec	0.99	0.28
	134299	AA487558	Hs.8135	ESTs	1.02	0.46
	134300	U81984	Hs.166082	endothelial PAS domain protein 1	0.86	0.42
65	134323	AA028976	Hs.8175	Homo sapiens mRNA; cDNA DKFZp564M0763 (f	1.19	0.27
	134343	D50683	Hs.82028	transforming growth factor; beta recepto	1.21	0.67
	134417	D87969	Hs.82921	solute carrier family 35 (CMP-sialic aci	1.28	1
	134561	U76421	Hs.85302	adenosine deaminase; RNA-specific; B1 (h	2.12	0.55
	134624	W67147	Hs.8700	deleted in liver cancer 1	2.35	2.74
70	134696	H88354	Hs.8861	ESTs	1.35	0.33
	134749	L10955	Hs.89485	carbonic anhydrase IV	0.89	0.2
	134786	L06139	Hs.89640	TEK tyrosine kinase; endothelial (venous	0.48	0.21
	134869	T35288	Hs.90421	ESTs; Moderately similar to !!!! ALU SUB	2.14	2.64
	135346	M21056	Hs.992	phospholipase A2; group IB (pancreas)	0.63	0.13
75	100113	D00591	Hs.84746	Chromosome condensation 1	1	2.15
	100147	D13666	Hs.136348	Homo sapiens mRNA for osteoblast specifi	0.5	2
	100280	D42085	Hs.155314	KIAA0095 gene product	1.02	1.39
	100335	D63391	Hs.6793	platelet-activating factor acetylhydrola	1	5.58
	100360	D78335	Hs.75939	Uridine monophosphate kinase	0.91	2.04
80	100372	D79997	Hs.184339	KIAA0175 gene product	0.75	2.03
	100486	HG1112-HT1112		TIGR: ras-like protein TC4	1.09	1.93
	100559	HG2197-HT2267		*collagen, type VII, alpha 1*	0.97	3.6
	100576	HG2290-HT2386		*calitonin/alpha-CGRP, alt. transcript	1	1
	100668	HG2981-HT3938		*TIGR: CD44 (epican, alt. transcript 12	0.85	1.9
85	100906	HG4716-HT5158		Guanosine 5'-Monophosphate Synthase	1.18	2.29
	100930	HG721-HT4827		*TIGR: placental protein 14, endometrial	1	1.45

	100960	J00124	Hs.117729	keratin 14 (epidermolysis bullosa simple	0.84	2.6
	101031	J05070	Hs.151738	*Matrix metalloproteinase 9 (gelatinase	0.77	1.52
	101111	L08424	Hs.1619	Achaete-scute complex (Drosophila) homol	1	1
5	101124	L10343	Hs.112341	*Protease inhibitor 3, skin-derived (SKA	0.62	2.67
	101175	L18920	Hs.36980	*Melanoma antigen, family A, 2"	1	1
	101204	L24203	Hs.82237	Ataxia-telangiectasia group D-associated	0.74	4.1
	101431	M19888	Hs.1076	Small proline-rich protein 1B (comifin)	0.85	2.51
	101448	M21389	Hs.195850	keratin 5 (epidermolysis bullosa simplex	0.61	8.83
10	101511	M27826	Hs.267319	Endogenous retroviral protease	1.03	1.13
	101526	M29540	Hs.220529	Carcinoembryonic antigen-related cell ad	1.07	4.61
	101548	M31328	Hs.71642	*Guanine nucleotide binding protein (G p	0.97	1.13
	101625	M57293		*Human parathyroid hormone-related pepti	1	1
	101649	M60047	Hs.1690	Heparin-binding growth factor binding pr	1	2.7
	101724	M69225	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	1	8.98
15	101748	M76482	Hs.1925	Desmoglein 3 (pemphigus vulgaris antigen	1	2.78
	101759	M80244	Hs.184601	*Solute carrier family 7 (cationic amino	1.07	2.45
	101804	M86699	Hs.169840	TTK protein kinase	1	1
	101806	M86757	Hs.112408	S100 calcium-binding protein A7 (psorias	0.74	1.76
20	101809	M86849		*Homo sapiens connexin 26 (GJB2) mRNA, c	1	7
	101845	M93426	Hs.78867	*Protein tyrosine phosphatase, receptor-	1	1
	101851	M94250	Hs.82045	Midkine (neurite growth-promoting factor	1.13	2.6
	102083	U10323	Hs.75117	*Interleukin enhancer binding factor 2,	1.03	1.61
	102154	U17760	Hs.75517	*Laminin, beta 3 (nicein (125kD), kalini	0.94	3.62
25	102193	U20758	Hs.313	secreted phosphoprotein 1 (osteopontin;	0.34	4.59
	102305	U33286	Hs.90073	chromosome segregation 1 (yeast homolog)	1.45	2.97
	102348	U37519	Hs.87539	Aldehyde dehydrogenase 8	0.52	2.25
	102581	U61145	Hs.77256	Enhancer of zeste (Drosophila) homolog 2	0.91	2.46
	102610	U65011	Hs.30743	Preferentially expressed antigen in mela	1	3.88
30	102623	U66083	Hs.37110	*Melanoma antigen, family A, 9 (MAGE-9)"	1	1
	102669	U71207	Hs.29279	Eyes absent (Drosophila) homolog 2	1	1
	102696	U74612	Hs.239	Forkhead box M1	1.06	2.77
	102829	U91618	Hs.80962	Neurotensin	1	1
	102888	X04741	Hs.76118	Ubiquitin carboxyl-terminal esterase L1	1.13	2.59
35	102913	X07696	Hs.80342	keratin 15	0.7	4.72
	102915	X07820	Hs.2258	Matrix Metalloproteinase 10 (Stromolysin	1.15	3.35
	102963	X15943	Hs.37058	*Calcitonin/calcitonin-related polypepti	1	1
	103021	X53587	Hs.85266	*Integrin, beta 4"	1.38	2.34
	103036	X54925	Hs.83169	Matrix metalloproteinase 1 (interstitial c	1	14.93
40	103058	X57348	Hs.184510	Stratiferin	1.25	4.17
	103060	X57766	Hs.155324	matrix metalloproteinase 11 (stromelysin	1	1.72
	103119	X63629	Hs.2877	*Cadherin 3, P-cadherin (placental)"	1.16	7.38
	103206	X72755	Hs.77367	monokine induced by gamma interferon	0.71	1.48
	103242	X76342	Hs.389	*Alcohol dehydrogenase 7 (class IV), mu	1	1
45	103312	X82693	Hs.3185	*Lymphocyte antigen 6 complex, locus D;	0.92	1.28
	103478	Y07755	Hs.38991	S100 calcium-binding protein A2	1.05	5.81
	103558	Z19574	Hs.2785	keratin 17	0.65	6.68
	103576	Z26317	Hs.2631	Desmoglein 2	0.79	1.73
	103587	Z29083	Hs.82128	5T4 Oncofetal antigen	1	3.93
50	103594	Z31560	Hs.816	*SRY (sex determining region Y)-box 2, p	0.71	7.23
	103768	AA089997		*ESTs, Highly similar to integral membra	0.99	1.8
	104158	AA454908	Hs.8127	KIAA0144 gene product	0.96	1.29
	104558	R56678	Hs.88959	Human DNA sequence from clone 967N21 on	1.23	7.23
	104689	AA010665		ESTs	0.96	2.11
55	104733	AA019498	Hs.23071	ESTs	1.18	1.88
	104906	AA055809	Hs.26802	Protein kinase domains containing protei	1.11	3.15
	104978	AA088458	Hs.19322	ESTs; Weakly similar to III ALU SUBFAMI	1.64	2.89
	105012	AA116036	Hs.9329	*Homo sapiens mRNA for fls353, complete	1.19	3.91
	105175	AA186804	Hs.25740	ESTs; Weakly similar to unknown [S.cerev	0.9	4.63
60	105263	AA227926	Hs.6682	ESTs	0.95	2.87
	105298	AA233459	Hs.26369	ESTs	1	1.13
	105312	AA233854	Hs.23348	S-phase kinase-associated protein 2 (p45	1.32	3.01
	105719	AA291644	Hs.36793	Hypothetical protein FLJ23188	1.28	2.31
	105743	AA293300	Hs.9598	ESTs	1	1
65	106012	AA411621	Hs.8895	ESTs; same as BFH67	0.94	2.04
	106231	AA429571	Hs.38002	KIAA1355 protein	1.04	1.5
	106540	AA454607	Hs.38114	Hypothetical protein FLJ11100	1.26	2.26
	106575	AA456039	Hs.105421	ESTs	1	2
	106632	AA459897	Hs.11950	GPI-anchored metastasis-associated prote	0.87	1.32
70	106727	AA465342	Hs.34045	Hypothetical protein FLJ20764	0.87	1.59
	106908	AA490237	Hs.222024	Transcription factor BMAL2 (cycle-like f	0.61	1.6
	107059	AA608545	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	0.48	2.67
	107104	AA609786	Hs.15243	Nucleolar protein 1 (120kD)	1.01	1.44
	107151	AA621169	Hs.8687	ESTs; procollagen I-N proteinase	0.97	2.89
75	107284	S74039	Hs.291904	Accessory proteins BAP31/BAP29	1.15	3.65
	107901	AA026418	Hs.91539	ESTs	0.72	3.44
	107922	AA028028	Hs.61460	Ig superfamily receptor LNIR precursor	1	2.48
	107932	AA029317	Hs.18878	Hypothetical protein FLJ21620	1	1
	108695	AA121315	Hs.70823	KIAA1077 protein	0.91	3.53
80	108857	AA133250	Hs.62180	ESTs	1	1
	108860	AA133334	Hs.129911	ESTs	0.73	7.3
	108990	AA152296	Hs.72045	ESTs	1	1
	109166	AA179845	Hs.73625	*RAB6 interacting, kinesin-like (rabkine	1	4.55
	109424	AA227919	Hs.85962	Hyaluronan synthase 3	1	1.28
85	109665	F05012	Hs.27027	Hypothetical protein DKFZp762H1311	1.42	2
	109970	H09281	Hs.13234	ESTs	1.13	2.16

	110015	H10998	Hs.7164	A disintegrin and metalloproteinase doma	0.84	1.95
	110156	H18957	Hs.4213	ESTs	0.94	1.41
	110561	H59617	Hs.5199	HSPC150 protein similar to ubiquitin-con	0.91	3.18
5	111223	N68921	Hs.34806	ESTs; Weakly similar to neogenin [H.sapi	0.91	3.13
	111345	N89820	Hs.14559	Hypothetical protein FLJ10540	1	1.25
	111876	R38239	Hs.293246	*ESTs, Weakly similar to putative p150 [0.83	1.27
	111902	R39191	Hs.109445	KIAA1020 protein	0.91	0.91
	112244	R51309	Hs.70823	KIAA1077 protein	0.77	3.01
10	112973	T17271		*cDNA FLJ13308 fis, clone OVARC1001436,	1	1
	112989	T23482	Hs.89981	*Diacylglycerol kinase, zeta (104kD)*	0.55	1.03
	113047	T25867	Hs.7549	ESTs	0.87	2
	113095	T40920	Hs.126733	ESTs	1	1
	113531	T90345	Hs.16740	Hypothetical protein FLJ11036	0.42	1.44
	113970	W86748	Hs.8109	ESTs	1.17	1.73
15	114346	Z41450	Hs.130489	*ATPase, aminophospholipid transporter-I	0.86	0.82
	114407	AA010188	Hs.103305	ESTs	0.8	1.88
	114471	AA028074	Hs.104613	RP42 homolog	1.06	1.34
	114509	AA043551	Hs.101799	KIAA1350 protein	1.82	2.32
20	115060	AA253214	Hs.198249	*Gap junction protein, beta 5 (connexin	0.79	1.49
	115091	AA255900	Hs.184523	KIAA0965 protein	0.72	1.92
	115123	AA256642	Hs.236894	*ESTs, High sim to LRP1_hu low density I	0.59	1.97
	115291	AA279943	Hs.122579	ESTs	1	1.25
	115506	AA292537	Hs.45207	Hypothetical protein KIAA1335	1.15	1.48
25	115522	AA331393	Hs.47378	ESTs	0.5	3.29
	115536	AA347193	Hs.62180	ESTs	1	1
	115697	AA411502	Hs.63325	Homo sapiens type II membrane serine pro	1	6.53
	115909	AA436666	Hs.59761	ESTs	1	6.98
	115978	AA447522	Hs.69517	Differentially expressed in Fanconi anem	1	2.31
30	116028	AA452112	Hs.42644	thioredoxin-like	0.99	1.68
	116107	AA456968	Hs.92030	ESTs	1.14	1.8
	116134	AA460246	Hs.50441	CGI-04 protein	1.11	1.86
	116157	AA461063	Hs.44298	Hypothetical protein	0.99	1.9
	116158	AA461187	Hs.61762	Hypoxia-inducible protein 2	0.44	0.86
35	116335	AA495830	Hs.87013	*Homo sapiens cDNA FLJ10238 fis, clone H	0.62	3.89
	116483	C14092	Hs.76118	Ubiquitin carboxyl-terminal esterase L1	1.04	2.36
	117320	N23239	Hs.211092	LUNX protein; PLUNC(palate lung & nasal	0.51	0.64
	117557	N33920	Hs.44532	Diubiquitin	1.11	2.63
	117693	N40939	Hs.112110	PTD007 protein	0.98	1.79
40	117881	N50073	Hs.260622	Butyrate-induced transcript 1	1	1.43
	118368	N64339	Hs.48956	ESTs	0.67	2.86
	118566	N68558	Hs.42824	Hypothetical protein FLJ10718	1.21	0.83
	118695	N71781	Hs.50081	KIAA1199 see CVA7.doc	0.88	1.63
	119780	W72967	Hs.191381	ESTs; Weakly similar to hypothetical pro	1	1
45	119845	W79920	Hs.58561	G protein-coupled receptor 87	1	1
	120102	W95428	Hs.132927	*ESTs, Moderately similar to p53 regulat	1	1
	120104	W95477	Hs.180479	ESTs	0.69	3.07
	120486	AA253400	Hs.137569	Tumor protein 63 kDa with strong homolog	1.08	12.05
50	120859	AA350158	Hs.1619	Achaete-scute complex (Drosophila) homol	1	1
	120880	AA360240	Hs.97019	EST	1	1
	120948	AA397822	Hs.104650	Hypothetical protein FLJ10292	1.04	2.15
	120983	AA398209	Hs.97587	EST	1	1
	121362	AA405500	Hs.97932	Chondromodulin I precursor	1	1
	121369	AA405657	Hs.128791	CGI-09 protein	1	1.8
55	121791	AA423978	Hs.293317	*ESTs, Weakly similar to JM27 [H.sapiens	1	1
	123005	AA479726	Hs.105577	ESTs	1	1
	123044	AA481549	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro	0.95	1.88
	123160	AA488687	Hs.284235	ESTs	1.59	4.98
	123479	AA599469	Hs.135056	clone RP5-850E9 on chromosome 20	1.19	1.64
60	123571	AA608956	Hs.112619	*ESTs, Weakly similar to PQ0109 Purkinje	1.03	1.14
	123829	AA620697	Hs.112208	XAGE-1 protein	1.39	2.2
	124006	D60302	Hs.108977	ESTs	1	4.85
	124059	F13673	Hs.99769	ESTs	1.49	8.62
	124960	T15386	Hs.194766	Seizure related gene 6 (mouse)-like	0.76	0.77
65	125218	W73561	Hs.110024	NADH:ubiquinone oxidoreductase MLRQ subu	1.33	1.77
	125453	R05041	Hs.18048	*Melanoma antigen, family A, 10*	0.8	1.42
	125759	AA425587	Hs.82226	Glycoprotein (transmembrane) nmb	1.52	2.26
	125972	AA434562	Hs.35406	*ESTs, Highly similar to unnamed protein	1.05	2.48
	125994	H55782	Hs.270799	EST	1	1.95
70	126395	N70192	Hs.278956	Hypothetical protein FLJ12929	1	1.35
	126645	AI167942	Hs.61635	STEAP1 (Homo sapiens BAC clone RG041D11	1	2.23
	127221	AI354332	Hs.72365	ESTs	0.73	3.27
	127479	AA513722	Hs.179729	collagen; type X; alpha 1 (Schmid metaph	0.51	1.94
	128192	AI204246		KIAA1085 protein	1.8	3.16
75	128610	L38608	Hs.10247	activated leucocyte cell adhesion molecu	0.89	0.97
	128777	U46006	Hs.10526	Cysteine and glycine-rich protein 2	1	1
	128924	AA234962	Hs.26557	Plakophilin 3	1.3	2.97
	129041	H58873	Hs.169902	*Solute carrier family 2 (facilitated gl	0.84	2.04
	129099	H50398	Hs.108660	*ATP-binding cassette, sub-family C (CFT	0.87	1.04
80	129404	AA172056	Hs.111128	ESTs	1	1
	129466	L42583		*Genbank Homo sapiens keratin 6 isoform	0.72	12.67
	129605	S72493	Hs.115947	Keratin 16 (focal non-epidermolytic palm	0.92	1.5
	129628	U26727	Hs.1174	*Cyclin-dependent kinase inhibitor 2A (m	0.85	1.93
	130023	X13461	Hs.239600	Calmodulin-like 3	0.84	1.22
	130080	X14850	Hs.147097	*H2A histone family, member X*	0.98	1.96
85	130385	AA126474	Hs.155223	stanniocalcin 2	1	1

	130410	V01514	Hs.155421	Alpha-fetoprotein	0.63	0.63
	130441	U35835	Hs.301387	"Human DNA-PK mRNA, partial cds"	1.15	3.65
	130482	L32866	Hs.1578	Baculoviral IAP repeat-containing 5 (sur	1	1.88
5	130553	AA430032	Hs.252587	Pituitary tumor-transforming 1	0.92	1.96
	130577	M35410	Hs.162	Insulin-like growth factor binding prote	1.17	4.7
	130627	L23808	Hs.1695	Matrix metalloproteinase 12 (macrophage	0.69	4.05
	130800	AA223386	Hs.19574	ESTs; Weakly similar to katanin p80 subu	1.13	2.41
	130939	AA598689	Hs.21400	ESTs	0.8	0.89
10	131046	X02530	Hs.2248	INTERFERON-GAMMA INDUCED PROTEIN PRECURS	0.8	1.15
	131244	D38076	Hs.24763	RAN binding protein 1	1.13	1.85
	131877	J04088	Hs.156346	Topoisomerase (DNA) II alpha (170kD)	1	1
	131927	AA461549	Hs.34780	"Doublecortin; lissencephaly, X-linked (0.81	0.62
	131965	W90146	Hs.35962	ESTs	0.74	3.27
	131978	D80008	Hs.36232	KIAA0186 gene product	1	1
15	132354	L05187	Hs.211913	Small proline-rich protein 1A	0.69	1.43
	132543	AA417152	Hs.5101	ESTs; Highly similar to protein regulati	0.79	4.27
	132632	N59764	Hs.5398	guanine-monophosphate synthetase	1	1.08
	132653	U31201	Hs.54451	"laminin gamma2 chain gene (LAMC2), exon	1	1
20	132659	Z75190	Hs.54481	"Low density lipoprotein receptor-relate	0.89	0.89
	132710	W93726	Hs.55279	"Serine (or cysteine) proteinase inhibit	0.64	4.41
	132758	W52432	Hs.56105	"ESTs, Weakly similar to WDNM RAT WDNM1	1.55	2.08
	132767	L05188	Hs.231622	Small proline-rich protein 2B	0.83	1.66
	132816	M74542	Hs.575	Aldehyde dehydrogenase 3	0.55	0.55
25	132990	AA458761	Hs.18387	transcription factor AP-2 alpha (activat	1	3.53
	133070	U69611	Hs.64311	"A disintegrin and metalloproteinase dom	1.16	2
	133282	U52960	Hs.286145	"SRB7 (suppressor of RNA polymerase B, y	1	2.7
	133317	AA215299	Hs.70830	U6 snRNA-associated Sm-like protein LSm7	0.95	1.42
	133370	AA156897	Hs.72157	Homo sapiens mRNA; cDNA DKFZp564I1922	1.12	2.55
30	133391	X57579	Hs.727	H.sapiens activin beta-A subunit (exon 2	1.65	1.76
	133832	H03387	Hs.241305	estrogen-responsive B box protein (EBBP)	1.02	1.39
	134032	Z81326	Hs.78589	"Serine (or cysteine) proteinase inhibit	1	1
	134168	AA398908	Hs.181634	"Homo sapiens cDNA: FLJ23602 fis, clone	0.95	1.53
	134218	AA227480	Hs.80205	Pim-2 oncogene	1.36	2.48
35	134405	R67275	Hs.82772	***collagen, type XI, alpha 1***	0.76	2.86
	134453	X70683	Hs.83484	SRY (sex determining region Y)-box 4	1.89	3.78
	134470	X54942	Hs.83758	CDC28 protein kinase 2	1.82	4.11
	134645	U87459	Hs.167379	"Cancer/testis antigen (NY-ESO-1, CTAG1,	0.82	0.83
	134781	M17183	Hs.89626	Parathyroid hormone-like hormone	1	1
40	135002	U19147	Hs.272484	G antigen 6	1	1
	100040	M97935		AFFX control: STAT1	0.92	1.25
	101201	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin;	2.92	8.5
	101664	M60752	Hs.121017	H2A histone family; member A	1	1
	102025	U03911	Hs.78934	mutS (E. coli) homolog 2 (colon cancer;	0.8	1.61
45	102031	U04898	Hs.2156	RAR-related orphan receptor A	1	1
	102221	U24576		LIM domain only 4	1	1
	102270	U30255	Hs.75888	phosphogluconate dehydrogenase	1.08	1.43
	102339	U37022	Hs.95577	cyclin-dependent kinase 4	0.88	1.32
	102391	U41668	Hs.77494	deoxyguanosine kinase	1.07	1.58
50	103000	X51956	Hs.146580	enolase 2; (gamma; neuronal)	0.91	1.49
	103395	X94754	Hs.119503	methionine-tRNA synthetase	0.89	1.32
	105638	AA281599	Hs.20418	Homo sapiens mRNA for for histone H2B; c	0.91	1.25
	105726	AA292328	Hs.9754	activating transcription factor 5	0.94	1.48
	114841	AA234722	Hs.55408	ESTs; Moderately similar to CALCIUM-DEPE	0.78	1.56
55	115206	AA262491	Hs.186572	ESTs	1	1
	115906	AA436616	Hs.82302	ESTs	0.74	2.52
	119132	R49046	Hs.107911	ATP-binding cassette; sub-family B (MDR/	1.1	1.51
	124163	H30539	Hs.189838	ESTs	1	1
	126487	AA482505	Hs.184601	solute carrier family 7 (cationic amino	1.01	1.46
60	127141	AA307960	Hs.75478	KIAA0956 protein	0.85	1.4
	128034	AA905754	Hs.75103	tyrosine 3-monooxygenase/tryptophan 5-mo	1	1.18
	128609	AA234365	Hs.102456	survival of motor neuron protein interac	1	1.5
	128895	R37753	Hs.106985	ESTs	1.7	2
	130199	Z48579	Hs.172028	a disintegrin and metalloprotease domain	1	1
65	130524	U89995	Hs.159234	forkhead box E1	1	1
	133000	U24152	Hs.62402	p21/Cdc42/Rac1-activated kinase 1 (yeast	1	1
	133658	M25756	Hs.75426	secretogranin II (chromogranin C)	1	1
	135047	AA460466	Hs.93597	ESTs	1	1
	100053	M27830		AFFX control: 28S ribosomal RNA	0.88	1.53
70	100114	D00596	Hs.82962	thymidylate synthetase	0.68	1.86
	100128	D11094	Hs.61153	proteasome (prosome; macropain) 26S subu	1.29	2.03
	100154	D14657	Hs.81892	KIAA0101 gene product	0.71	4.26
	100161	D14694	Hs.77329	phosphatidylserine synthase 1	1.02	1.56
	100168	D14874	Hs.394	adrenomedullin	0.46	1.17
75	100187	D17793	Hs.78183	aldo-keto reductase family 1; member C3	1	1
	100188	D21063	Hs.57101	minichromosome maintenance deficient (S.	0.97	1.4
	100217	D26600	Hs.89545	proteasome (prosome; macropain) subunit;	1.13	1.9
	100220	D28364		***Human mRNA for annexin II, 5'UTR (seq	1.11	1.53
	100287	D43950	Hs.1600	chaperonin containing TCP1; subunit 5 (e	1.13	2.09
80	100297	D49489	Hs.182429	protein disulfide isomerase-related prot	0.92	1.78
	100330	D55716	Hs.77152	minichromosome maintenance deficient (S.	1.07	1.61
	100355	D78129		***Homo sapiens mRNA for squalene epoxid	0.96	1.87
	100364	D78586	Hs.154868	carbamoyl-phosphate synthetase 2; aspart	1.49	2.46
	100368	D79987	Hs.153479	extra spindle poles; S. cerevisiae; homo	0.59	1.32
	100398	D84557	Hs.155462	minichromosome maintenance deficient (ml	1.08	1.9
85	100438	D87448	Hs.91417	topoisomerase (DNA) II binding protein	1	2.15

	100455	D87953	Hs.75789	N-myc downstream regulated	0.91	1.48
	100491	HG1153-HT1153		Nucleoside Diphosphate Kinase Nm23-H2s	0.99	1.41
	100518	HG174-HT174		Desmoplakin I	1.28	3.17
5	100528	HG1828-HT1857		***Nexin, Glia-Derived***	0.68	1.9
	100661	HG2874-HT3018		Ribosomal Protein L39 Homolog	1.1	5.44
	100667	HG2981-HT3127		***Epican, Alt. Splice 11***	0.8	1.97
	100830	HG4074-HT4344		Rad2	1.01	2.12
	101061	K03515	Hs.944	glucose phosphate isomerase	0.91	1.79
10	101131	L10838	Hs.167460	splicing factor; arginine/serine-rich 3	1.23	1.87
	101162	L14595	Hs.174203	solute carrier family 1 (glutamate/neutral)	1.35	2.73
	101181	L19686	Hs.73798	macrophage migration inhibitory factor (1.03	1.78
	101183	L19779	Hs.795	H2A histone family; member O	0.57	1.3
	101216	L25876	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	0.7	2.2
15	101228	L27706	Hs.82916	chaperonin containing TCP1; subunit 6A (0.99	1.99
	101233	L29008	Hs.878	sorbitol dehydrogenase	0.82	2.11
	101247	L33801	Hs.78802	glycogen synthase kinase 3 beta	1.2	1.91
	101332	L47276		***Homo sapiens (cell line HL-6) alpha t	0.69	2.78
	101342	L76191	Hs.182018	interleukin-1 receptor-associated kinase	1.04	1.84
20	101396	M15796	Hs.78996	proliferating cell nuclear antigen	0.95	3.55
	101423	M18391	Hs.89839	EphA1	1	1.5
	101445	M21259	Hs.1066	small nuclear ribonucleoprotein polypept	1.21	1.96
	101505	M27396	Hs.75692	asparagine synthetase	0.93	1.6
	101525	M29536	Hs.12163	eukaryotic translation initiation factor	1.19	1.93
25	101535	M30448	Hs.251669	casein kinase 2; beta polypeptide	0.96	1.42
	101607	M38690	Hs.1244	CD9 antigen (p24)	1.11	1.25
	101624	M55998		***Human alpha-1 collagen type I gene, 3	1.17	1.98
	101758	M77836	Hs.79217	pyrroline-5-carboxylate reductase 1	1.77	3.45
	101839	M93036	Hs.692	membrane component; chromosomal 4; surfa	0.71	1.45
30	101853	M94362	Hs.76084	lamin B2	0.84	1.19
	101977	S83364		***putative Rab5-interacting protein (cl	0.89	1.9
	101992	U01038	Hs.77597	polo (Drosophila)-like kinase	0.66	1.46
	102009	U02680	Hs.82643	protein tyrosine kinase 9	1.23	3.35
	102012	U03057	Hs.118400	singed (Drosophila)-like (sea urchin fas	0.85	1.88
35	102039	U05861	Hs.201957	aldo-keto reductase family 1; member C1	0.93	2.32
	102123	U14518	Hs.1594	centromere protein A (17kD)	1	4.28
	102130	U15009	Hs.1575	small nuclear ribonucleoprotein D3 polyp	0.89	1.42
	102148	U16954	Hs.75823	ALL1-fused gene from chromosome 1q	0.8	2.95
	102210	U23028	Hs.2437	eukaryotic translation initiation factor	1.01	1.34
40	102220	U24389	Hs.65436	lysyl oxidase-like 1	1.15	2.34
	102260	U28386	Hs.159557	karyopherin alpha 2 (RAG cohort 1; impor	1.14	2.69
	102330	U35451	Hs.77254	chromobox homolog 1 (Drosophila HP1 beta	1.05	1.7
	102423	U44754	Hs.179312	small nuclear RNA activating complex; po	1.14	2.99
	102455	U48705	Hs.75562	discoidin domain receptor family; member	1.05	2.01
45	102499	U51478	Hs.76941	ATPase; Na+/K+ transporting; beta 3 poly	1.27	1.92
	102522	U53347	Hs.183556	solute carrier family 1 (neutral amino a	0.84	1.31
	102590	U62136		***Homo sapiens enterocyte differentiati	1.11	1.6
	102676	U72514	Hs.12045	putative protein	1.04	2.17
	102687	U73379	Hs.93002	ubiquitin carrier protein E2-C	0.86	2.28
50	102704	U76538	Hs.54089	BRCA1 associated RING domain 1	1.12	1.63
	102781	U83843		***Human HIV-1 Nef interacting protein (0.9	1.39
	102784	U85658	Hs.61796	transcription factor AP-2 gamma (activa	0.98	2.16
	102827	U91327	Hs.6456	chaperonin containing TCP1; subunit 2 (b	0.96	1.62
	102935	X13482	Hs.80506	small nuclear ribonucleoprotein polypept	1.21	4.2
55	102972	X16662	Hs.87268	annexin A8	1.25	2.32
	102983	X17620	Hs.118638	non-metastatic cells 1; protein (NM23A)	1.03	1.83
	103023	X53793	Hs.117950	multifunctional polypeptide similar to S	1.58	5.44
	103038	X54941	Hs.77550	CDC28 protein kinase 1	1.32	3.79
	103075	X59543	Hs.2934	ribonucleotide reductase M1 polypeptide	1.11	2.58
60	103168	X68314	Hs.2704	glutathione peroxidase 2 (gastrointestin	0.75	3.05
	103185	X69910	Hs.74368	transmembrane protein (63kD); endoplasm	1.01	1.97
	103212	X73874	Hs.2393	phosphorylase kinase; alpha 1 (muscle)	0.95	1.72
	103223	X74801	Hs.1708	chaperonin containing TCP1; subunit 3 (g	0.97	1.77
	103260	X78416	Hs.3155	casein; alpha	1	1
65	103262	X78565	Hs.204133	hexabrachion (tenascin C; cytotoxicin)	1.23	3.09
	103330	X85373	Hs.77496	small nuclear ribonucleoprotein polypept	1.12	2.25
	103364	X90872	Hs.75854	SULT1C sulfotransferase	2.85	4.62
	103375	X91868	Hs.54416	sine oculis homeobox (Drosophila) homolo	1	2.48
	103391	X94453	Hs.114366	pyrroline-5-carboxylate synthetase (glut	1	1.53
70	103404	X95586	Hs.78596	proteasome (prosome; macropain) subunit;	0.92	1.53
	103437	X98260	Hs.82254	M-phase phosphoprotein 11	0.92	1.54
	103448	X99133	Hs.204238	lipocalin 2 (oncogene 24p3)	0.55	0.96
	103605	Z35402	Hs.194657	cadherin 1; E-cadherin (epithelial)	1.32	2.51
	103646	Z68228	Hs.2340	junction plakoglobin	0.88	1.28
75	103658	Z74615	Hs.172928	collagen; type I; alpha 1	1.06	2.98
	103774	AA092898	Hs.92918	ESTs; Weakly similar to R07G3.8 [C.elega	1.88	4.66
	104261	AF008442	Hs.5409	RNA polymerase I subunit	0.87	2.17
	104276	C02193	Hs.85222	ESTs; Weakly similar to R27090_2 [H.sapi	1.4	2.49
	104289	C16281	Hs.75478	KIAA0956 protein	1.15	1.68
80	104434	L02870	Hs.1640	collagen; type VII; alpha 1 (epidermolys	1.04	1.49
	104453	M19169	Hs.123114	cystatin SN	0.38	0.76
	104611	R98280	Hs.125845	ribulose-5-phosphate-3-epimerase	1.08	2.25
	104758	AA024661	Hs.7010	ESTs; Weakly similar to ACYL-COA DEHYDRO	1.14	1.65
	105114	AA156532	Hs.11801	adenosine A2b receptor pseudogene	0.91	1.38
	105132	AA159501	Hs.247280	HBV associated factor	1.08	1.7
85	105174	AA186613	Hs.34744	ESTs	0.95	2.05

	105280	AA232215	Hs.14600	ESTs	1	1.4
	105344	AA235303	Hs.8645	ESTs	0.72	2.02
	105516	AA257971	Hs.21214	ESTs	1.35	3.56
5	105621	AA280865	Hs.6375	Homo sapiens mRNA; cDNA DKFZp564K0222 (f	1.23	1.82
	105698	AA287393	Hs.15202	ESTs; Weakly similar to oligodendrocyte-	0.98	1.28
	105705	AA290767	Hs.101282	Homo sapiens mRNA; cDNA DKFZp434B102 (fr	0.92	1.32
	105724	AA292098	Hs.22934	ESTs; Weakly similar to ZINC FINGER PROT	0.99	1.41
	105782	AA350215	Hs.21580	ESTs	1	1
10	105799	AA372018	Hs.24743	ESTs	1.08	1.78
	105807	AA393803	Hs.16869	ESTs; Moderately similar to COLLAGEN ALP	0.95	1.34
	105891	AA400768	Hs.26662	ESTs; Weakly similar to tumor necrosis f	0.87	2.25
	105936	AA404338		ESTs	1.14	1.46
	106069	AA417741	Hs.29899	ESTs; Weakly similar to ZINC FINGER PROT	1	1
	106103	AA421104	Hs.12094	ESTs	1.04	1.44
15	106140	AA424524	Hs.14912	KIAA0286 protein	1.23	2.11
	106149	AA424881	Hs.256301	ESTs	0.83	1.48
	106154	AA425304	Hs.6994	ESTs	0.77	2.05
	106182	AA426609	Hs.10862	ESTs	0.74	2.23
20	106220	AA428582	Hs.32196	ESTs; Moderately similar to metargidin p	0.97	1.99
	106228	AA429290	Hs.17719	ESTs	0.99	1.54
	106318	AA436570	Hs.9605	pre-mRNA cleavage factor Im (25kD)	0.95	2.09
	106341	AA441798	Hs.5243	ESTs; Moderately similar to p1L2 hypothe	0.98	2.66
	106432	AA448850	Hs.17138	ESTs	0.95	1.93
25	106474	AA450212	Hs.42484	Homo sapiens mRNA; cDNA DKFZp564C053 (fr	1	1
	106483	AA451676	Hs.30299	IGF-II mRNA-binding protein 2	1.4	2.29
	106599	AA457235	Hs.12842	ESTs; Moderately similar to non-function	1	1.82
	106611	AA458904	Hs.26267	ESTs; Weakly similar to torsinA [H.sapie	1.49	2.78
	106654	AA460449	Hs.3784	ESTs; Highly similar to phosphoserine am	1	1.4
30	107076	AA609145	Hs.21143	ESTs; Weakly similar to fos39554_1 [H.s.a	1.11	1.49
	107115	AA610108	Hs.27693	ESTs; Highly similar to CGI-124 protein	1	1.03
	107129	AA620553	Hs.4756	flap structure-specific endonuclease 1	1.13	3.63
	107159	AA621340	Hs.10600	ESTs; Weakly similar to ORF YKR081c [S.c	1.05	2.09
	107444	W28391	Hs.5181	proliferation-associated 2G4; 38kD	1.18	1.9
35	107481	W58247	Hs.27437	Homo sapiens kinesin superfamily motor K	0.99	2.74
	107516	X56597	Hs.99853	fibrillarin	0.94	1.77
	107529	Y12065	Hs.5092	nucleolar protein (KKE/D repeat)	1.05	2.29
	107531	Y13936	Hs.17883	protein phosphatase 1G (formerly 2C); ma	1.06	1.62
	107801	AA019433	Hs.173100	ESTs	1.03	1.4
40	107957	AA031948	Hs.57548	ESTs	0.95	1.46
	108565	AA085342	Hs.1526	ATPase; Ca++ transporting; cardiac muscul	0.59	1.35
	108780	AA128561	Hs.117938	collagen; type XVII; alpha 1	1	7.63
	108828	AA131584	Hs.71435	DKFZP564O0463 protein	1.33	2.56
	109060	AA160879	Hs.241551	chloride channel; calcium activated; fam	0.67	1.42
45	109112	AA169379	Hs.72865	ESTs	1.03	2.31
	109344	AA213696	Hs.86559	poly(A)-binding protein-like 1	0.97	1.55
	109412	AA227145	Hs.209473	ESTs; Weakly similar to REGULATOR OF MIT	0.76	1.87
	110780	N23174	Hs.22891	solute carrier family 7 (cationic amino	0.9	0.95
	110958	N50550	Hs.24587	signal transduction protein (SH3 contain	1.17	2.26
50	111018	N54067	Hs.3628	mitogen-activated protein kinase kinase	1.21	1.85
	111337	N79612	Hs.16607	ESTs; Highly similar to Myosin heavy cha	1	1.45
	112305	R54822	Hs.26244	ESTs	1	1
	112401	R61279	Hs.237536	ESTs; Weakly similar to F25B5.3 [C.elega	1.24	1.64
	112853	T02843	Hs.4351	EST	1.56	1.96
55	112869	T03313	Hs.4747	dyskeratosis congenita 1; dyskerin	1.03	1.57
	112992	T23513	Hs.7147	ESTs	1	1
	113048	T25895	Hs.184008	ESTs; Weakly similar to RNA-binding prot	1.37	2.26
	113063	T32438	Hs.5027	ESTs	1	1
	113179	T55182	Hs.152571	ESTs; Highly similar to IGF-II mRNA-bind	1.33	2.7
60	113573	T91166	Hs.15990	ESTs	0.76	1.47
	113811	W44928	Hs.4878	ESTs	0.79	1.51
	114086	Z38266	Hs.12770	Homo sapiens PAC clone DJ0777Q23 from 7p	0.9	1.34
	114587	AA070827	Hs.180320	ESTs; Weakly similar to GOLGI 4-TRANSMEM	1.02	1.76
	114846	AA234929	Hs.44343	ESTs	1.32	2.36
65	114964	AA243873	Hs.82184	ring finger protein 3	1.1	1.84
	115047	AA252627	Hs.22554	homeo box B5	1.01	2.36
	115166	AA258409	Hs.198907	myelin protein zero-like 1	1.05	2.31
	115167	AA258421	Hs.43728	hypothetical protein	1.52	2.52
	115239	AA278650	Hs.73291	ESTs; Weakly similar to similar to the b	0.7	2.57
70	115278	AA279757	Hs.67466	ESTs; Weakly similar to BACN32G11.d [D.m	1.14	2.12
	115652	AA405098	Hs.38178	ESTs	0.82	4.67
	115875	AA433943	Hs.43946	ESTs; Weakly similar to Weak similarity	1.2	1.98
	116004	AA449122	Hs.76086	ESTs; Highly similar to small zinc finger	0.96	1.31
	116121	AA459254	Hs.48855	ESTs	0.97	1.55
75	116129	AA459956	Hs.49163	ESTs; Highly similar to putative ribonuc	1.08	2.73
	116190	AA464963	Hs.67776	ESTs	0.8	1.57
	116312	AA490494	Hs.65403	ESTs	1.37	2.65
	116732	F13779	Hs.165909	ESTs	0.92	1.8
	117602	N35020	Hs.44685	ESTs; Weakly similar to GOLIATH PROTEIN	1.15	1.84
80	117950	N51394	Hs.75478	KIAA0956 protein	1.04	2.36
	117992	N52000	Hs.172089	Homo sapiens mRNA; cDNA DKFZp586B0222 (f	0.62	1.29
	118785	N75386	Hs.111867	GLI-Kruppel family member GLI2	1	1
	119717	W69134	Hs.67987	ESTs	1	1.4
	119814	W74069	Hs.58350	ESTs	0.78	1.77
85	120128	Z38499	Hs.91448	MKP-1 like protein tyrosine phosphatase	0.86	1.46
	120242	Z98443	Hs.86366	ESTs	0.83	2.01

	120483	AA252994	Hs.1578	apoptosis inhibitor 4 (survivin)	0.74	1.64
	121054	AA398604	Hs.97387	ESTs	1.05	1.93
	121326	AA404246	Hs.97031	ESTs; Weakly similar to Similar to phyto	0.98	1.3
5	121376	AA405699	Hs.166232	ESTs; Moderately similar to SODIUM- AND	0.91	1.83
	121457	AA411448	Hs.208985	ESTs	0.91	1.59
	121780	AA422086	Hs.124660	ESTs	0.46	0.55
	121781	AA422150	Hs.98370	cytochrome P540 family member predicted	1.07	1.54
	121844	AA425732	Hs.98485	gap junction protein; beta 2; 26kD (conn	0.94	1.4
10	122059	AA431737	Hs.98749	EST	1.93	2.33
	122338	AA443311	Hs.98998	ESTs	1	1
	122354	AA443772	Hs.186692	ESTs	0.88	1.39
	122591	AA453265	Hs.99311	ESTs; Weakly similar to MRJ (H.sapiens)	2.28	2.93
	122790	AA460156	Hs.99556	ESTs	0.88	1.3
	123398	AA521265	Hs.105514	ESTs	1	1.93
15	123518	AA608531	Hs.170313	ESTs	1	1
	123673	AA609471	Hs.112712	ESTs	1	1.15
	124000	D57317	Hs.74861	activated RNA polymerase II transcriptio	0.74	1.12
	124367	N24006	Hs.99348	distal-less homeo box 5	0.67	1.1
20	124447	N48000	Hs.140945	Homo sapiens mRNA; cDNA DKFZp586L141 (fr	1.19	1.7
	125756	W25498	Hs.81634	ATP synthase; H+ transporting; mitochond	0.93	1.59
	125769	AI382972	Hs.82128	5T4 oncofetal trophoblast glycoprotein	1.65	6.76
	125852	H09290	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (f	0.72	2.26
	125924	AA526849	Hs.82109	syndecan 1	1.22	2.25
25	126037	M85772	Hs.6066	KIAA1112 protein	1.36	1.63
	126214	N29455	Hs.74316	desmoplakin (DPI; DPII)	1.93	3.55
	126414	N78770	Hs.223439	ESTs	1.21	1.66
	126737	AA488132	Hs.62741	ESTs	1	1
	126743	AA179253	Hs.172182	poly(A)-binding protein; cytoplasmic 1	1.3	2.16
30	126926	AA179546	Hs.832	ESTs; Highly similar to INTEGRIN BETA-8	2.53	2.8
	127432	AA501734	Hs.170311	heterogeneous nuclear ribonucleoprotein	1.57	2.12
	128218	H02682	Hs.99189	ESTs; Moderately similar to recombinaio	1.24	2.09
	128527	M31523	Hs.101047	transcription factor 3 (E2A immunoglobul	1.08	1.78
	128568	X60673	Hs.247568	adenylate kinase 3	1.23	3.48
35	128584	M11433	Hs.101850	retinol-binding protein 1; cellular	0.87	2.42
	128628	C14037	Hs.251978	EST	1.22	1.9
	128691	W27939	Hs.103834	ESTs	1.1	1.73
	128714	V00599	Hs.179661	Homo sapiens clone 24703 beta-tubulin mR	0.92	1.17
	128733	AA328993	Hs.104558	ESTs	1.34	1.94
40	128781	X85372	Hs.105465	small nuclear ribonucleoprotein polypept	0.9	1.34
	129052	AA496297	Hs.182740	ribosomal protein S11	2.59	3.19
	129095	L12350	Hs.108623	thrombospondin 2	1.04	3.2
	129241	AA435665	Hs.109706	ESTs; Moderately similar to HN1 [M.muscu	0.95	1.61
	129665	M88458	Hs.118778	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	1.28	2.63
45	129703	AA401348	Hs.179999	ESTs	0.97	1.63
	129720	AA476582	Hs.12152	ESTs; Moderately similar to SIGNAL RECOG	1.09	1.79
	129850	N20593	Hs.56845	GDP dissociation inhibitor 2	0.74	1.68
	129896	AA043021	Hs.13225	UDP-Gal:betaGlcNAc beta 1;4- galactosylt	1.43	4.19
	130069	AA055896	Hs.146428	collagen; type V; alpha 1	1.17	1.98
50	130405	H88359	Hs.155396	nuclear factor (erythroid-derived 2)-lik	1.26	1.79
	130541	X05608	Hs.211584	neurofilament; light polypeptide (68kD)	1	1
	130599	M91670	Hs.174070	ubiquitin carrier protein	1.07	1.66
	130867	J04093	Hs.2056	UDP glycosyltransferase 1	1	4.8
55	131009	AA063596	Hs.22142	ESTs; Weakly similar to NADH-CYTOCHROME	0.93	1.05
	131028	U20240	Hs.2227	CCAAT/enhancer binding protein (C/EBP);	1	1.23
	131083	U66661	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	1.1	1.8
	131091	T35341	Hs.22880	ESTs; Highly similar to dipeptidyl pepti	1.28	1.98
	131144	C14412	Hs.23528	ESTs; Highly similar to HSPC038 protein	1.43	2.06
	131148	C00038	Hs.23579	ESTs	0.88	3.38
60	131164	Y00503	Hs.182265	keratin 19	1.19	2.77
	131185	M25753	Hs.23960	cyclin B1	0.86	3.84
	131219	C00476	Hs.24395	small inducible cytokine subfamily B (Cy	0.66	2.96
	131454	AA455896	Hs.2699	glypican 1	0.99	1.54
	131687	L11066	Hs.3069	heat shock 70kD protein 9B (mortalin-2)	1	1.18
65	131689	AA599653	Hs.30696	transcription factor-like 5 (basic helix	1	1.95
	131692	D50914	Hs.30736	KIAA0124 protein	1.55	2.39
	131786	AA135554	Hs.32125	ESTs	1	1.33
	131843	AA195893	Hs.184062	ESTs; Moderately similar to putative Rab	0.83	1.63
	131860	U02082	Hs.334	Oncogene TIM	1.08	2.2
70	131884	H90124	Hs.3463	ribosomal protein S23	1.23	1.24
	131903	AA481723	Hs.3436	deleted in oral cancer (mouse; homolog)	0.91	1.18
	131945	M87339	Hs.35120	replication factor C (activator 1) 4 (37	1	2.8
	131958	AA093998	Hs.3566	ESTs; Highly similar to phosphorylation	0.87	1.36
	131964	W42508	Hs.3593	ESTs	1	1.25
75	132001	J00277	Hs.37003	v-Ha-ras Harvey rat sarcoma viral oncoge	1.12	1.43
	132040	AA146843	Hs.172894	BH3 interacting domain death agonist	1	1.55
	132065	D82226	Hs.211594	proteasome (prosome; macropain) 26S subu	0.89	1.27
	132109	AA599801	Hs.40098	ESTs	1	1.05
	132112	AA150661	Hs.40154	jumonji (mouse) homolog	0.99	1.44
80	132123	AA447123	Hs.250705	ESTs	1.05	2.46
	132162	H89551	Hs.41241	ESTs	1.08	2.46
	132180	AA405569	Hs.418	fibroblast activation protein; alpha; se	1.02	4.56
	132309	AA460917	Hs.2780	jun D proto-oncogene	1.16	1.8
	132371	AA235448	Hs.46677	ESTs	0.8	1.26
85	132618	AA253330	Hs.5344	adaptor-related protein complex 1; gamma	0.5	1.49
	132736	U68019	Hs.211578	MAD (mothers against decapentaplegic; Dr	1.21	1.81

	132771	AA488432	Hs.56407	phosphoserine phosphatase	1	1.3
	132833	U78525	Hs.57783	eukaryotic translation initiation factor	0.91	1.43
	132922	T23641	Hs.60666	KIAA1112 protein	1.16	1.53
5	132959	AA028103	Hs.61472	ESTs; Weakly similar to unknown [S.cerev	1.02	1.88
	132994	AA505133	Hs.7594	solute carrier family 2 (facilitated glu	0.72	2.97
	133005	C21400	Hs.103329	KIAA0970 protein	0.88	1.34
	133065	X62535	Hs.172690	diacylglycerol kinase; alpha (80kD)	0.93	1.23
	133083	N70633	Hs.6456	chaperonin containing TCP1; subunit 2 (p	1.14	1.76
10	133086	L17131	Hs.139800	high-mobility group (nonhistone chromoso	0.97	1.43
	133134	T89703	Hs.65648	RNA binding motif protein 8	1.1	1.8
	133195	AA350744	Hs.181409	KIAA1007 protein	2.29	2.69
	133313	AA249427	Hs.70704	ESTs	1.07	1.68
	133331	T62039	Hs.158675	ribosomal protein L14	0.85	1.18
15	133438	D13370	Hs.73722	APEX nuclease (multifunctional DNA repai	0.91	1.45
	133445	T99303	Hs.73797	guanine nucleotide binding protein (G pr	0.94	1.68
	133483	X52426	Hs.74070	keratin 13	0.85	1.14
	133492	L40397	Hs.74137	transmembrane trafficking protein	1.1	1.69
	133504	W95070	Hs.74316	desmoplakin (DPI; DPL)	0.7	6.21
20	133517	X52947	Hs.74471	gap junction protein; alpha 1; 43kD (con	0.95	1.3
	133540	D78151	Hs.74619	proteasome (prosome; macropain) 26S subu	0.91	1.25
	133594	L07758	Hs.172589	nuclear phosphoprotein similar to S. cer	0.84	1.29
	133627	U09587	Hs.75280	glycyl-URNA synthetase	1.09	1.99
	133671	T25747	Hs.75471	zinc finger protein 146	1.02	1.5
25	133859	U86782	Hs.178761	26S proteasome-associated pad1 homolog	1.11	3.33
	133865	F09315	Hs.170290	discs; large (Drosophila) homolog 5	1.84	6.7
	133913	W84712	Hs.7753	calumenin	1.15	1.86
	133963	L34587	Hs.184693	transcription elongation factor B (SIII)	1.3	1.91
	133982	U47621	Hs.207251	nucleolar autoantigen (55kD) similar to	1.3	1.99
30	134100	L07540	Hs.171075	replication factor C (activator 1) 5 (36	0.72	1.65
	134110	U41060	Hs.79136	LIV-1 protein; estrogen regulated	1.04	1.62
	134158	U15174	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	1	1.55
	134161	U97188	Hs.79440	IGF-II mRNA-binding protein 3	0.82	1.95
	134193	F09570	Hs.7980	ESTs	0.98	1.48
35	134367	X54199	Hs.82285	phosphoribosylglycinamide formyltransfer	1	2.8
	134402	U25165	Hs.82712	fragile X mental retardation; autosomal	1.26	2
	134457	D86963	Hs.174044	dishevelled 3 (homologous to Drosophila	1	1.47
	134469	X17567	Hs.83753	small nuclear ribonucleoprotein polypept	0.94	1.57
	134498	M63180	Hs.84131	threonyl-URNA synthetase	1.2	2.64
40	134501	W84870	Hs.211568	eukaryotic translation initiation factor	0.84	1.36
	134507	M63488	Hs.84318	replication protein A1 (70kD)	1.7	2.93
	134548	U41515	Hs.85215	Deleted in split-hand/split-foot 1 regio	1.46	2.73
	134599	X99226	Hs.86297	Fanconi anemia; complementation group A	1.36	2.22
	134692	R73567	Hs.8850	a disintegrin and metalloproteinase doma	0.77	1.64
45	134693	N70361	Hs.8854	ESTs	1.09	1.82
	134806	Z49099	Hs.89718	spermine synthase	0.98	1.35
	134821	Z34974	Hs.198382	plakophilin 1 (ectodermal dysplasia/skin	0.99	1.4
	134864	Y08999	Hs.90370	actin related protein 2/3 complex; subun	0.95	1.42
	134914	U29615	Hs.91093	chitinase 1 (chilotriosidase)	1.16	1.29
50	134953	L10678	Hs.91747	profilin 2	0.95	1.76
	134993	AA282343	Hs.9242	purine-rich element binding protein B	0.98	1.73
	135051	C15324	Hs.93668	ESTs	1.35	2.11
	135158	U51711		Human desmocollin-2 mRNA; 3' UTR	0.86	1.16

Table 1B shows the accession numbers for those pkeys in Table 1A lacking unigenal/D's. For each probaset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the Accession column.

Pkey: Unique Eos probaset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT	Accessions
65	100661 23182_1	BE623001 L05096 AA383604 AW966416 N53295 AA460213 AW571519 AA603655
	100667 26401_3	L05424 X56794 S66400 X55150 W60071 AW351820 X55938 M83326 BE005289 BE070059 M83324 BE005248 BE069717 BE181648 BE069700 AW606203 BE069721 AW382138 AW803776 BE463954 BE005334 BE005274 T27386 AA932714 AA972695 AW377728 A1632506 T29066 A1783934 AW377727 BE163715 AL047291 AA279047 AA523003 BE008048 BE440141 W23614 BE090519 BE092193 N29181 N20358 N44153 BE546944 T69231 AW377441 AA907406 H50799 AW051416 A1420712 BE620922 A1279161 AA992549 W47198 BE005241 A1342696 H50700 A1969974 A1863855 AA374490 AW130675 A1950633 AA146687 H99482 X55150 BE005414 BE005339 N28294 A1673068 A1887890 AW804171 A1675961 AW804172 AA778841 AL048050 A1127757 A1095568 AW204965 AW468978 W31898 A1052595 A1278771 BE464018 A1081503 A1824196 AA513211 AA411062 AW084376 N48752 AA703209 N35580 AW059918 AA054563 A1280942 T27619 BE621435 N66010 AW589527 A1160414 AA283090 AA962536 H82726 W52115 W45432 W60433 AA577548 AA146714 BE150994 AA054615 AW796025 AW382768 BE565671 C00444 AA054555
75	100668 26401_3	L05424 X56794 S66400 X55150 W60071 AW351820 X55938 M83326 BE005289 BE070059 M83324 BE005248 BE069717 BE181648 BE069700 AW606203 BE069721 AW382138 AW803776 BE463954 BE005334 BE005274 T27386 AA932714 AA972695 AW377728 A1632506 T29066 A1783934 AW377727 BE163715 AL047291 AA279047 AA523003 BE008048 BE440141 W23614 BE090519 BE092193 N29181 N20358 N44153 BE546944 T69231 AW377441 AA907406 H50799 AW051416 A1420712 BE620922 A1279161 AA992549 W47198 BE005241 A1342696 H50700 A1969974 A1863855 AA374490 AW130675 A1950633 AA146687 H99482 X55150 BE005414 BE005339 N28294 A1673068 A1887890 AW804171 A1675961 AW804172 AA778841 AL048050 A1127757 A1095568 AW204965 AW468978 W31898 A1052595 A1278771 BE464018 A1081503 A1824196 AA513211 AA411062 AW084376 N48752 AA703209 N35580 AW059918 AA054563 A1280942 T27619 BE621435 N66010 AW589527 A1160414 AA283090 AA962536 H82726 W52115 W45432 W60433 AA577548 AA146714 BE150994 AA054615 AW796025 AW382768 BE565671 C00444 AA054555
80		J04088 NM_001067 AF071747 AJ011741 N85424 AL042407 AA218572 BE296748 BE083981 AL040877 AW499918 AW675045 H17813 BE081283 AA670403 AW504327 BE094229 AA104024 A1471482 A1970337 AA737616 A1827444 AW003286 A1742333 A1344044 A1765634
85	101332 25130_1	

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AI948838 AW253336 AW172827 AA095289 BE046383 AI734240 W16699 AI660329 AI289433 AA933778 AW469242 AA468838 AA806983
AA625873 W78031 BE206307 AA550803 AI743147 AI990075 AA948274 AA129533 AI635399 AA605313 AI624669 AW594319 AI221834 AI337434
AI307706 BE550282 AI760467 AI630636 AI221521 AW674314 AW078889 AI933732 AI686989 AI186928 AW074595 AI127486 AL079644
AI910815 H17814 AA310903 AW137854 T19279 AA026682 AA306035 AW383390 AW383389 AW383422 AW383395 H09977
AA306247 AA352501 AW403639 F05421 AA224473 AA305321 H93904 AA089612 AW391543 AW402915 AW173382 AW402701 AW403113
R94438 N73126 H93466 AA090928 AA095051 T29025 AW951071 L47277 L47276 AI375913 BE384156 W24652 AA746288 AA568223 BE090591
H93033 N57027 AA504348 AA327653 AW959913 N53767 AA843715 AI453437 AW263710 AI076594 AA583483 AW873194 AW575166 AI128799
AI803319 AL042776 AW074313 AI887722 AI032284 AA447521 AI123885 N29334 AI354911 AW090687 AA237663 AA435535 AI2236910
AA047124 AA236734 AW514610 H93467 AA962007 AI446783 AA127259 AI613495 AI686720 AI587374 AA936731 AA702453 AI859757
AA216786 AI251819 AI469227 AA806022 AI092324 N71868 AA968782 AA236919 AA809450 AA227220 AA765284 AI192007 AW768810
AA805794 AA729280 AA806238 AW768817 N71879 AI050685 AA505822 AA668974 AI688160 BE045915 AW466315 AA731314 AA649568
AA834316 AW591901 AW063876 AW294770 AI300266 AI336094 AI560380 AA721755 H09978 D20305 D29155 AW821790 BE150864 F01675
AI457474 AW466316 AA550969 AA630788
100780 458_127 BE561958 BE561728 BE397612 BE514391 BE269037 BE514207 BE562381 BE514256 BE514403 BE514250 BE397832 BE269598 BE559865
BE396881 BE560031 BE514199 BE560037 BE560454
100830 4002_1 AC004770 W05005 AA356068 AA094281 H29358 T56781 AW875313 L37374 BE312466 BE311755 BE207106 BE293320 BE018115 AW239090
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AA188808 AA186879 AA565243 AL040655 AA456177 AI750722 AA045756 AA213580 C16936 AW578747 AW753731 H41632 N44761 R58560
R61260 AA039902 N59721 AW992543 R68380 AA149686 T29017 H03739 BE383822 BE387105 BE408251 BE410425 H41560 AA247591
BE389677 AI752233 AI566195 AA868004 AI424523 AW753720 AA852159 BE386803
NM_000094 L02870 D13694 S51236 M96984 AW946290 M65158 AI285422 D29523 AL119886 AW630655 L06862 AI884355 AW168737 T29085
AW797005 AW801340 AI355504 AW079048 AW801337 AI690455 AI972063 AW268565 W68588 AA587326 AA883498 AI033523 AW510356
AW591998 H98463 AL043852 AI150055 AI566239 AI624803 AA844717 H40670 AA922334 AI864424 AW615094 AW451233 AI302203 F31221
AI872170 W68589 AA904478 AI917631 AW014208 AW450759 AA847625 AI284033 AA848176 AA598507
X00356 NM_001741 M26095 X03662 M12667 X02330 X02330 AA716058 AW296074 X04861 AI695720 AA719597
N22401
N22401
M55998
M57293
AL037551 AI804716 AW439811 AI569470 AA075299 AI738572 AI270388 AI816783 AW263026 AI633951 AI655285 AI990572 AI950425
AW241533 AA916883 AA576693 AA160156 AA613783 AW078884 AI888282 AI275241 AI133467 AA164921

Tables 2A-8C were previously filed on November 9, 2001 in USSN 60/339,245 (18501-004100US)

Table 2A shows 504 genes down-regulated in lung tumors relative to normal lung and chronically diseased lung. Chronically diseased lung samples represent chronic non-malignant lung diseases such as fibrosis, emphysema, and bronchitis. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: 90th percentile of AI for normal lung samples divided by the 80th percentile of AI for adenocarcinoma and squamous cell carcinoma lung tumor samples.
 R2: median of AI for normal lung samples divided by 90th percentile of AI for adenocarcinoma and squamous cell carcinoma lung tumor samples.
 R3: median of AI for normal lung samples minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples divided by the 90th percentile of AI for adenocarcinoma and squamous cell carcinoma lung tumor samples minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples.
 R4: average of AI for normal lung samples divided by average AI for squamous cell carcinoma and adenocarcinoma lung tumors.
 R5: median of AI for normal lung samples divided by the 90th percentile of AI for adenocarcinomas.
 R6: median of AI for normal lung samples minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples divided by the 90th percentile of AI for adenocarcinomas minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples.
 R7: average of AI for normal lung samples divided by the 90th percentile of AI for squamous cell carcinomas.
 R8: median of AI for normal lung samples minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples divided by the 90th percentile of AI for squamous cell carcinomas minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples.

	Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2	R3	R4	R5	R6	R7	R8
	100095	Z97171	Hs.78454	myocilin; trabecular meshwork inducible	40.20							
	100115	NM_002084	Hs.336920	glutathione peroxidase 3 (plasma)								3.46
	100138	U83508	Hs.2463	angiotensinogen 1			2.30					
	100299	D49493	Hs.2171	growth differentiation factor 10		11.00						
	100306	U86749	Hs.80598	transcription elongation factor A (SII);						3.06		
	100447	NM_014767	Hs.74583	KIAA0275 gene product								3.16
	100458	S74019	Hs.247979	Vpre-B	42.40							
	100862	AA005247	Hs.285754	Hepatocyte Growth Factor Receptor						4.13		
	100959	AA359129	Hs.118127	actin; alpha; cardiac muscle				125.60				
	101032	BE206854	Hs.46039	phosphoglycerate mutase 2 (muscle)	36.40							
	101081	AF047347	Hs.4880	amyloid beta (A4) precursor protein-bind				34.60				
	101088	X70697	Hs.553	solute carrier family 6 (neurotransmitter)				193.20				
	101125	AJ250562	Hs.82749	transmembrane 4 superfamily member 2						3.10		
	101180	U11874	Hs.846	interleukin 8 receptor; beta				54.86				
	101308	L41390		"Homo sapiens core 2 beta-1,6-N-acetylgl	33.20							
	101330	L43821	Hs.80261	enhancer of filamentation 1 (cas-like do				36.40				
	101345	NM_005795	Hs.152175	Calcitonin receptor-like			2.29					
	101346	AI738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N				70.55				
	101397	M26380	Hs.180878	lipoprotein lipase								3.54
	101414	NM_000066	Hs.38069	complement component 8; beta polypeptide							3.81	
	101435	NM_001100	Hs.1288	actin; alpha 1; skeletal muscle				34.60				
	101507	X16896	Hs.82112	interleukin 1 receptor; type I				37.60				
	101530	M29874	Hs.1360	cytochrome P450; subfamily IIB (phenobar								4.25
	101537	AI469059	Hs.184915	zinc finger protein; Y-linked			2.54					
	101542	NM_000102	Hs.1363	cytochrome P450; subfamily XVII (steroid		5.50						
	101545	BE246154	Hs.154210	EDG1; endothelial differentiation, sphin	39.40							
	101554	BE207611	Hs.123078	thyroid stimulating hormone receptor		13.00						
	101560	AW958272	Hs.83733	Intercellular adhesion molecule 2, exon								3.38
	101574	M34182	Hs.158029	protein kinase; cAMP-dependent; catalyti						4.37		
	101605	M37984	Hs.118845	troponin C; slow								3.80
	101621	BE391804	Hs.62661	guanylate binding protein 1; interferon-	30.20							
	101680	AA299330	Hs.1042	Sjogren syndrome antigen A1 (52kD; ribon							2.75	
	101829	AW452398	Hs.129763	solute carrier family 8 (sodium/calcium						3.37		
	101842	M93221	Hs.75182	mannose receptor; C type 1				38.20				
	101961	AW004056	Hs.168357	"Hs-TBX2=T-box gene (T-box region) [huma			2.32					
	101994	T92248	Hs.2240	uteroglobin								6.85
	102020	AU077315	Hs.154970	transcription factor CP2			2.45					
	102091	BE280901	Hs.83155	aldehyde dehydrogenase 7								6.75
	102112	AW025430	Hs.155591	forkhead box F1	54.60							
	102190	AA723157	Hs.73769	folate receptor 1 (adult)								3.98
	102202	NM_000507	Hs.574	fructose-bisphosphatase 1								3.62
	102241	NM_007351	Hs.268107	Multimerin			2.32					
	102310	U33839		Accession not listed in Genbank		7.00						
	102397	U41898		"Human sodium cotransporter RKST1 mRNA,	29.40							
	102571	U60115	Hs.239069	"Homo sapiens skeletal muscle LIM-protei								3.75
	102620	AA976427	Hs.121513	Human clone W2-6 mRNA from chromosome X						3.07		
	102636	U67092		"Human ataxia-telangiectasia locus prote								
	102667	U70867	Hs.83974	solute carrier family 21 (prostaglandin			2.40					
	102675	U72512	Hs.7771	"Human B-cell receptor associated protei			3.15					
	102698	M18667	Hs.1867	progastrin (pepsinogen C)								4.51
	102727	U79251	Hs.99902	opioid-binding protein/cell adhesion mol					12.00			
	102852	V00571	Hs.75294	corticotropin releasing hormone	37.40							
	103026	X54162	Hs.79386	thyroid and eye muscle autoantigen D1 (6					13.00			
	103028	X54380	Hs.74094	pregnancy-zone protein	28.80							
	103098	M86361		Human mRNA for T cell receptor; clone IG					10.00			
	103117	X63578	Hs.295449	parvalbumin		6.00						
	103241	X76223		H.sapiens MAL gene exon 4			2.47					
	103280	U84722	Hs.76206	Cadherin 5, VE-cadherin (vascular epithe			2.69					
	103360	Y16791	Hs.73082	keratin; hair; acidic; 5							2.16	

	103496	Y09267	Hs.132821	flavin containing monooxygenase 2					3.27	5.97
	103508	Y10141		*H.sapiens DAT1 gene, partial, VNTR						
	103561	NM_001843	Hs.143434	contactin 1	2.40					
	103569	NM_005512	Hs.151641	glycoprotein A repetitions predominant	2.99					
5	103575	Z26256		*H.sapiens isoform 1 gene for L-type cal					4.18	
	103627	Z48513		H.sapiens XG mRNA (clone PEP6)					3.44	
	103767	BE244667	Hs.296155	CGI-100 protein				2.25		
	103850	AA187101	Hs.213194	Hypothetical protein MGC10895; sim to SR		46.55				
10	104078	AA402801	Hs.303276	ESTs					3.05	
	104326	AW732858	Hs.143067	ESTs					3.54	
	104352	BE219898	Hs.173135	dual-specificity tyrosine-(Y)-phosphoryl					3.16	
	104398	AI423930	Hs.36790	ESTs; Weakly similar to putative p150 [H	64.80					
	104473	AI904823	Hs.31297	ESTs						3.38
	104493	AW960427	Hs.79059	ESTs; Moderately similar to TGF-BETA REC		2.47				
15	104495	AW975687	Hs.292979	ESTs	28.60					
	104595	AI799603	Hs.271568	ESTs					3.42	
	104597	AI364504	Hs.93967	ESTs; Weakly similar to Slit-1 protein [6.00				
	104659	AW969769	Hs.105201	ESTs	34.00					
20	104686	AA010539	Hs.18912	ESTs		11.00				
	104691	U29690	Hs.37744	ESTs; Beta-1-adrenergic receptor	56.80					
	104764	AI039243	Hs.278585	ESTs			60.40			
	104776	AA026349		ESTs	34.20					
	104825	AA035613	Hs.141883	ESTs		3.03				
	104865	T79340	Hs.22575	Homo sapiens cDNA: FLJ21042 fis, clone C	41.20					
25	104942	NM_016348	Hs.10235	ESTs						3.27
	104989	R65998	Hs.285243	ESTs			40.00			
	105062	AW954355	Hs.36529	ESTs						3.20
	105101	H63202	Hs.38163	ESTs	34.20					
30	105173	U54617	Hs.8364	ESTs						4.17
	105194	R06780	Hs.19800	ESTs		16.00				
	105226	R58958	Hs.26608	ESTs			2.34			
	105256	AA430650	Hs.16529	transmembrane 4 superfamily member (tetr			2.72			
	105394	BE245812	Hs.8941	ESTs			2.61			
	105647	Y09306	Hs.30148	homeodomain-interacting protein kinase 3	33.60					
35	105789	AF105941	Hs.18142	arrestin; beta 2						3.59
	105817	AA397825		synaptopodin				4.46		
	105847	AW964490	Hs.32241	ESTs			35.40			
	105894	AI904740	Hs.25691	calcitonin receptor-like receptor activi		3.43				
40	105999	BE268786	Hs.21543	ESTs	7.00					
	106075	AA045290	Hs.25930	ESTs			42.60			
	106178	AL049935	Hs.301763	KIAA0554 protein	34.80					
	106381	AB040916	Hs.24106	ESTs			12.00			
	106467	AA450040	Hs.154162	ADP-ribosylation factor-like 2				3.69		
45	106536	AA329648	Hs.23804	ESTs			96.40			
	106569	R20909	Hs.300741	sorcin			47.20			
	106605	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (fr			220.40			
	106842	AF124251	Hs.26054	novel SH2-containing protein 3		2.55				
	106844	AA485055	Hs.158213	sperm associated antigen 6	39.20					
50	106870	AI983730	Hs.26530	serum deprivation response (phosphatidyl)		2.28				
	106943	AW888222	Hs.9973	ESTs						4.28
	106954	AF128847	Hs.204038	ESTs						4.32
	107106	AA862496	Hs.28482	ESTs			10.45			
	107163	AF233588	Hs.27018	ESTs		2.57				
55	107201	D20378	Hs.30731	EST				3.84		
	107238	D59362	Hs.330777	EST		8.00				
	107376	U90545	Hs.327179	solute carrier family 17 (sodium phospho		10.67				
	107530	Y13622	Hs.85087	latent transforming growth factor beta b		2.32				
	107688	AW082221	Hs.60536	ESTs			34.60			
60	107706	AA015579	Hs.29276	ESTs	28.40					
	107723	AA015967		EST				3.29		
	107727	AA149707	Hs.173091	DKFZP434K151 protein			80.80			
	107750	AA017291	Hs.60781	ESTs			51.40			
	107751	AA017301	Hs.235390	ESTs				3.14		
65	107873	AK000520	Hs.143811	ESTs		9.00				
	107899	BE019261	Hs.83869	ESTs; Weakly similar to !!! ALU SUBFAM1				3.65		
	107994	AA036811	Hs.48469	ESTs			44.60			
	107997	AL049176	Hs.82223	Human DNA sequence from clone 141H5 on c			32.00			
	108041	AW204712	Hs.61957	ESTs			30.80			
70	108048	AI797341	Hs.165195	ESTs				4.75		
	108338	AA070773		*zm53g11.s1 Stratagene fibroblast (#9372		2.33				
	108434	AA078899		*zm94b1.s1 Stratagene colon HT29 (#93722				2.92		
	108447	AA079126		*zm92a11.s1 Stratagene ovarian cancer (#						
	108480	AL133092	Hs.68055	ESTs			34.00			
75	108499	AA083103		*zn1b12.s1 Stratagene hNT neuron (#93723						3.36
	108535	R13949	Hs.226440	Homo sapiens clone 24881 mRNA sequence			19.00			
	108550	AA084867		*zn11f6.s1 Stratagene hNT neuron (#93723			12.00			
	108604	AA934589	Hs.49696	ESTs		2.33				
	108625	AW972330	Hs.283022	ESTs						5.82
80	108629	AA102425		*zn24c6.s1 Stratagene neuroepithelium NT				3.42		
	108655	AA099960		*zm65c6.s1 Stratagene fibroblast (#93721		7.00				
	108756	AA127221	Hs.117037	Homo sapiens mRNA; cDNA DKFZp564N1164 (f		6.05				
	108864	AI733852	Hs.199957	ESTs	28.80					
	108895	AL138272	Hs.62713	ESTs	32.80					
	108921	AI568801	Hs.71721	ESTs			57.80			
85	108967	AA142989	Hs.71730	ESTs	28.80					

	109001	AJ056548	Hs.72116	ESTs; Moderately similar to hedgehog-int	2.57				
	109003	AA147497	Hs.71825	ESTs				2.11	
	109004	AA156235	Hs.139077	EST	5.60				
5	109065	AA161125	Hs.252739	EST			10.00		
	109250	H83784	Hs.62113	ESTs; Weakly similar to PHOSPHATIDYLETHA				3.44	
	109490	AA233416	Hs.139202	ESTs				2.92	
	109510	AJ798863	Hs.87191	ESTs		2.40			
	109578	F02208	Hs.27214	ESTs	10.00				
10	109601	F02695	Hs.311662	EST			40.80		
	109613	H47315	Hs.27519	ESTs			54.40		
	109650	R31770	Hs.23540	ESTs	31.20				
	109682	H18017	Hs.22869	ESTs		8.40			
	109724	D59899	Hs.127842	ESTs			29.40		
15	109782	AB020644	Hs.14945	long fatty acyl-CoA synthetase 2 gene			8.00		
	109833	R79854	Hs.29889	ESTs		10.00			
	109837	H00656	Hs.29792	ESTs		6.49			
	109977	T64183	Hs.282982	ESTs				2.75	
	109984	AI796320	Hs.10299	ESTs			107.00		
20	110146	H41324	Hs.31581	ESTs; Moderately similar to SYNTAXIN 1B				2.22	
	110271	H28985	Hs.31330	ESTs				3.48	
	110280	AW874263	Hs.32468	ESTs	44.20				
	110420	R93141	Hs.184261	ESTs			32.00		
	110578	T62507	Hs.11038	ESTs	28.40				
	110634	R98905	Hs.35992	ESTs			20.00		
25	110726	AW961818	Hs.24379	potassium voltage-gated channel; shaker-					4.15
	110837	H03109	Hs.108920	ESTs; Weakly similar to semaphorin F (H.			56.80		
	110875	N35070	Hs.26401	tumor necrosis factor (ligand) superfamily		3.13			
	110894	R92356	Hs.66881	ESTs; Moderately similar to cytoplasmic		5.33			
30	110971	AJ760098	Hs.21411	ESTs			44.60		
	111023	AV655386	Hs.7645	ESTs	32.40				
	111057	T79639	Hs.14629	ESTs			17.14		
	111247	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f				4.58	
	111330	BE247767	Hs.18166	KIAA0870 protein					3.42
	111374	BE250726	Hs.283724	ESTs; Moderately similar to HYA22 (H.sap					3.91
35	111442	AW449573	Hs.181003	ESTs			33.20		
	111737	H04607	Hs.9218	ESTs			53.00		
	111747	AJ741471	Hs.23666	ESTs	46.20				
	111807	R33508	Hs.18827	ESTs		16.00			
40	111862	R37472	Hs.21559	EST				3.91	
	112045	AJ372588	Hs.8022	TU3A protein					2.74
	112057	R43713	Hs.22945	EST					4.92
	112214	AW148652	Hs.167398	ESTs			13.00		
	112263	R52393	Hs.25917	ESTs		2.43			
45	112314	AW206093	Hs.748	ESTs		9.00			
	112324	R55965	Hs.26479	limbic system-associated membrane protei			14.00		
	112362	AW300887	Hs.26638	ESTs; Weakly similar to CD20 receptor (H		2.49			
	112380	H63010	Hs.5740	ESTs		2.34			
	112425	AA324998	Hs.321677	ESTs; Weakly similar to !!!! ALU SUBFAM		8.00			
50	112473	R65993	Hs.279798	pregnancy specific beta-1-glycoprotein 9				4.53	
	112492	N51620	Hs.28694	ESTs			29.80		
	112541	AF038392	Hs.116674	ESTs				3.62	
	112620	R80552	Hs.29040	ESTs		2.37			
	112623	AW373104	Hs.25094	ESTs		2.26			
55	112867	T03254	Hs.167393	ESTs			12.00		
	112894	T08188	Hs.3770	ESTs		6.50			
	112954	AA928953	Hs.6655	ESTs		7.00			
	113029	AW081710	Hs.7369	ESTs; Weakly similar to !!!! ALU SUBFAM					4.39
	113086	AA346839	Hs.209100	DKFZP434C171 protein					4.47
60	113140	T50405	Hs.175967	ESTs			10.00		
	113252	NM_004469	Hs.11392	c-fos induced growth factor (vascular en		14.00			
	113257	AJ821378	Hs.159367	ESTs				3.72	
	113394	T81473	Hs.177894	ESTs				3.60	
	113437	T85349	Hs.15923	EST	35.00				
65	113454	AJ022166	Hs.16188	ESTs		6.00			
	113502	T89130	Hs.16026	ESTs	39.60				
	113552	AJ654223	Hs.16026	ESTs					3.88
	113645	T95358	Hs.333181	ESTs				2.58	
	113691	T96935	Hs.17932	EST			38.20		
70	113706	AA004693	Hs.269192	ESTs				3.09	
	113883	U89281	Hs.11958	oxidative 3 alpha hydroxysteroid dehydro		2.31			
	113924	BE178285	Hs.170056	Homo sapiens mRNA; cDNA DKFZp586B0220 (f	30.40				
	114035	W92798	Hs.269181	ESTs			13.00		
	114058	AK002016	Hs.114727	ESTs					5.00
75	114084	AA708035	Hs.12248	ESTs			40.60		
	114121	H05785	Hs.25425	ESTs		2.31			
	114124	W57554	Hs.125019	Human lymphoid nuclear protein (LAF-4)		7.00			
	114275	AW515443	Hs.306117	interleukin 13 receptor; alpha 1		6.00			
	114297	AA149707	Hs.173091	DKFZP434K151 protein			48.80		
80	114427	AA017176	Hs.33532	ESTs; Highly similar to Miz-1 protein (H				3.45	
	114449	AA020736	Hs.243010	*ze63b11.s1 Soares retina N2b4HR Homo sa			10.00		
	114452	AJ369275	Hs.243010	ESTs; Moderately similar to RTCO_HUMAN G		14.00			
	114609	AA079505	Hs.243010	*zm97a5.s1 Stratagene colon HT29 (#93722				3.13	
	114648	AA101056	Hs.243010	*zn25b3.s1 Stratagene neuroepithelium NT			35.40		
85	114731	BE094291	Hs.155651	Homo sapiens HNF-3beta mRNA for hepatocy					3.42
	114762	AA146979	Hs.288464	ESTs	33.00				

	114776	AA151719	Hs.95834	ESTs	34.40				
	115009	AA251561	Hs.48689	ESTs	30.20				
	115272	AW015947		ESTs; Weakly similar to hypothetical L1	32.60				
5	115279	AW964897	Hs.290825	ESTs		6.00			
	115302	AL109719	Hs.47578	ESTs			12.00		
	115365	AW976252	Hs.268391	ESTs				3.32	
	115559	AL079707	Hs.207443	ESTs			48.00		
	115566	AI142336	Hs.43977	ESTs			56.20		
10	115683	AF255910	Hs.54650	ESTs, Weakly similar to (define not ava	31.40				
	115744	AA418538	Hs.43945	ESTs; Highly similar to dJ1178H5.3 [H.s			33.60		
	115819	AA486620	Hs.41135	Endomucin 2			74.40		
	115949	AI478427	Hs.43125	ESTs		3.18			
	115965	AA001732	Hs.173233	ESTs			388.80		
	116035	AA621405	Hs.184664	ESTs			33.20		
15	116049	AA454033	Hs.41644	ESTs			45.80		
	116081	AI190071	Hs.55278	ESTs				3.57	
	116082	AB029495	Hs.59729	ESTs		3.06			
	116213	AA292105	Hs.326740	leucine rich repeat (in FLII) interactin	50.60				
20	116228	AI767947	Hs.50841	ESTs; Weakly similar to tutelin [M.musc		3.85			
	116250	N76712	Hs.44829	ESTs		6.00			
	116419	AI613480	Hs.47152	ESTs; Weakly similar to testicular tekti			30.00		
	116617	D80761	Hs.45220	EST		2.27			
	116784	AB007979	Hs.301281	tenascin R (restriclin; janusin)	47.20				
25	116835	N39230	Hs.38218	ESTs			41.20		
	116970	AB023179	Hs.9059	KIAA0962 protein			91.00	11.00	
	117023	AW070211	Hs.102415	ESTs					
	117027	AW085208	Hs.130093	ESTs	49.40				
	117036	H88908	Hs.41192	EST			32.60		
30	117110	AA160079	Hs.172932	ESTs		8.67			
	117209	W03011	Hs.306881	ESTs			30.60		
	117325	N23599	Hs.43396	ESTs				9.29	
	117454	N29569	Hs.44055	ESTs					3.19
	117475	N30205	Hs.93740	ESTs	44.00				
35	117543	BE219453	Hs.42722	ESTs		16.00			
	117567	AW444761	Hs.44565	ESTs			12.00		
	117570	N48649	Hs.44583	ESTs			11.00		
	117600	N34963	Hs.44676	EST				3.74	
	117730	N45513	Hs.46608	ESTs		6.00			
40	117791	N48325	Hs.93956	EST		9.00			
	117929	N51075	Hs.47191	ESTs			29.20		
	117990	AA446167	Hs.47385	ESTs		8.00			
	118224	N62275	Hs.48503	EST	31.40				
	118244	N62516	Hs.48556	ESTs	32.80				
45	118357	AL109667	Hs.124154	Homo sapiens mRNA full length insert cDN			2.40		
	118446	N66361	Hs.269121	ESTs			2.28		
	118447	N66399	Hs.49193	EST	30.80				
	118530	N67900	Hs.118446	ESTs				3.10	
	118549	N68163	Hs.322954	EST				3.41	
50	118823	W03754	Hs.50813	ESTs; Weakly similar to long chain fatty		3.94			
	118862	W17065	Hs.54522	ESTs				3.58	
	118935	AI979247	Hs.247043	KIAA0525 protein			33.00		
	118944	AI734233	Hs.226142	ESTs; Weakly similar to !!!! ALU SUBFAM				11.43	
	118995	N94591	Hs.323056	ESTs		14.00			
55	119073	BE245360	Hs.279477	ERG-2/ERG-1; V-ets avian erythroblastosi			52.60		
	119268	T16335	Hs.65325	EST	31.40				
	119514	W37937		Accession not listed in Genbank				3.50	
	119824	W74536	Hs.184	advanced glycosylation end product-speci		2.75			
60	119831	AL117664	Hs.58419	DKFZP586L2024 protein					3.21
	119861	W78816	Hs.49943	ESTs; Moderately similar to !!!! ALU SUB			33.80		
	119889	W84346	Hs.58671	ESTs			30.03		
	119921	W86192	Hs.58815	ESTs	29.00				
	120082	H80286	Hs.40111	ESTs				3.80	
	120094	AA811339	Hs.124049	ESTs		6.00			
65	120132	W57554	Hs.125019	Human lymphoid nuclear protein (LAF-4)			36.60		
	120378	AA223249	Hs.285728	ESTs		12.00			
	120404	AB023230	Hs.96427	KIAA1013 protein	39.40				
	120504	AA256837		ESTs			8.00		
	120512	N55761	Hs.194718	ESTs	33.00				
70	120667	AA287740	Hs.78335	microtubule-associated protein; RP/EB fa			46.60		4.18
	120777	AA287702	Hs.10031	KIAA0955 protein			39.00		
	121082	AA398722		ESTs					
	121191	AA400205	Hs.104447	ESTs	41.60				
	121248	AA400914	Hs.97827	EST				5.08	
75	121363	AI287280	Hs.97933	ESTs			12.00		
	121366	AI743515		ESTs			20.00		
	121483	AI660332	Hs.25274	ESTs; Moderately similar to putative sev				3.32	
	121518	AA412155		ESTs			30.20		
	121545	AA412442	Hs.98132	ESTs		2.29			
80	121622	AA416931	Hs.126065	ESTs		9.00			
	121665	AA416556	Hs.98234	ESTs			34.80		
	121709	AI338247	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (f	34.80				
	121730	AI140683	Hs.98328	ESTs	38.80				
	121740	AA421138	Hs.98334	EST		7.00			
85	121772	AI590770	Hs.110347	Homo sapiens mRNA for alpha integrin bin	36.20				
	121821	AL040235	Hs.3346	ESTs				3.61	

	121835	AB033030	Hs.300670	ESTs	2.34				
	121841	AA427794	Hs.104864	ESTs	2.61				
	121885	AA934883	Hs.98467	ESTs				2.25	
	121888	AA426429	Hs.98463	ESTs				2.92	
5	121938	AA428659	Hs.98610	ESTs		46.80			
	121950	AA429515	EST			31.40			
	122030	AA431310	Hs.98724	ESTs	34.40				
	122054	AA431725	Hs.98746	EST				3.58	
10	122211	AA300900	Hs.98849	ESTs; Moderately similar to bithoraxoid-	49.40				
	122233	AA436455	Hs.98872	EST	29.80				
	122247	AA436676	Hs.98890	EST		39.80			
	122253	AA436703	Hs.104936	ESTs; Weakly similar to hypothetical pro	9.00				
	122266	AA436840	Hs.98907	EST				3.60	
	122285	AA436981	Hs.121602	EST				3.14	
15	122409	AA446830	Hs.99081	ESTs	30.80				
	122485	AA524547	Hs.160318	phospholemman		2.65			
	122697	AA420683	Hs.98321	Homo sapiens cDNA FLJ14103 fis, clone MA	15.00				
	122772	AW117452	Hs.99489	ESTs	6.67				
20	122831	AI857570	Hs.5120	ESTs				3.37	
	122913	AI638774	Hs.105328	ESTs		32.20			
	123049	BE047680	Hs.211869	ESTs		41.80			
	123076	AI345569	Hs.190046	ESTs	35.80				
	123136	AW451999	Hs.194024	ESTs				2.58	
25	123309	N52937	Hs.102679	ESTs		19.00			
	123455	AA353113	Hs.112497	ESTs		82.80			
	123691	AA609579	Hs.112724	ESTs				3.95	
	123756	AA609971	Hs.112795	EST	35.40				
	123802	AA620448	Homo sapiens clone 24760 mRNA sequence	58.00					
30	123837	AI807243	Hs.112893	ESTs		32.40			
	123844	AA938905	Hs.120017	olfactory receptor, family 7; subfamily		2.63			
	123936	NM_004673	Hs.241519	ESTs	29.00				
	123987	C21171	Hs.95497	ESTs; Weakly similar to GLUCOSE TRANSPOR		70.60			
	124013	AI521936	Hs.107149	ESTs; Weakly similar to PTB-ASSOCIATED S	28.40				
35	124160	R40290	Hs.124685	ESTs		13.00			
	124205	H77570	Hs.108135	ESTs				4.74	
	124226	AA618527	Hs.190266	ESTs		2.35			
	124246	H67680	Hs.270952	ESTs		29.40			
40	124348	AI796320	Hs.10299	ESTs	17.00				
	124358	AW070211	Hs.102415	*yw35g11.s1 Morton Fetal Cochlea Homo sa		3.07			
	124409	AI814166	Hs.107197	ESTs				3.14	
	124442	AW663632	Hs.285625	TATA box binding protein (TBP)-associate		2.48			
	124468	N51413	Hs.109284	ESTs		30.80			
	124479	AB011130	Hs.127436	calcium channel; voltage-dependent; alph				6.03	
45	124519	AI670056	Hs.137274	ESTs; Weakly similar to SPLICEOSOME ASSO		2.50			
	124711	NM_004657	Hs.26530	serum deprivation response (phosphatidyl	59.20				
	124866	AI768289	Hs.304389	ESTs	8.00				
	124874	BE550182	Hs.127826	ESTs		37.60			
	125097	AW576389	Hs.335774	ESTs		10.00			
50	125179	AW205468	Hs.103118	ESTs				3.12	
	125200	AW836591	Hs.103156	ESTs				2.79	
	125299	T32982	Hs.102720	ESTs		34.20			
	125400	AL110151	Hs.128797	DKFZP586D0824 protein	29.00				
	125810	H00083		aryl hydrocarbon receptor-interacting pr	32.20				
55	126176	BE242256	Hs.2441	KIAA0022 gene product		12.00			
	126303	D78841		HUM525A05B Human placenta polyA+ (TFuj		33.60			
	126403	AW629054	Hs.125976	ESTs; Weakly similar to metalloprotease/	35.80				
	126507	AL040137	Hs.23964	ESTs; Weakly similar to HC1 ORF [M.muscu		29.80			
	126773	AA648284	Hs.187584	ESTs	39.60				
60	127307	AW962712	Hs.126712	ESTs; Weakly similar to pL2 hypotheticala	28.80				
	127462	AA760776	Hs.293977	aa59b04.s1 NCL CGAP_GCB1 Homo sapiens c		34.40			
	127486	AW002846	Hs.105468	ESTs	9.00				
	127572	AA594027	Hs.191788	ESTs		2.36			
	127609	X80031	Hs.530	ESTs		29.40			
65	127832	AW976035	Hs.292396	ESTs		37.20			
	127898	AA774725	Hs.128970	ESTs				4.42	
	128073	AW340720	Hs.125983	ESTs		38.40			
	128101	AA905730	Hs.128254	ESTs	7.33				
	128149	NM_012214	Hs.177576	mannosyl (alpha-1;3-)-glycoprotein beta-				2.58	
70	128212	W27411	Hs.336920	glutathione peroxidase 3 (plasma)		3.09			
	128333	W68800	Hs.12126	ESTs; Weakly similar to LR8 [H.sapiens]		34.40			
	128364	N76462	Hs.269152	ESTs; Weakly similar to ZINC FINGER PROT	10.00				
	128426	AI265784	Hs.145197	ESTs				4.31	
	128598	AA305407	Hs.102308	potassium inwardly-rectifying channel; s	31.20				
75	128634	AA464918		ESTs; Moderately similar to !!!! ALU SUB		41.60			
	128687	AW271273	Hs.23767	ESTs		87.00			
	128726	AI311238	Hs.104476	ESTs				4.02	
	128773	NM_004131	Hs.1051	granzyme B (granzyme 2; cytotoxic T-lymp		9.00			
	128833	W26667	Hs.184581	ESTs				3.76	
80	128870	H39537	Hs.75309	eukaryotic translation elongation factor	2.66				
	128878	R25513	Hs.10683	ESTs				3.10	
	128885	AF134803	Hs.180141	cofilin 2 (muscle)		11.00			
	128998	W04245	Hs.107761	ESTs; Weakly similar to PUTATIVE RHO/RAC				3.21	
	129000	AA744902	Hs.107767	ESTs; Moderately similar to CaM-KII inh					3.68
	129038	AW156903	Hs.108124	ribosomal protein L41				3.17	
85	129098	AW580945	Hs.330466	ESTs	34.60				

	129210	AL039940	Hs.202949	KIAA1102 protein					4.09
	129240	AA361258	Hs.237868	interleukin 7 receptor	2.29				
	129262	BE222198	Hs.109843	ESTs			3.30		
5	129301	AF182277	Hs.330780	Human cytochrome P450-IIB (hIIB3) mRNA;					4.05
	129331	AW167668	Hs.279772	ESTs; Highly similar to CGI-38 protein [4.09
	129381	AW245805	Hs.110903	claudin 5 (transmembrane protein deleted	2.93				
	129565	X77777	Hs.198726	vasoactive intestinal peptide receptor 1		160.80			
	129595	U09550	Hs.1154	oviductal glycoprotein 1; 120kD			10.00		
10	129613	AW978517	Hs.172847	ESTs; Weakly similar to collagen alpha 1				3.40	
	129782	AW016932	Hs.104105	EST	9.00				
	129950	F07783	Hs.1369	decay accelerating factor for complement		87.80			
	129958	R27496	Hs.1378	annexin A3		44.60			
	129959	AL036554	Hs.274463	defensin; alpha 1; myeloid-related seque	2.72				
15	130160	AA305688	Hs.267695	UDP-Gal:betaGlcNAc beta 1;3-galactosyltr		42.20			
	130259	NM_000328	Hs.153614	retinitis pigmentosa GTPase regulator	2.54				
	130273	AW972422	Hs.153863	MAD (mothers against decapentaplegic; Dr		51.60			
	130312	AF056195	Hs.15430	DKFZP586G1219 protein				3.16	
	130436	NM_001928	Hs.155597	D component of complement (adipsin)					4.11
20	130523	AA999702	Hs.214507	ESTs				4.77	
	130799	AB028945	Hs.12696	ESTs	6.00				
	130885	NM_005883	Hs.20912	adenomatous polyposis coli like				3.54	
	131002	AL050295	Hs.22039	KIAA0758 protein					3.50
	131012	AL039940	Hs.202949	KIAA1102 protein	20.00				
25	131031	NM_001650	Hs.288650	aquaporin 4	41.20				
	131061	N64328	Hs.268744	ESTs; Moderately similar to KIAA0273 [H.		31.40			
	131066	AW169287	Hs.22588	ESTs		29.60			
	131082	AI091121	Hs.246218	ESTs; Weakly similar to zinc finger prot			9.00		
	131087	AF147709	Hs.22824	ESTs; Weakly similar to p160 myb-binding					3.86
30	131161	AF033382	Hs.23735	potassium voltage-gated channel; subfam				3.14	
	131179	AA171368	Hs.184482	DKFZP586D0624 protein				3.80	
	131182	AI824144	Hs.23912	ESTs					3.67
	131205	NM_003102	Hs.2420	superoxide dismutase 3; extracellular	2.98				
	131277	AA131466	Hs.23767	ESTs	3.15				
35	131281	AA251716	Hs.25227	ESTs		32.20			
	131282	X03350	Hs.4	alcohol dehydrogenase 3 (class I); gamma					3.44
	131285	AI567943	Hs.25274	ESTs; Moderately similar to putative sev				6.40	
	131355	R52804	Hs.25956	DKFZP564D206 protein	8.00				
	131391	AW085781	Hs.26270	ESTs	10.00				
40	131461	AA992841	Hs.27263	butyrate response factor 2 (EGF-response	28.80				
	131487	F13036	Hs.27373	Homo sapiens mRNA; cDNA DKFZp564O1763 (f					4.03
	131517	AB037789	Hs.263395	ESTs; Highly similar to semaphorin VIa [39.00				
	131545	AL137432	Hs.28564	ESTs			11.00		
	131583	AK000383	Hs.323092	ESTs; Weakly similar to dual specificity			10.00		
45	131647	AA359615	Hs.30089	ESTs	2.47				
	131675	H15205	Hs.30509	ESTs				3.06	
	131676	AI126821	Hs.30514	ESTs	45.80				
	131708	S60415	Hs.30941	calcium channel; voltage-dependent; beta	2.28				
	131717	X94630	Hs.3107	CD97 antigen					3.78
50	131756	AA443966	Hs.31595	ESTs		40.60			
	131762	AA744902	Hs.107767	ESTs; Moderately similar to CaM-KII inhi					3.67
	131821	AA017247	Hs.164577	ESTs	2.87				
	131839	AB014533	Hs.33010	KIAA0633 protein					3.48
55	131861	AL096858	Hs.184245	KIAA0929 protein Mx2 interacting nuclea	54.00				
	132015	AI418006	Hs.3731	ESTs		49.20			
	132070	BE622641	Hs.38489	ESTs		34.80			
	132242	AA332697	Hs.42721	ESTs	2.68				
	132334	AW080704	Hs.45033	lacrima proline rich protein	4.66				
	132476	AL119844	Hs.49476	Homo sapiens clone TUA8 Cri-du-chat regi	34.20				
60	132490	NM_001290	Hs.4980	LIM binding domain 2	2.66				
	132533	AI922988	Hs.172510	ESTs	13.00				
	132598	X80031	Hs.530	collagen; type IV; alpha 3 (Goodpasture		30.60			
	132619	H28855	Hs.53447	ESTs; Moderately similar to kinesin lig				4.02	
	132652	N41739	Hs.61260	ESTs				3.18	
65	132726	N52298	Hs.55608	ESTs; Weakly similar to cDNA EST yk484g1			11.43		
	133028	R51604	Hs.300842	ESTs	2.37				
	133071	BE384932	Hs.64313	ESTs	2.27				
	133120	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein	2.63				
	133129	AA428580	Hs.65551	ESTs					5.49
70	133147	AA026533	Hs.66	interleukin 1 receptor-like 1	6.20				
	133151	NM_014051	Hs.94896	ESTs				3.69	
	133213	AA903424	Hs.6786	ESTs		31.40			
	133276	AW978439	Hs.69504	ESTs			9.00		
75	133377	AJ131245	Hs.7239	SEC24 (S. cerevisiae) related gene famil	41.20				
	133407	AF017987	Hs.7306	secreted frizzled-related protein 1	50.20				
	133535	AL134030	Hs.284180	protocadherin 2 (cadherin-like 2)				3.72	
	133537	U41518	Hs.74602	aquaporin 1 (channel-forming integral pr					3.35
	133656	BE149455	Hs.75415	Accession not listed in Genbank	2.65				
	133689	NM_001872	Hs.75572	carboxypeptidase B2 (plasma)		90.80			
80	133779	T58486	Hs.222566	ESTs				3.05	
	133978	AF035718	Hs.78061	transcription factor 21	2.92				
	133985	L34657	Hs.78146	platelet/endothelial cell adhesion molec					3.45
	134000	AW175787	Hs.334841	selenium binding protein 1					4.05
	134111	AI372588	Hs.8022	TU3A protein	4.49				
85	134185	AA285136	Hs.301914	Homo sapiens mRNA; cDNA DKFZp586K1220 (f					3.27
	134204	AI873257	Hs.7994	ESTs; Weakly similar to CGI-69 protein [40.80			

	134641	AI092634	Hs.156114	protein tyrosine phosphatase; non-recept				3.76
	134677	AA251363	Hs.177711	ESTs		32.20		
	134745	NM_000685	Hs.89472	angiotensin receptor 1B	15.00			
5	134749	T28499	Hs.89485	carbonic anhydrase IV		3.05		
	134786	T29618	Hs.89640	angiotensin 1 receptor; TEK tyrosine ki			57.80	
	134825	U33749	Hs.197764	thyroid transcription factor 1				3.73
	134978	AI829008	Hs.333333	ficolin (collagen/fibrinogen domain-cont		2.52		
	135010	N50465	Hs.92927	ESTs		31.60		
10	135053	AW796190	Hs.93678	ESTs			3.21	
	135081	AF069517	Hs.173993	RNA binding motif protein 6	28.80			
	135091	AA493650	Hs.94367	ESTs				4.24
	135135	AA775910	Hs.95011	syntrophin; beta 1 (dystrophin-associate		8.00		
	135203	C15737	Hs.269386	ESTs			4.31	
15	135236	AI636208	Hs.96901	ESTs	43.00			
	135266	R41179	Hs.97393	Human mRNA for KIAA0328 gene; partial cd			6.42	
	135346	NM_000928	Hs.992	phospholipase A2; group I3 (pancreas)		3.82		
	135378	AW961818	Hs.24379	potassium voltage-gated channel; shaker-		4.15		
	135387	NM_001972	Hs.99863	elastase 2; neutrophil	37.20			
20	135388	W27965	Hs.99865	EST	38.80			
	135402	L12398	Hs.99922	dopamine receptor D4			4.21	

TABLE 2B shows the accession numbers for those primekeys lacking unigenelD's for Table 2A. For each probe set we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probe set identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

Pkey	CAT number	Accessions
35	108447	43452_7 AA079126
	108550	120073_1 AA084867 AA084996
	108655	127522_1 AA099960 AA113013
	102397	44371_1 U41898
	126303	1525933_1 D78841 D78880
40	125810	1554054_1 H00083 R81062
	103627	2615_2 Z48513 Z48512
	121366	280401_1 AI743515 AA405617 AW276706
	114609	116777_1 AA079505 AA079537
	115272	172113_1 AW015947 AA211890 AA279425
45	108338	112186_1 AA070773 AA070774
	108434	114012_1 AA078899 AA078782 AA075788
	123802	genbank_AA620448 AA620448
	102310	NOT_FOUND_entrez_U33839 U33839
	102636	entrez_U67092 U67092
50	104776	genbank_AA026349 AA026349
	120504	genbank_AA256837 AA256837
	113502	genbank_T89130T89130
	108499	genbank_AA083103 AA083103
	101308	entrez_L41390 L41390
55	108629	genbank_AA102425 AA102425
	103098	Z21_215 M86361 Z26593 X02850 D13070 AE000659 M17649 M87869 M87871 X61077 M16286 AF018169 X61079 S59351 X60142 AF043169
	103241	entrez_X76223 X76223
	103508	entrez_Y10141 Y10141
	103575	entrez_Z26256 Z26256
60	119514	NOT_FOUND_entrez_W37937 W37937
	121082	genbank_AA398722 AA398722
	128634	AA464918_at AA464918
	105817	genbank_AA397825 AA397825
	121518	genbank_AA412155 AA412155
65	114449	genbank_AA020736 AA020736
	114648	genbank_AA101056 AA101056
	121950	genbank_AA429515 AA429515
	107723	genbank_AA015967 AA015967

Table 3A shows 452 genes up-regulated in chronically diseased lung relative to normal lung. Chronically diseased lung samples represent chronic non-malignant lung diseases such as fibrosis, emphysema, and bronchitis. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

5	Pkey:	Unique Eos probeset identifier number					
	ExAccn:	Exemplar Accession number, Genbank accession number					
	UnigeneID:	Unigene number					
	Unigene Title:	Unigene gene title					
10	R1:	80th percentile of AI for chronically diseased lung samples divided by the 90th percentile of AI for normal lung samples.					
	R2:	80th percentile of AI for chronically diseased lung samples divided by the 90th percentile of normal lung samples, squamous cell carcinomas and adenocarcinomas					
	R3:	70th percentile of AI for chronically diseased lung samples minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples divided by the 90th percentile of normal lung samples, squamous cell carcinomas and adenocarcinomas minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples					
15							
	Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2	R3
20	135423	U50531	Hs.138751	Human BRCA2 region, mRNA sequence CG030	12.40		
	135378	AW961818	Hs.24379	MUM2 protein			2.13
	135346	NM_000928	Hs.992	phospholipase A2, group IB (pancreas)			
	135235	AW298244	Hs.293507	ESTs	12.40		
	135057	U90268	Hs.93810	cerebral cavernous malformations 1	11.67		
25	134951	BE305081	Hs.169358	hypothetical protein		8.00	
	134799	M36821	Hs.89690	GRO3 oncogene		8.20	
	134786	T29618	Hs.89640	TEK tyrosine kinase, endothelial (venous			
	134772	NM_000829	Hs.163697	glutamate receptor, ionotropic, AMPA 4	29.80		
	134752	BE246762	Hs.89499	arachidonate 5-lipoxygenase			1.93
	134749	T28499	Hs.89485	carbonic anhydrase IV			2.07
30	134696	BE326276	Hs.8861	ESTs			
	134636	NM_005582	Hs.87205	lymphocyte antigen 64 (mouse) homolog, r	13.60		
	134627	AI018768	Hs.12482	glyceronephosphate O-acyltransferase			1.92
	134622	AW975159	Hs.293097	ESTs, Weakly similar to A55380 facio geni			1.92
35	134570	U66615	Hs.172280	SWI/SNF related, matrix associated, acti	13.20		
	134561	U76421	Hs.85302	adenosine deaminase, RNA-specific, B1 (h			1.78
	134468	NM_001772	Hs.83731	CD33 antigen (gp67)		6.20	
	134417	NM_006416	Hs.82921	solute carrier family 35 (CMP-sialic aci			
	134343	D50683	Hs.82028	transforming growth factor, beta recepto			
40	134323	BE170651	Hs.8700	deleted in liver cancer 1			
	134300	NM_001430	Hs.8136	endothelial PAS domain protein 1			
	134299	AW580939	Hs.97199	complement component C1q receptor			
	134253	X52075	Hs.80738	sialophorin (gpL115, leukosialin, CD43)	20.60		
	134182	D52059	Hs.7972	KIAA0871 protein	12.20		
45	133985	L34657	Hs.78146	platelet/endothelial cell adhesion molec			
	133978	AF035718	Hs.78061	transcription factor 21			
	133835	AI677897	Hs.76640	RGC32 protein			
	133651	AI301740	Hs.173381	dihydropyrimidinase-like 2			
	133633	D21262	Hs.75337	nucleolar and coiled-body phosphoprotein	15.20		
50	133565	AW955776	Hs.313500	ESTs, Moderately similar to ALU7_HUMAN A			
	133548	AW946384	Hs.178112	DNA segment, single copy probe LNS-CAI/L			1.77
	133488	AA335295	Hs.74120	adipose specific 2			
	133478	X83703	Hs.31432	cardiac ankyrin repeat protein			2.08
	133337	AF085983	Hs.293676	ESTs		9.60	
55	133200	AB037715	Hs.183639	hypothetical protein FLJ10210			1.77
	133153	AF070592	Hs.66170	HSKM-B protein	30.60		
	133130	AI128606	Hs.6557	zinc finger protein 161	22.60		
	133120	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein			
	132928	AW168082	Hs.169449	protein kinase C, alpha	13.80		
60	132836	AB023177	Hs.29900	KIAA0960 protein			
	132799	W73311	Hs.169407	SAC2 (suppressor of actin mutations 2,	41.60		
	132742	AA025480	Hs.292812	ESTs, Weakly similar to T33468 hypotheti	40.40		
	132548	X12830	Hs.193400	interleukin 6 receptor		7.20	
	132476	AL119844	Hs.49476	Homo sapiens clone TUA8 Cri-du-chat regi		4.76	
65	132439	AK001942	Hs.4863	hypothetical protein DKFZp566A1524			1.88
	132240	AB018324	Hs.42676	KIAA0781 protein	21.20		
	132210	NM_007203	Hs.42322	A kinase (PRKA) anchor protein 2			1.99
	132199	AL041299	Hs.165084	ESTs	15.20		
	131751	T96555	Hs.31562	ESTs			1.76
70	131745	AI828559	Hs.31447	ESTs, Moderately similar to A46010 X-li	27.80		
	131694	NM_000246	Hs.3076	MHC class II transactivator		4.00	
	131686	NM_012296	Hs.30687	GRB2-associated binding protein 2			
	131676	AI126821	Hs.30514	ESTs		6.20	
	131629	Z45794	Hs.238809	ESTs	21.40		
75	131589	C18825	Hs.29191	epithelial membrane protein 2			
	131536	AA019201	Hs.269210	ESTs		9.40	
	131517	AB037789	Hs.263395	sema domain, transmembrane domain (TM),		3.59	
	131355	R52804	Hs.25956	DKFZP564D206 protein		4.48	
	131253	R71802	Hs.24853	ESTs	15.00		
80	131207	AF104266	Hs.24212	latrophilin			1.75
	131156	AI472209	Hs.323117	ESTs			1.84
	131066	AW169287	Hs.22588	ESTs		3.54	
	131061	N64328	Hs.268744	KIAA1796 protein			
	131053	AA348541	Hs.296261	guanine nucleotide binding protein (G pr			1.93
	130895	AA641767	Hs.21015	hypothetical protein DKFZp564L0864 simil	16.60		
85	130762	D84371	Hs.1898	paraoxonase 1	12.00		

	130657	AW337575	Hs.201591	ESTs		
	130655	AI831962	Hs.17409	cysteine-rich protein 1 (intestinal)		
	130589	AL110226	Hs.16441	DKFZP434H204 protein		2.08
5	130562	D50402	Hs.182611	solute carrier family 11 (proton-coupled)		1.91
	130555	R69743	Hs.116774	integrin, alpha 1	9.60	
	130365	W56119	Hs.155103	eukaryotic translation initiation factor	11.60	
	130273	AW972422	Hs.153863	MAD (mothers against decapentaplegic, Dr	6.60	
	130259	NM_000328	Hs.153614	retinitis pigmentosa GTPase regulator		1.91
10	130090	H97878	Hs.132390	zinc finger protein 36 (KOX 18)	21.20	
	129958	R27496	Hs.1378	annexin A3	5.05	
	129898	AI672731	Hs.13256	ESTs		
	129875	AA181018	Hs.13056	hypothetical protein FLJ13920	18.60	
	129699	AB007899	Hs.12017	homolog of yeast ubiquitin-protein ligas		
	129626	F13272	Hs.111334	feritin, light polypeptide		
15	129598	N30436	Hs.11556	Homo sapiens cDNA FLJ12566 fis, clone NT	22.63	
	129593	AI338247	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (f		
	129565	X77777	Hs.198726	vasoactive intestinal peptide receptor 1		2.53
	129527	AA769221	Hs.270847	delta-tubulin	39.20	
	129402	W72062	Hs.11112	ESTs		2.11
20	129385	AA172106	Hs.110950	Rag C protein	15.20	
	129315	NM_014563	Hs.174038	spondyloepiphyseal dysplasia, late	12.40	
	129312	T97579	Hs.110334	ESTs, Weakly similar to I78885 serine/th	20.83	
	129240	AA361258	Hs.237868	interleukin 7 receptor		1.95
	129210	AL039940	Hs.202949	KIAA1102 protein		
25	129122	AW958473	Hs.301957	nudix (nucleoside diphosphate linked moi	4.20	
	129057	N90866	Hs.276770	CDW52 antigen (CAMPATH-1 antigen)		
	128946	Y13153	Hs.107318	kynurenine 3-monooxygenase (kynurenine 3	5.20	
	128798	AF015525	Hs.302043	chemokine (C-C motif) receptor-like 2		
30	128789	AW368576	Hs.139851	caveolin 2		2.24
	128778	AA504776	Hs.186709	ESTs, Weakly similar to I38022 hypothet	12.20	
	128766	AW160432	Hs.296460	craniofacial development protein 1	26.40	
	128631	R44238	Hs.155546	KIAA1080 protein; Golgi-associated, gamm		1.78
	128624	BE154765	Hs.102647	ESTs, Weakly similar to TRHY_HUMAN TRICH		2.51
	128609	NM_003616	Hs.102456	survival of motor neuron protein interac	16.00	
35	128603	NM_004915	Hs.10237	ATP-binding cassette, sub-family G (WHIT	12.80	
	128598	AA305407	Hs.102308	potassium inwardly-rectifying channel, s		4.00
	128458	H55864	Hs.56340	ESTs		
	128061	AF150882	Hs.186877	sodium channel, voltage-gated, type XII,	17.20	
40	127968	AA830201	Hs.124347	ESTs	21.30	
	127959	AI302471	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L		
	127944	AI557081	Hs.262476	S-adenosylmethionine decarboxylase 1	10.60	
	127925	AA805151	Hs.3628	mitogen-activated protein kinase kinase	13.40	
	127896	AI669586	Hs.222194	ESTs	7.00	
	127859	AA761802	Hs.291559	ESTs	14.00	
45	127817	AA836641	Hs.163085	ESTs	14.00	
	127742	AW293496	Hs.180138	ESTs	11.00	
	127628	AI240102	Hs.322430	NDRG family, member 4	11.10	
	127609	X80031	Hs.530	collagen, type IV, alpha 3 (Goodpasture		
50	127582	AA908954	Hs.130844	ESTs	19.60	
	127543	AK000787	Hs.157392	Homo sapiens cDNA FLJ20780 fis, clone CO	15.40	
	127535	AA568424	Hs.164450	ESTs	17.50	
	127404	AI379920	Hs.270224	ESTs	14.60	
	127396	L31968	Hs.187991	DKFZP564A122 protein	15.40	
55	127374	AA442797	Hs.312110	ESTs, Weakly similar to I38022 hypothet	14.60	
	127346	AA203616	Hs.44896	DnaJ (Hsp40) homolog, subfamily B, membe	21.00	
	127340	BE047653	Hs.119183	ESTs, Weakly similar to ZN91_HUMAN ZINC	15.80	
	127307	AW962712	Hs.126712	ESTs, Weakly similar to AF191020 I E2IG5		
	127242	AW390395	Hs.181301	cathepsin S	22.60	
60	127167	AA625690	Hs.190272	ESTs	21.40	
	127046	AA321948	Hs.293968	ESTs	41.20	
	126928	AA480902	Hs.137401	ESTs	11.00	
	126900	AF137386	Hs.12701	plasmolipin		1.78
	126852	AA399961		gb:zu68c01.r1 Soares_testis_NHT Homo sap	5.60	
65	126816	AA248234		gb:csq2228.seq.F Human fetal heart, Lamb	12.20	
	126812	AB037860	Hs.173933	nuclear factor I/A	17.19	
	126666	AA648886	Hs.151999	ESTs	13.57	
	126645	AA316181	Hs.61635	six transmembrane epithelial antigen of	15.40	
	126592	AI611153	Hs.6093	Homo sapiens cDNA: FLJ22783 fis, clone K	4.67	
70	126556	AF255303	Hs.112227	membrane-associated nucleic acid binding	18.00	
	126433	AA325606		gb:EST28707 Cerebellum II Homo sapiens c	16.77	
	126299	AW979155	Hs.298275	amino acid transporter 2	14.60	
	126218	AL049801	Hs.13649	Novel human gene mapping to chromosome 13	3.50	
	126182	AA721331	Hs.293771	ESTs	13.40	
75	126177	AW752782	Hs.129750	hypothetical protein FLJ10546	18.20	
	126142	H86261	Hs.40568	ESTs	14.00	
	126077	M78772	Hs.210836	ESTs	16.59	
	125994	AI990529	Hs.270799	ESTs	17.40	
	125934	AA193325	Hs.32646	hypothetical protein FLJ21901	13.00	
80	125847	AW161885	Hs.249034	ESTs	49.57	
	125831	H04043		gb:yj45c03.r1 Soares_placenta Nb2HP Homo		
	125731	R61771	Hs.26912	ESTs	13.20	
	125676	BE612918	Hs.151973	hypothetical protein FLJ23511	11.20	
	125561	F18572	Hs.22978	ESTs, Weakly similar to ALU4_HUMAN ALU S		
	125552	H09701	Hs.278366	ESTs, Weakly similar to I38022 hypotheti	12.60	
85	125489	H49193	Hs.124984	ESTs, Moderately similar to ALU7_HUMAN A	33.40	

	125422	AA903229	Hs.153717	ESTs		1.80
	125331	AI422996	Hs.161378	ESTs	38.00	
	125309	T12411	Hs.183745	hypothetical protein FLJ13456	18.20	
5	125167	AL137540	Hs.102541	netrin 4		1.95
	125139	AW194933	Hs.9788	hypothetical protein MGC10924 similar to		1.84
	125042	T78906	Hs.269432	ESTs, Moderately similar to ALU1_HUMAN	21.80	
	124711	NM_004657	Hs.26530	serum deprivation response (phosphatidyl		10.60
	124631	NM_014053	Hs.270594	FLVCR protein	23.20	
10	124578	N58321	Hs.231500	EST	21.43	
	124574	AL036596	Hs.42322	A kinase (PRKA) anchor protein 2		1.77
	124472	N52517	Hs.102670	EST	37.20	
	124438	BE178536	Hs.11090	membrane-spanning 4-domains, subfamily A		
	124357	N22401		gb:yyw37g07.s1 Morton Fetal Cochlea Homo	14.64	
15	124306	AW973078	Hs.293039	ESTs		4.00
	124214	H58608	Hs.151323	ESTs		
	124097	AW298235	Hs.101689	ESTs	27.20	
	123978	T89832	Hs.170278	ESTs		2.03
	123972	T46848	Hs.70337	immunoglobulin superfamily, member 4	6.00	
20	123961	AL050184	Hs.21610	DKFZP434B203 protein		1.79
	123936	NM_004673	Hs.241519	angiotensin-like 1	15.80	
	123802	AA620448		gb:ae58c09.s1 Stratagene lung carcinoma	4.23	
	123734	AA609861	Hs.312447	ESTs	4.20	
	123619	AA602964		gb:nc97c02.s1 NCI_CGAP_Pr2 Homo sapiens	33.60	
25	123596	AA421130	Hs.112640	EST	10.93	
	123476	AA384564	Hs.108829	ESTs		2.18
	123340	AA504264	Hs.182937	peptidylprolyl isomerase A (cyclophilin	11.20	
	123190	AA489212	Hs.105228	EST	14.20	
	123136	AW451999	Hs.194024	ESTs		7.00
30	123073	AA485061	Hs.105652	ESTs	31.20	
	123055	AA482005	Hs.105102	ESTs, Weakly similar to reverse transcri		4.80
	122699	AA456130	Hs.301721	KIAA1255 protein		5.00
	122679	AA811286	Hs.192837	ESTs, Weakly similar to ALU5_HUMAN ALU S	14.40	
	122633	NM_001546	Hs.34853	Inhibitor of DNA binding 4, dominant neg		
35	122553	AA451884	Hs.190121	ESTs	40.00	
	122544	AW973253	Hs.292689	ESTs	15.40	
	122485	AA524547	Hs.160318	FXD domain-containing ion transport reg		1.81
	122211	AA300900	Hs.98849	ESTs, Moderately similar to AF161511.1 H	12.10	
	122127	AW207175	Hs.106771	ESTs		1.95
40	122011	AA431082		gb:zw78a10.s1 Soares_testis_NHT Homo sap		1.89
	121992	AI860775	Hs.98506	ESTs	3.60	
	121989	W55487	Hs.193784	Homo sapiens mRNA; cDNA DKFZp586K1922 (f		2.01
	121835	AB033030	Hs.300670	KIAA1204 protein		1.85
	121726	AF241254	Hs.178098	angiotensin I converting enzyme (peptidy	12.43	
45	121690	AV660305	Hs.110286	ESTs		1.82
	121643	AA640987	Hs.193767	ESTs		
	121633	AA417011	Hs.98175	EST	14.00	
	121622	AA416931	Hs.126065	ESTs		16.40
	121497	AA412031	Hs.97901	EST	11.20	
50	121351	AW206227	Hs.287727	hypothetical protein FLJ23132	12.20	
	121314	W07343	Hs.182538	phospholipid scramblase 4		1.83
	121242	AA400857	Hs.97509	ESTs	22.40	
	121059	AA393283		gb:zt74e03.r1 Soares_testis_NHT Homo sap	14.80	
	120934	AA226198		gb:nc26a07.s1 NCI_CGAP_Pr1 Homo sapiens	21.20	
55	120755	AA312934	Hs.190745	Homo sapiens cDNA: FLJ21326 fis, clone		1.79
	120637	AA811804		gb:ob39a05.s1 NCI_CGAP_GCB1 Homo sapiens	20.00	
	120484	AA253170	Hs.96473	EST	40.20	
	120336	N85785	Hs.181165	eukaryotic translation elongation factor		6.60
	120266	AI807264	Hs.205442	ESTs, Weakly similar to T34036 hypotheti	16.80	
60	120132	W57554	Hs.125019	ESTs		4.73
	120041	AA830882	Hs.59368	ESTs		1.75
	119996	W88996	Hs.59134	EST	7.20	
	119970	AA767718	Hs.93581	hypothetical protein FLJ10512	11.20	
	119861	W78816	Hs.49943	ESTs, Weakly similar to S65657 alpha-1C-		3.78
65	119824	W74536	Hs.184	advanced glycosylation end product-speci		
	119740	AW021407	Hs.21068	hypothetical protein	20.20	
	119271	AI061118	Hs.65328	Fanconi anemia, complementation group F	15.20	
	119221	C14322	Hs.250700	trypsin beta 1		
	119126	R45175	Hs.117183	ESTs	12.60	
70	119073	BE245360	Hs.279477	ESTs		
	118928	AA312799	Hs.283689	activator of CREM in testis		10.00
	118901	AW282577	Hs.94445	ESTs	3.96	
	118661	AL137554	Hs.49927	protein kinase NYD-SP15	9.60	
	118607	AI377444	Hs.54245	ESTs, Weakly similar to S65824 reverse t	10.40	
75	118449	AI813865	Hs.164478	hypothetical protein FLJ21939 similar to		1.90
	118416	N56028	Hs.49105	FKBP-associated protein	16.20	
	118379	N54491	Hs.48990	ESTs		4.00
	118329	N63520		gb:yy62f01.s1 Soares_multiple_sclerosis_		6.60
	118320	N63451	Hs.141600	ESTs, Weakly similar to alternatively s		3.80
80	118253	AA497044	Hs.20887	hypothetical protein FLJ10392	17.60	
	118124	N56968	Hs.46707	chromosome 21 open reading frame 37	14.00	
	118056	AB037746	Hs.42768	hypothetical protein DKFZp761O0113		1.86
	118032	N52802	Hs.47544	EST		5.00
	117840	T26379	Hs.48802	Homo sapiens clone 23632 mRNA sequence		4.00
	117404	N39725	Hs.15220	zinc finger protein 106		1.90
85	117314	N32498	Hs.42829	ESTs	14.20	

	117209	W03011	Hs.306881	MSTP043 protein			
	117023	AW070211	Hs.102415	Homo sapiens mRNA; cDNA DKFZp586N0121 (f	20.20	2.31	
	116814	H50834		gb:yp86a10.s1 Soares fetal liver spleen			
5	116784	AB007979	Hs.301281	Homo sapiens mRNA, chromosome 1 specific		3.51	
	116766	AI608557	Hs.95097	ESTs	16.20		
	116712	AW901618	Hs.61935	Homo sapiens mRNA; cDNA DKFZp7611071 (fr		6.80	
	116707	H10344	Hs.49050	ESTs, Weakly similar to A Chain A, Human	18.60		
	116351	AL133623	Hs.82501	similar to mouse Xrn1 / Dhms2 protein	19.40		
10	116279	AW971248	Hs.291289	ESTs, Weakly similar to ALU1_HUMAN ALU S			
	116166	AL039940	Hs.202949	KIAA1102 protein		2.13	
	116152	AL040521	Hs.15220	zinc finger protein 106		1.75	
	116117	BE613410	Hs.31575	SEC63, endoplasmic reticulum translocon	13.20		
	116107	AL133916	Hs.172572	hypothetical protein FLJ20093	30.11		
15	115965	AA001732	Hs.173233	hypothetical protein FLJ10970		2.36	
	115955	AF263613	Hs.44198	intracellular membrane-associated calciu	18.20		
	115844	AI373062	Hs.332938	hypothetical protein MGC5370	18.57		
	115683	AF255910	Hs.54650	junctional adhesion molecule 2		23.00	
	115673	AA406341	Hs.269908	Homo sapiens cDNA FLJ11991 fis, clone HE	11.82		
20	115672	AI889110	Hs.73251	ESTs	10.60		
	115566	AI142336	Hs.43977	Human DNA sequence from clone RP11-196N1		1.76	
	115313	AA808001	Hs.184411	albumin	25.20		
	115279	AW964897	Hs.290825	ESTs		8.00	
	115230	AA278300	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L		1.80	
25	115110	AK001671	Hs.11387	KIAA1453 protein	14.20		
	114999	BE246481	Hs.87856	ESTs	19.20		
	114930	AA237022	Hs.188717	ESTs		5.60	
	114922	AA235672	Hs.87491	ESTs		3.60	
	114837	BE244930	Hs.166895	ESTs	43.70		
30	114769	AA149060	Hs.296100	ESTs	11.00		
	114761	AA143781	Hs.126280	hypothetical protein FLJ23393	14.00		
	114736	AI610347	Hs.103812	ESTs, Moderately similar to ALU1_HUMAN A		4.20	
	114596	AA310162	Hs.169248	cytochrome c	10.71		
	114518	AW163267	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like	20.40		
35	114455	H37908	Hs.271616	ESTs, Weakly similar to ALU8_HUMAN ALU S	20.40		
	114452	AI369275	Hs.243010	Homo sapiens cDNA FLJ14445 fis, clone HE		17.20	
	114359	NM_016929	Hs.283021	chloride intracellular channel 5		2.09	
	114357	R41677	Hs.6107	Homo sapiens cDNA FLJ14839 fis, clone OV	12.40		
	114251	H15261	Hs.21948	ESTs		2.00	
40	114138	AW384793	Hs.15740	Homo sapiens mRNA; cDNA DKFZp434E033 (fr		11.40	
	114124	W57554	Hs.125019	ESTs		6.04	
	113946	AW083883	Hs.37896	Homo sapiens cDNA FLJ13510 fis, clone PL		1.82	
	113695	T96965	Hs.17948	ESTs, Weakly similar to ALUB_HUMAN !!!!			
	113606	NM_013343	Hs.278951	NAG-7 protein		2.15	
45	113590	R49642	Hs.142447	ESTs, Weakly similar to ALU1_HUMAN ALU S		3.60	
	113560	T91015	Hs.268626	ESTs	32.00		
	113552	AI654223	Hs.16026	hypothetical protein FLJ23191			
	113540	AW152618	Hs.16757	ESTs			
50	113502	T89130		gb:ye12d01.s1 Stratagene lung (937210) H		8.35	
	113288	AI076838	Hs.12967	ESTs	12.40		
	113252	NM_004469	Hs.11392	c-fos induced growth factor (vascular en		4.27	
	113238	R45467	Hs.189813	ESTs			
	113203	AA743563	Hs.10305	ESTs	21.20		
	113195	H83265	Hs.8881	ESTs, Weakly similar to S41044 chromosom		1.92	
55	113089	T40707	Hs.270862	ESTs	14.33		
	113076	AF033199	Hs.8198	zinc finger protein 204		6.00	
	113009	T23699	Hs.7246	ESTs		9.40	
	112937	AI694320	Hs.6295	ESTs, Weakly similar to T17248 hypotheli		12.20	
	112891	T03927	Hs.293147	ESTs, Moderately similar to A46010 X-li	10.57		
60	112794	R97018		gb:yq74b08.s1 Soares fetal liver spleen	26.60		
	112691	R88708	Hs.220647	ESTs	15.33		
	112602	AW004045	Hs.203365	ESTs	15.60		
	112366	AF035318	Hs.12533	Homo sapiens clone 23705 mRNA sequence	15.40		
	112210	R49645	Hs.7004	ESTs	14.00		
65	112064	AL049390	Hs.22689	Homo sapiens mRNA; cDNA DKFZp586O1318 (f	13.00		
	111998	R42379	Hs.138283	ESTs	11.00		
	111987	NM_015310	Hs.6763	KIAA0942 protein	22.40		
	111803	AA593731	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A		1.77	
	111737	H04607	Hs.9218	ESTs		1.86	
70	111605	T91081	Hs.194178	ESTs, Moderately similar to PC4259 ferri	23.00		
	111510	R07856	Hs.16355	ESTs	11.02		
	111341	AL157484	Hs.22483	Homo sapiens mRNA; cDNA DKFZp762M127 (fr		1.88	
	111280	AA373527	Hs.19385	CGI-58 protein	18.40		
	111247	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f			
75	111232	AI247763	Hs.16928	ESTs	27.60		
	110942	R63503	Hs.28419	ESTs	14.80		
	110924	AW058463	Hs.12940	zinc-fingers and homeoboxes 1	24.71		
	110837	H03109	Hs.108920	HT018 protein		2.18	
	110824	AI767183	Hs.26942	ESTs	12.20		
80	110776	AB032417	Hs.19545	frizzled (Drosophila) homolog 4		1.75	
	110576	H60869	Hs.37889	ESTs	13.00		
	110369	AK000768	Hs.107872	hypothetical protein FLJ20761		5.60	
	110099	R44557	Hs.23748	ESTs		2.31	
	109984	AI796320	Hs.10299	Homo sapiens cDNA FLJ13545 fis, clone PL			
85	109958	AA001266	Hs.133521	ESTs	11.25		
	109893	AA884208	Hs.30484	ESTs		2.68	

	109842	AW818435	Hs.23590	solute carrier family 16 (monocarboxylic	23.83		
	109837	H00656	Hs.29792	ESTs, Weakly similar to I38022 hypothe		3.91	
	109796	AI800515	Hs.12024	ESTs		17.20	
5	109688	R41900	Hs.22245	ESTs		9.60	
	109648	H17800	Hs.7154	ESTs	22.80		
	109613	H47315	Hs.27519	ESTs			
	109550	AW021488	Hs.26981	ESTs			
	109523	AW193342	Hs.24144	ESTs		1.89	
10	109472	AK001989	Hs.91165	hypothetical protein		6.00	
	109355	AA524525	Hs.48297	DKFZP586C1620 protein	15.00		
	109260	AW978515	Hs.131915	KIAA0863 protein	25.60		
	108781	AA128554		gbzn98g07.s1 Stratagene fetal retina 93	14.20		
	108663	BE219231	Hs.292653	ESTs, Weakly similar to T26845 hypothe	11.00		
15	108573	AA086005		gbzl84c04.s1 Stratagene colon (937204)	26.00		
	108480	AL133092	Hs.68055	hypothetical protein DKFZp434I0428			
	108382	NM_006770	Hs.67726	macrophage receptor with collagenous str		1.83	
	108174	AA055632	Hs.303070	ESTs	15.20		
	108138	AL049990	Hs.51515	Homo sapiens mRNA; cDNA DKFZp564G112 (fr		3.60	
20	108087	AA045708	Hs.40545	ESTs	15.44		
	108048	AI797341	Hs.165195	Homo sapiens cDNA FLJ14237 fis, clone NT		11.40	
	108041	AW204712	Hs.61957	ESTs			
	107997	AL049176	Hs.82223	chordin-like		4.76	
	107994	AA036811	Hs.48469	LIM domains containing 1			
25	107922	BE153855	Hs.61460	Ig superfamily receptor LNIR	14.20		
	107681	BE379594	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	51.80		
	107666	AA010611	Hs.60418	EST	29.20		
	107332	T87750	Hs.183297	DKFZP566F2124 protein	10.73		
	107292	BE166479	Hs.4789	Homo sapiens serologically defined breas	32.00		
30	107230	AI034467	Hs.34650	ESTs	17.40		
	107168	W57578	Hs.237955	RAB7, member RAS oncogene family	10.43		
	107160	AA314490	Hs.27669	KIAA1563 protein	11.40		
	107054	AI076459	Hs.15978	KIAA1272 protein			
	107029	AF264750	Hs.288971	myeloid/lymphoid or mixed-lineage leukem	21.40		
35	106999	H93281	Hs.10710	hypothetical protein FLJ20417	35.80		
	106954	AF128847	Hs.204038	indolethylamine N-methyltransferase		1.76	
	106870	AI983730	Hs.26530	serum deprivation response (phosphatidyl			
	106865	AW192535	Hs.19479	ESTs	13.40		
	106844	AA485055	Hs.158213	sperm associated antigen 6		7.13	
40	106820	NM_016831	Hs.12592	period (Drosophila) homolog 3		7.00	
	106818	AK002135	Hs.3542	hypothetical protein FLJ11273	13.00		
	106797	AI768801	Hs.169943	Homo sapiens cDNA FLJ13569 fis, clone PL		2.05	
	106773	AA478109	Hs.188833	ESTs			
	106747	NM_007118	Hs.171957	triple functional domain (PTPRF interact	12.60		
45	106743	BE613328	Hs.21938	hypothetical protein FLJ12492	10.60		
	106667	AW360847	Hs.16578	ESTs			
	106605	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (fr		2.40	
	106567	AW450408	Hs.86412	chromosome 9 open reading frame 5		1.78	
	106562	AL031846	Hs.152151	plakophilin 4		1.76	
50	106536	AA329648	Hs.23804	ESTs, Weakly similar to PN0099 son3 prot		2.19	
	106533	AL134708	Hs.145998	ESTs	23.20		
	106507	AA259068	Hs.267819	protein phosphatase 1, regulatory (inhib	15.20		
	106490	AA404265	Hs.115537	putative dipeptidase			
	106474	BE383668	Hs.42484	hypothetical protein FLJ10618	10.44		
55	106211	AA428240	Hs.126083	ESTs		29.80	
	105986	AB037722	Hs.8707	KIAA1301 protein		3.70	
	105894	AI904740	Hs.25691	receptor (calcitonin) activity modifying		1.94	
	105847	AW964490	Hs.32241	ESTs, Weakly similar to S65657 alpha-1C-		1.75	
	105803	AW747996	Hs.160999	ESTs, Moderately similar to A56194 throm		2.47	
60	105731	AA834664	Hs.29131	nuclear receptor coactivator 2	10.71		
	105729	H46612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds			
	105688	AI299139	Hs.17517	ESTs	23.40		
	105510	Z42047	Hs.283978	Homo sapiens PRO2751 mRNA, complete cds	37.20		
	105101	H63202	Hs.38163	ESTs		8.30	
65	104989	R65998	Hs.285243	hypothetical protein FLJ22029		8.09	
	104986	AW088826	Hs.117176	poly(A)-binding protein, nuclear 1		1.92	
	104969	AI670947	Hs.78406	phosphatidylinositol-4-phosphate 5-kinas		5.40	
	104903	AI436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,		7.60	
	104896	AW015318	Hs.23165	ESTs	13.80		
70	104865	T79340	Hs.22575	Homo sapiens cDNA: FLJ21042 fis, clone C			
	104825	AA035613	Hs.141883	ESTs		1.87	
	104781	AA099904	Hs.21610	DKFZP434B203 protein		1.93	
	104776	AA026349		gb:zj99f01.s1 Soares_pregnant_uterus_NbH		10.20	
	104691	U29690	Hs.37744	Homo sapiens beta-1 adrenergic receptor		5.69	
75	104667	AI239923	Hs.30098	ESTs		3.82	
	104404	H58762		gb:EST00057 HE6W Homo sapiens cDNA clone		4.20	
	104392	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	27.20		
	104212	AB002298	Hs.173035	KIAA0300 protein		1.91	
	104074	AL162039	Hs.31422	Homo sapiens mRNA; cDNA DKFZp434M229 (fr	11.20		
80	103749	AL135301	Hs.8768	hypothetical protein FLJ10849	10.86		
	103645	AW246253	Hs.7043	succinate-CoA ligase, GDP-forming, alpha	12.00		
	103554	AI878826	Hs.323469	caveolin 1, caveolae protein, 22kD		1.80	
	103541	AI815601	Hs.79197	CD83 antigen (activated B lymphocytes, i			
	103496	Y09267	Hs.132821	flavin containing monooxygenase 2			
85	103428	BE383507	Hs.78921	A kinase (PRKA) anchor protein 1	11.20		
	103353	X89399	Hs.119274	RAS p21 protein activator (GTPase activa	19.80		

5	103295	X81479	Hs.2375	egf-like module containing, mucin-like,	3.60	
	103280	U84722	Hs.76206	cadherin 5, type 2, VE-cadherin (vascula		
	103100	NM_005574	Hs.184585	LIM domain only 2 (rhombotin-like 1)		1.76
	103025	NM_002837	Hs.123641	protein tyrosine phosphatase, receptor t		2.15
	102698	M18667	Hs.1867	progastricsin (pepsinogen C)		
	102659	BE245169	Hs.211610	CUG triplet repeat, RNA-binding protein	11.00	
	102580	U60808	Hs.152981	CDP-diacylglycerol synthase (phosphatida	25.40	
	102417	AA034127	Hs.153487	signal transducing adaptor molecule (SH3	14.00	
10	102363	NM_003734	Hs.198241	amine oxidase, copper containing 3 (vasc		
	102302	AA306342	Hs.69171	protein kinase C-like 2	10.86	
	102283	AW161552	Hs.83381	guanine nucleotide binding protein 11		
	102188	U20350	Hs.78913	chemokine (C-X3-C) receptor 1		7.40
	102151	T27013	Hs.3132	steroidogenic acute regulatory protein	16.40	
15	101957	L28824	Hs.74101	spleen tyrosine kinase	15.40	
	101842	M93221	Hs.75182	mannose receptor, C type 1		
	101771	NM_002432	Hs.153837	myeloid cell nuclear differentiation ant		
	101764	A1198550	Hs.81256	S100 calcium-binding protein A4 (calcium		1.78
	101716	AF050658	Hs.2563	tachykinin, precursor 1 (substance K, su	18.80	
20	101678	M62505	Hs.2161	complement component 5 receptor 1 (C5a1		2.22
	101447	M21305		gb:Human alpha satellite and satellite 3	504.80	
	101383	NM_000132	Hs.79345	coagulation factor VIII, procoagulant co		31.00
	101346	A1738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N		1.75
	101345	NM_005795	Hs.152175	calcitonin receptor-like		
25	101338	NM_006732	Hs.75678	FBJ murine osteosarcoma viral oncogene h		2.24
	101330	L43821	Hs.80261	enhancer of filamentation 1 (cas-like do		
	101277	BE297626	Hs.296049	microfibrillar-associated protein 4		
	101262	L35854		gb:Human dystrophin (dp140) mRNA, 5' end	19.00	
	101168	NM_005308	Hs.211569	G protein-coupled receptor kinase 5		2.01
30	101102	NM_003243	Hs.79059	transforming growth factor, beta recepto		
	101088	X70697	Hs.553	solute carrier family 6 (neurotransmitte		7.52
	101066	AW970254	Hs.889	Charot-Leyden crystal protein	19.38	
	100971	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte		1.91
	100893	BE245294	Hs.180789	S164 protein	15.40	
35	100770	W25797.comp	Hs.177486	amyloid beta (A4) precursor protein (pro	11.20	
	100716	X89887	Hs.172350	HIR (histone cell cycle regulation defec	14.80	
	100555	M69181		gb:Human nonmuscle myosin heavy chain-B	33.00	
	100425	NM_014747	Hs.78748	KIAA0237 gene product	16.20	
	100408	D86640	Hs.56045	src homology three (SH3) and cysteine ri		4.00
40	100382	D83407	Hs.156007	Down syndrome critical region gene 1-lik		4.24
	100351	D64158				6.20
	100299	D49493	Hs.2171	growth differentiation factor 10		21.20
	100134	AA305746	Hs.49	macrophage scavenger receptor 1		
	100108	U09577	Hs.76873	hyaluronoglucosaminidase 2		1.79
45	100095	Z97171	Hs.78454	myocilin, trabecular meshwork inducible		5.40
	100066				11.29	

TABLE 3B shows the accession numbers for those primekeys lacking unigenelD's for Table 3A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accessions
60	123619	371681_1 AA602964 AA609200
	126433	127143_1 AA325606 AA099517 N89423
	125831	1522905_1 H04043 D60988 D60337
65	126816	122973_1 AA248234 AA090985
	126852	136135_1 AA399961 AA128347
	121059	273450_1 AA393283 AA398628
	120637	200885_1 AA811804 AA809404 AA286907 AW977624
	122011	7617_-2 AA431082
70	120934	177521_1 AA226198 AA226513 AA383773
	123802	genbank_AA620448 AA620448
	116814	genbank_H50834 H50834
	118329	genbank_N63520 N63520
	104404	H58762_at H58762
75	104776	genbank_AA026349 AA026349
	113502	genbank_T89130T89130
	101262	entrez_L35854 L35854
	108573	genbank_AA086005 AA086005
	101447	entrez_M21305 M21305
80	124357	genbank_N22401 N22401
	108781	genbank_AA128654 AA128654
	112794	genbank_R97018 R97018
	100351	entrez_D64158 D64158
85	100555	tigr_HT2245 M69181 M81105 U51039

Table 4A shows 202 genes up-regulated in samples from patients treated with chemotherapy or radiotherapy. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: average of AI for samples from patients treated with chemotherapy or radiotherapy divided by the average of AI for normal lung samples.

Pkey	ExAccn	UnigenelD	Unigene Title	R1
100113	NM_001269	Hs.84746	chromosome condensation 1	27.20
100187	D17793	Hs.78183	aldo-keto reductase family 1, member C3	20.60
100210	D26361	Hs.3104	KIAA0042 gene product	20.40
100225	D28539	Hs.167185	glutamate receptor, metabotropic 5	20.60
100269	NM_001949	Hs.1189	E2F transcription factor 3	29.40
100438	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	23.50
100877	X80821	Hs.27973	KIAA0874 protein	35.56
100893	BE245294	Hs.180789	S164 protein	43.40
101273	Z11933	Hs.182505	POU domain, class 3, transcription facto	21.80
101447	M21305		gb:Human alpha satellite and satellite 3	193.60
101649	AW959908	Hs.1690	heparin-binding growth factor binding pr	38.40
101724	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	198.80
101748	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	78.60
101809	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	162.20
101879	AA176374	Hs.243886	nuclear autoantigenic sperm protein (his	50.00
101915	AF207881	Hs.155185	cytosolic ovarian carcinoma antigen 1	26.00
101973	U41514	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	37.20
102025	U04045	Hs.78934	mutS (E. coli) homolog 2 (colon cancer,	
102031	U04898	Hs.2156	RAR-related orphan receptor A	32.00
102052	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	51.20
102391	AA296874	Hs.77494	deoxyguanosine kinase	13.90
102420	U44060	Hs.14427	Homo sapiens cDNA: FLJ21800 fis, clone H	28.80
102610	U65011	Hs.30743	preferentially expressed antigen in mela	110.60
102829	NM_006183	Hs.80962	neurotensin	116.80
103000	NM_001975	Hs.146580	enolase 2, (gamma, neuronal)	2.30
103036	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	181.40
103507	AJ000512	Hs.296323	serum/glucocorticoid regulated kinase	49.20
103587	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	86.60
104660	BE298665	Hs.14846	Homo sapiens mRNA; cDNA DKFZp564D016 (fr	42.60
104896	AW015318	Hs.23165	ESTs	29.40
105038	AW503733	Hs.9414	KIAA1488 protein	21.50
105298	BE387790	Hs.26369	hypothetical protein FLJ20287	32.80
105510	Z42047	Hs.283978	Homo sapiens PRO2751 mRNA, complete cds	20.20
105667	AA767526	Hs.22030	paired box gene 5 (B-cell lineage specif	28.40
106073	AL157441	Hs.17834	downstream neighbor of SON	25.40
106205	AW965058	Hs.111583	ESTs, Weakly similar to I38022 hypotheti	32.00
106516	AL137311	Hs.234074	Homo sapiens mRNA; cDNA DKFZp761G02121 (40.60
106533	AL134708	Hs.145998	ESTs	59.80
106575	AW970602	Hs.105421	ESTs	43.40
106654	AW075485	Hs.286049	phosphoserine aminotransferase	50.80
106851	A1458623		gb:tk04g09.x1 NCI_CGAP_Lu24 Homo sapiens	53.40
106995	AB023139	Hs.37892	KIAA0922 protein	20.88
107332	T87750	Hs.183297	DKFZP566F2124 protein	23.60
107532	AA443473	Hs.173684	Homo sapiens mRNA; cDNA DKFZp762G207 (fr	57.20
107922	BE153855	Hs.61460	Ig superfamily receptor LNIR	49.00
108609	BE409857	Hs.69499	hypothetical protein	19.67
108780	AU076442	Hs.117938	collagen, type XVII, alpha 1	48.17
109166	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	59.20
109260	AW978515	Hs.131915	KIAA0863 protein	28.60
109280	AK001355	Hs.279610	hypothetical protein FLJ10493	22.80
109292	AW975746	Hs.188662	KIAA1702 protein	
109384	AA219172	Hs.85849	ESTs	21.00
109415	U80736	Hs.110826	trinucleotide repeat containing 9	31.60
109445	AA232103	Hs.189915	ESTs	24.20
109502	AW967069	Hs.211556	hypothetical protein MGC5487	21.40
109633	AW003785	Hs.170267	ESTs	20.40
109786	AI989482	Hs.146286	kinesin family member 13A	19.60
109958	AA001266	Hs.133521	ESTs	24.00
110920	N47224	Hs.20521	HMT1 (hnRNP methyltransferase, S. cerevi	28.40
110924	AW058463	Hs.12940	zinc-fingers and homeoboxes 1	36.00
111084	H44186	Hs.15456	PDZ domain containing 1	61.20
111132	AB037807	Hs.83293	hypothetical protein	24.60
111229	AW389845	Hs.110855	ESTs	27.20
111337	AA837396	Hs.263925	LIS1-interacting protein NUDE1, rat homo	48.00
111987	NM_015310	Hs.6763	KIAA0942 protein	37.80
112046	AA383343	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	26.80
112268	W39609	Hs.22003	soluble carrier family 6 (neurotransmitte	63.80
112685	R87650	Hs.33439	ESTs, Weakly similar to ALU1_HUMAN ALU	26.40
112871	AL110216	Hs.12285	ESTs, Weakly similar to I55214 salivary	47.64
112897	AW206453	Hs.3782	ESTs	22.00
112973	AB033023	Hs.318127	hypothetical protein FLJ10201	65.00
112992	AL157425	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (f	42.00
113073	N39342	Hs.103042	microtubule-associated protein 1B	55.40

	113494	T91451	Hs.86538	ESTs	22.80
	113560	T91015	Hs.268626	ESTs	22.80
	113849	AA457211	Hs.8858	bromodomain adjacent to zinc finger doma	51.80
5	113950	AI267652	Hs.30504	Homo sapiens mRNA; cDNA DKFZp434E082 (tr	28.20
	114339	AA782845	Hs.22790	ESTs	20.20
	114365	H42169	Hs.18653	hypothetical protein FLJ14627	21.00
	114455	H37908	Hs.271616	ESTs, Weakly similar to ALU8_HUMAN ALU S	25.80
	114518	AW163267	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like	23.60
10	114824	AA960961	Hs.305953	zinc finger protein 83 (HPF1)	27.20
	114837	BE244930	Hs.166895	ESTs	30.20
	114974	AW956931	Hs.179562	nucleosome assembly protein 1-like 1	20.80
	115075	AA814043	Hs.88045	ESTs	30.60
	115084	BE383668	Hs.42484	hypothetical protein FLJ10618	28.86
	115291	BE545072	Hs.122579	hypothetical protein FLJ10461	38.00
15	115313	AA808001	Hs.184411	albumin	22.60
	115697	D31382	Hs.63325	transmembrane protease, serine 4	173.60
	115909	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	27.77
	116090	AI591147	Hs.61232	ESTs	20.80
20	116107	AL133916	Hs.172572	hypothetical protein FLJ20093	164.20
	116399	AA889120	Hs.110637	homeo box A10	38.00
	117099	H93699		gb:yy16a11.s1 Soares fetal liver spleen	21.60
	117881	AF161470	Hs.260622	butyrate-induced transcript 1	49.40
	118091	AW005054	Hs.47883	ESTs, Weakly similar to KCC1_HUMAN CALCI	22.40
25	118138	AA374756	Hs.93560	Homo sapiens mRNA for KIAA1771 protein,	22.00
	118720	N73515		gb:za49d07.s1 Soares fetal liver spleen	20.00
	118873	AI824009	Hs.44577	ESTs	19.40
	119126	R45175	Hs.117183	ESTs	111.20
	119717	AA918317	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	33.00
30	119940	AL050097	Hs.272531	DKFZP586B0319 protein	31.00
	120266	AI807264	Hs.205442	ESTs, Weakly similar to T34036 hypotheti	20.20
	120515	AA258356		gb:zr59c10.s1 Soares_NhHMPu_S1 Homo sapi	25.00
	120859	AA826434	Hs.1619	achaete-scute complex (Drosophila) homol	95.40
	120983	AA398209	Hs.97587	EST	105.20
35	121054	AW976570	Hs.97387	ESTs	38.80
	121369	AW450737	Hs.128791	CGI-09 protein	41.60
	122335	AA443258	Hs.241551	chloride channel, calcium activated, fam	30.80
	122612	AA974832	Hs.128708	ESTs	19.60
	123130	AA487200		gb:ab19f02.s1 Stratagene lung (937210) H	33.20
40	123440	AI733692	Hs.112488	ESTs	23.17
	123596	AA421130	Hs.112640	EST	23.00
	123619	AA602964		gb:no97c02.s1 NCI_CGAP_Pr2 Homo sapiens	28.80
	124006	AI147155	Hs.270016	ESTs	77.60
	124169	BE079334	Hs.271630	ESTs	22.20
45	124281	AI333756	Hs.111801	arsenate resistance protein ARS2	42.20
	124472	N52517	Hs.102670	EST	32.60
	124617	AW628168	Hs.152684	ESTs	21.80
	124631	NM_014053	Hs.270594	FLVCR protein	30.40
	124839	R55784	Hs.140942	ESTs	21.20
50	125186	AA610620	Hs.181244	major histocompatibility complex, class	42.80
	125321	T86652	Hs.178294	ESTs	27.00
	125535	NM_013243	Hs.22215	secretogranin III	23.80
	125646	AA628962	Hs.75209	protein kinase (cAMP-dependent, catalyti	23.20
	125684	AW589427	Hs.158849	Homo sapiens cDNA: FLJ21663 fis, clone C	21.20
55	125724	AL360190	Hs.295978	Homo sapiens mRNA full length insert cDN	48.80
	125847	AW161885	Hs.249034	ESTs	31.00
	125934	AA193325	Hs.32646	hypothetical protein FLJ21901	21.20
	126077	M78772	Hs.210836	ESTs	49.80
	126299	AW979155	Hs.298275	amino acid transporter 2	21.80
60	126395	AI468004	Hs.278956	hypothetical protein FLJ12929	71.00
	126433	AA325606		gb:EST28707 Cerebellum II Homo sapiens c	23.20
	126509	R47400	Hs.23850	ESTs	23.80
	126538	AB030656	Hs.17377	coronin, actin-binding protein, 1C	23.10
	126666	AA648886	Hs.151999	ESTs	36.00
65	126812	AB037860	Hs.173933	nuclear factor I/A	20.80
	126872	AW450979		gb:UI-H-BI3-ala-a-12-0-UI.s1 NCI_CGAP_Su	46.29
	127046	AA321948	Hs.293968	ESTs	22.80
	127431	AW771958	Hs.175437	ESTs, Moderately similar to PC4259 ferri	30.00
	127489	AA650250	Hs.272076	ESTs	20.80
70	127521	AW297206	Hs.164018	ESTs	25.20
	127742	AW293496	Hs.180138	ESTs	28.00
	127925	AA805151	Hs.3628	mitogen-activated protein kinase kinase	21.20
	127930	AA809672	Hs.123304	ESTs	20.54
	127968	AA830201	Hs.124347	ESTs	28.20
75	127987	AI022103	Hs.124511	ESTs	19.60
	128116	H07103	Hs.286014	Homo sapiens, clone IMAGE:3867243, mRNA	20.40
	128609	NM_003616	Hs.102456	survival of motor neuron protein interac	34.40
	128777	AI878918	Hs.10526	cysteine and glycine-rich protein 2	53.80
	128949	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	23.00
80	129168	AI132988	Hs.109052	chromosome 14 open reading frame 2	37.60
	129404	AI267700	Hs.317584	ESTs	28.60
	129527	AA769221	Hs.270847	delta-tubulin	40.80
	129574	AA026815	Hs.11463	UMP-CMP kinase	31.20
	129598	N30436	Hs.11556	Homo sapiens cDNA FLJ12566 fis, clone NT	29.60
	129785	H19006	Hs.184780	ESTs	72.20
85	129970	AV655806	Hs.296198	chromosome 12 open reading frame 4	22.20

	130149	AW067805	Hs.172665	methylenetetrahydrofolate dehydrogenase	29.60
	130199	Z48579	Hs.172028	a disintegrin and metalloproteinase doma	27.60
	130441	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	28.36
5	130466	W19744	Hs.180059	Homo sapiens cDNA FLJ20653 fis, clone KA	20.20
	130482	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	22.40
	130617	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	19.60
	130703	R77776	Hs.18103	ESTs	19.40
	130732	AW890487	Hs.63984	cadherin 13, H-cadherin (heart)	21.40
10	130867	NM_001072	Hs.284239	UDP glycosyltransferase 1 family, polype	110.00
	131028	A1879165	Hs.2227	CCAAT/enhancer binding protein (C/EBP),	25.20
	131086	AL035461	Hs.2281	chromogranin B (secretogranin 1)	40.60
	131284	NM_001429	Hs.25272	E1A binding protein p300	24.60
	131775	AB014548	Hs.31921	KIAA0648 protein	21.00
15	131860	BE383676	Hs.334	Rho guanine nucleotide exchange factor (33.40
	131945	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	60.80
	132040	NM_001196	Hs.315689	Homo sapiens cDNA: FLJ22373 fis, clone H	20.40
	132084	NM_002267	Hs.3886	karyopherin alpha 3 (importin alpha 4)	29.40
	132389	AA310393	Hs.190044	ESTs	32.40
20	132437	AA152106	Hs.4859	cyclin L ania-6a	27.40
	132550	AW969253	Hs.170195	bone morphogenetic protein 7 (osteogenic	75.60
	132617	AF037335	Hs.5338	carbonic anhydrase XII	31.36
	132632	AU076916	Hs.5398	guanine monophosphate synthetase	32.40
	132672	W27721	Hs.54697	Cdc42 guanine exchange factor (GEF) 9	23.40
25	132742	AA025480	Hs.292812	ESTs, Weakly similar to T33468 hypothe	61.20
	132771	Y10275	Hs.56407	phosphoserine phosphatase	22.33
	133070	U92649	Hs.64311	a disintegrin and metalloproteinase doma	23.50
	133153	AF070592	Hs.66170	HSKM-B protein	30.00
	133181	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	23.80
30	133282	AA449015	Hs.286145	SRB7 (suppressor of RNA polymerase B, ye	51.60
	133350	AI499220	Hs.71573	hypothetical protein FLJ10074	33.00
	133592	AV652066	Hs.75113	general transcription factor IIIA	82.00
	133658	AA319146	Hs.75426	secretogranin II (chromogranin C)	
35	133865	AB011155	Hs.170290	discs, large (Drosophila) homolog 5	69.33
	134032	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibito	33.20
	134125	NM_014781	Hs.50421	KIAA0203 gene product	31.60
	134158	U15174	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	30.60
	134321	BE538082	Hs.8172	ESTs, Moderately similar to A46010 X-lin	23.40
	134367	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	49.20
40	134570	U66615	Hs.172280	SWI/SNF related, matrix associated, acti	20.20
	134753	NM_006482	Hs.173135	dual-specificity tyrosine-(Y)-phosphoryl	20.80
	135002	AA448542	Hs.251677	G antigen 7B	37.60
	135029	H58818	Hs.187579	hydroxysteroid (17-beta) dehydrogenase	53.40
45	135047	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	31.60
	135345	X53655	Hs.99171	neurotrophin 3	28.80

TABLE 4B shows the accession numbers for those primekeys lacking unigenes/D's for Table 4A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accessions
123619	371681_1	AA602964 AA609200
126433	127143_1	AA325605 AA099517 N89423
126872	142696_1	AW450979 AA136653 AA136656 AW419381 AA984358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359 BE011367 BE011368 BE011362 BE011215 BE011365 BE011363
106851	322947_1	AI458623 AA639708 AA485409 R22065 AA485570
118720	genbank_N73515	N73515
120515	genbank_AA258356	AA258356
117099	321871_1	H93699 H97976 H80036
101447	entrez_M21305	M21305
123130	genbank_AA487200	AA487200

Table 5A shows 680 genes up-regulated in squamous cell carcinoma or adenocarcinoma lung tumors relative to normal lung and chronically diseased lung. These genes were selected from 59680 probesets on the Eos/Affymatrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

5	Pkey:	Unique Eos probeset identifier number							
	ExAccn:	Exemplar Accession number, Genbank accession number							
	UnigenelD:	Unigene number							
	Unigene Title:	Unigene gene title							
10	R1:	70th percentile of AI for squamous cell carcinoma and adenocarcinoma lung tumor samples divided by the 90th percentile of AI for normal and chronically diseased lung samples.							
	R2:	80th percentile of AI adenocarcinoma lung tumor samples divided by the 90th percentile of AI for normal and chronically diseased lung samples.							
	R3:	80th percentile of AI squamous cell carcinoma lung tumor samples divided by the 90th percentile of AI for normal and chronically diseased lung samples.							
	R4:	80th percentile of AI adenocarcinoma lung tumor samples divided by the 80th percentile of AI for squamous cell carcinoma lung tumor samples.							
15	R5:	70th percentile of AI for squamous cell carcinoma and adenocarcinoma lung tumor samples minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples divided by 90th percentile of AI for normal and chronically diseased lung samples minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples							
20	Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2	R3	R4	R5
	100035			AFFX control: GAPDH					6.76
	100036			AFFX control: GAPDH					5.77
	100037			AFFX control: GAPDH					5.75
25	100071	A28102		Human GABAA receptor alpha-3 subunit		8.00			
	100114	X02308	Hs.82962	thymidylate synthetase					5.71
	100154	H60720	Hs.81892	KIAA0101 gene product	3.84				
	100187	D17793	Hs.78183	aldo-keto reductase family 1, member C3	3.33				
	100188	AW247090	Hs.57101	minichromosome maintenance deficient (S.					4.52
	100202	BE294407	Hs.99910	phosphofructokinase, platelet					5.49
30	100216	AA489908	Hs.1390	proteasome (prosome, macropain) subunit,					5.67
	100269	NM_001949	Hs.1189	E2F transcription factor 3	2.55				
	100287	AU076657	Hs.1600	chaperonin containing TCP1, subunit 5 (e					5.66
	100297	AU077258	Hs.182429	protein disulfide isomerase-related prot					3.81
	100330	AW410976	Hs.77152	minichromosome maintenance deficient (S.					4.50
35	100335	AW247529	Hs.6793	platelet-activating factor acetylhydrola	5.07				
	100360	W70171	Hs.75939	uridine monophosphate kinase					4.82
	100372	NM_014791	Hs.184339	KIAA0175 gene product					3.79
	100474	NM_000699	Hs.300280	amylase, alpha 2A; pancreatic				15.65	
	100486	T19006	Hs.10842	RAN, member RAS oncogene family					5.49
40	100491	D56165	Hs.275163	non-metastatic cells 2, protein (NM23B)					4.17
	100516	D90278	Hs.11	carcinoembryonic antigen-related cell ad		7.20			
	100522	X51501	Hs.99949	prolactin-induced protein				14.20	
	100559	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	3.10				
	100576	X00356	Hs.37058	calcitonin/calcitonin-related polypeptid				9.30	
45	100629	AA015693	Hs.21291	mitogen-activated protein kinase kinase				20.60	
	100661	BE623001	Hs.132748	Homo sapiens ribosomal protein L39 mRNA,	3.85				
	100677	AA353686	Hs.57813	zinc ribbon domain containing, 1		8.60			
	100696	D14887	Hs.121686	general transcription factor IIA, 1 (37k				10.00	
	100709	N26539	Hs.100469	myeloid/lymphoid or mixed-lineage leukem			24.80		
50	100761	BE208491	Hs.295112	KIAA0618 gene product		7.60			
	100830	AC004770	Hs.4756	flap structure-specific endonuclease 1					7.99
	100867	U14622		gb:Human transketolase-like protein gene		10.20			
	100902	M16029	Hs.287270	ret proto-oncogene (multiple endocrine n		8.00			
	100906	AU076916	Hs.5398	guanine monophosphate synthetase					5.16
55	100960	J00124	Hs.117729	keratin 14 (epidermolysis bullosa simple	2.57				
	101045	J05614		gb:Human proliferating cell nuclear anti					4.69
	101061	NM_000175	Hs.180532	glucose phosphate isomerase					4.19
	101071	L02840	Hs.84244	potassium voltage-gated channel, Shab-re		12.91			
	101124	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	3.12				
60	101175	U82671	Hs.36980	melanoma antigen, family A, 2	3.50				
	101181	BE262621	Hs.73798	macrophage migration inhibitory factor (5.69
	101204	L24203	Hs.82237	ataxia-telangiectasia group D-associated	4.08				
	101210	L29301	Hs.2353	opioid receptor, mu 1			6.40		
	101216	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	2.53				
65	101228	AA333387	Hs.82916	chaperonin containing TCP1, subunit 6A (7.90
	101233	AL135173	Hs.878	sorbitol dehydrogenase					4.45
	101273	Z11933	Hs.182505	POU domain, class 3, transcription facto	8.50				
	101342	U52112	Hs.182018	interleukin-1 receptor-associated kinase					4.17
	101346	A1738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N				21.89	
70	101369	NM_000892	Hs.1901	kallikrein B, plasma (Fletcher factor) 1				12.80	
	101396	BE267931	Hs.78996	proliferating cell nuclear antigen	3.24				
	101431	BE185289	Hs.1076	small protine-rich protein 1B (cornifin)					7.90
	101448	NM_000424	Hs.195850	keratin 5 (epidermolysis bullosa simplex	8.31				
	101462	AL035668	Hs.73853	bone morphogenetic protein 2				38.80	
75	101466	BE262660	Hs.170197	glutamic-oxaloacetic transaminase 2, mit					4.01
	101484	AA053486	Hs.20315	interferon-induced protein with tetratri				12.00	
	101502	M26958		gb:Human parathyroid hormone-related pro	10.50				
	101505	AA307680	Hs.75692	asparagine synthetase					4.46
	101526	NM_002197	Hs.154721	aconitase 1, soluble	4.02				
80	101535	X57152	Hs.99853	fibrillarin					4.65
	101577	M34353	Hs.1041	v-ros avian UR2 sarcoma virus oncogene h				9.09	
	101649	AW959908	Hs.1690	heparin-binding growth factor binding pr	54.00				
	101663	NM_003528	Hs.2178	H2B histone family, member Q	5.59				
	101664	AA436989	Hs.121017	H2A histone family, member A	7.00				
85	101669	L24498	Hs.80409	growth arrest and DNA-damage-inducible,		7.60			

5	101695	M69136	Hs.135626	chymase 1, mast cell	4.79			
	101724	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	15.21			
	101748	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen)	55.50			
	101759	M80244	Hs.184601	solute carrier family 7 (cationic amino			4.10	
	101771	NM_002432	Hs.153837	myeloid cell nuclear differentiation ant			18.57	
10	101804	M86699	Hs.169840	TTK protein kinase	4.50			
	101809	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	140.00			
	101833	AU076442	Hs.117938	collagen, type XVII, alpha 1	2.56			
	101842	M93221	Hs.75182	mannose receptor, C type 1			12.80	
	101851	BE260964	Hs.82045	midkine (neurite growth-promoting factor			5.88	
15	102002	NM_002484	Hs.81469	nucleotide binding protein 1 (E.coli Min	7.80			
	102039	AL134223	Hs.306098	aldo-keto reductase family 1, member C1			4.35	
	102072	U09410	Hs.78743	zinc finger protein 131 (clone pHZ-10)		7.40		
	102083	T35901	Hs.75117	interleukin enhancer binding factor 2, 4			5.12	
	102111	L36196	Hs.81884	sulfotransferase family, cytosolic, 2A,			12.00	
20	102123	NM_001809	Hs.1594	centromere protein A (17kD)	6.20			
	102154	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin	2.62			
	102193	AL036335	Hs.313	secreted phosphoprotein 1 (osteopontin,	5.85			
	102217	AA829978	Hs.301613	JTV1 gene			6.18	
	102224	NM_002810	Hs.148495	proteasome (prosome, macropain) 26S subu			4.49	
25	102234	AW163390	Hs.278554	heterochromatin-like protein 1			5.80	
	102251	NM_004398	Hs.41706	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	4.50			
	102305	AL043202	Hs.90073	chromosome segregation 1 (yeast homolog)			5.15	
	102330	BE298063	Hs.77254	chromobox homolog 1 (Drosophila HP1 beta			4.17	
	102340	U37055	Hs.278657	macrophage stimulating 1 (hepatocyte gro			9.33	
30	102348	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	8.87			
	102368	U39817	Hs.36820	Bloom syndrome	15.91			
	102394	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma		19.20		
	102404	NM_005429	Hs.79141	vascular endothelial growth factor C			14.00	
	102537	U57094	Hs.50477	RAB27A, member RAS oncogene family			12.00	
35	102581	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2			4.57	
	102605	AI435128	Hs.181369	ubiquitin fusion degradation 1-like			3.98	
	102610	U65011	Hs.30743	preferentially expressed antigen in mela	77.50			
	102623	AW249285	Hs.37110	melanoma antigen, family A, 9	12.50			
	102642	AA205847	Hs.23016	G protein-coupled receptor		22.00		
40	102654	AV649989	Hs.24385	Human hbc647 mRNA sequence		12.00		
	102659	BE245169	Hs.211610	CUG triplet repeat, RNA-binding protein			12.80	
	102669	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	6.50			
	102672	U72066	Hs.29287	retinoblastoma-binding protein 8	8.50			
	102687	NM_007019	Hs.93002	ubiquitin carrier protein E2-C			9.24	
45	102696	BE540274	Hs.239	forkhead box M1			5.54	
	102768	U82321		gb:Homo sapiens clone 14.9B mRNA sequenc	6.60			
	102781	BE258778	Hs.108809	chaperonin containing TCP1, subunit 7 (e			3.78	
	102784	U85658	Hs.61795	transcription factor AP-2 gamma (activat			4.26	
	102824	U90916	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H		14.40		
50	102829	NM_006183	Hs.80962	neurotensin	8.00			
	102888	AI346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1			5.50	
	102892	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin		6.70		
	102913	NM_002275	Hs.80342	keratin 15	4.64			
	102935	BE561850	Hs.80506	small nuclear ribonucleoprotein polypept	2.93			
55	102951	X15218	Hs.2969	v-ski avian sarcoma viral oncogene homol			11.40	
	102983	BE387202	Hs.118638	non-metastatic cells 1, protein (NM23A)			7.26	
	103023	AW500470	Hs.117950	multifunctional polypeptide similar to S	3.01			
	103036	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	27.90			
	103038	AA926960	Hs.334883	CDC28 protein kinase 1			8.79	
60	103060	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromalysin			4.27	
	103099	AI693251	Hs.8248	NADH dehydrogenase (ubiquinone) Fe-S pro		9.80		
	103119	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	4.05			
	103168	X53463	Hs.2704	glutathione peroxidase 2 (gastrointestin	3.07			
	103185	NM_006825	Hs.74368	transmembrane protein (63kD), endoplasm			5.62	
65	103192	M22440	Hs.170009	transforming growth factor, alpha		7.40		
	103223	BE275607	Hs.1708	chaperonin containing TCP1, subunit 3 (g			4.70	
	103242	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o		100.00		
	103316	X83301	Hs.324728	SMA5			9.80	
	103375	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	9.71			
70	103376	AL036166	Hs.323378	coated vesicle membrane protein	14.00			
	103385	NM_007069	Hs.37189	similar to rat HREV107			11.00	
	103391	X94453	Hs.114366	pyrroline-5-carboxylate synthetase (glut	2.93			
	103404	BE394784	Hs.78596	proteasome (prosome, macropain) subunit,			5.15	
	103430	BE564090	Hs.20716	translocase of inner mitochondrial membr			3.98	
75	103446	X98834	Hs.79971	sal (Drosophila)-like 2			21.40	
	103476	Y07701	Hs.293007	aminopeptidase puromycin sensitive		13.00		
	103477	AJ011812	Hs.119018	transcription factor NRF		6.40		
	103478	BE514982	Hs.38991	S100 calcium-binding protein A2	5.02			
	103515	Y10275	Hs.56407	phosphoserine phosphatase	10.50			
80	103558	BE616547	Hs.2785	keratin 17	6.41			
	103580	AA328046	Hs.46405	polymerase (RNA) II (DNA directed) polyp			3.84	
	103587	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	78.50			
	103594	AI368680	Hs.816	SRY (sex determining region Y)-box 2	6.51			
	103636	NM_006235	Hs.2407	POU domain, class 2, associating factor	3.50			
85	103768	AF086009		gb:Homo sapiens full length insert cDNA			4.48	
	103841	AA314821	Hs.38178	hypothetical protein FLJ23468	8.00			
	103847	AF219946	Hs.102237	tubby super-family protein	10.40			
	103913	AW967500	Hs.133543	ESTs			15.60	
	104094	AA418187	Hs.330515	ESTs		6.60		

	104150	AL122044	Hs.331633	hypothetical protein DKFZp566N034			26.00	
	104257	BE560621	Hs.9222	estrogen receptor binding site associate	6.80			
	104261	AW248364	Hs.5409	RNA polymerase I subunit			3.98	
5	104331	AB040450	Hs.279862	cdk inhibitor p21 binding protein	6.80			
	104415	BE410992	Hs.258730	heme-regulated initiation factor 2-alpha	10.29			
	104558	R56578	Hs.88959	hypothetical protein MGC4816	4.21			
	104590	AW373062	Hs.83623	nuclear receptor subfamily 1, group I, m			15.79	
	104658	AA360954	Hs.27268	Homo sapiens cDNA: FLJ21933 fis, clone H			17.40	
10	104660	BE298665	Hs.14846	Homo sapiens mRNA: cDNA DKFZp564D016 (fr	6.40			
	104689	AA420450	Hs.292911	ESTs, Highly similar to S60712 band-6-pr			6.55	
	104754	AI206234	Hs.155924	cAMP responsive element modulator			10.00	
	104758	BE560269	Hs.7010	NPD002 protein			4.47	
	104971	BE311926	Hs.15830	hypothetical protein FLJ12691	2.87			
15	105011	BE091926	Hs.16244	mitotic spindle coiled-coil related prot	3.83			
	105012	AF098158	Hs.9329	chromosome 20 open reading frame 1	2.86			
	105026	AA809485	Hs.124219	hypothetical protein FLJ12934	11.00			
	105076	AI598252	Hs.37810	hypothetical protein MGC14833			5.01	
	105132	AA148164	Hs.247280	HBV associated factor			3.99	
20	105143	AI368836	Hs.24808	ESTs, Weakly similar to I38022 hypotheti		11.00		
	105158	AW976357	Hs.234545	hypothetical protein NUF2R	16.00			
	105175	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	4.32			
	105200	AA328102	Hs.24641	cytoskeleton associated protein 2	3.00			
	105264	AA227934		gb:zr57e08.s1 Soares_NhHMPu_S1 Homo sapi			10.00	
25	105298	BE387790	Hs.26369	hypothetical protein FLJ20287	3.69			
	105409	AW505076	Hs.301855	DiGeorge syndrome critical region gene 8			9.20	
	105460	AW296078	Hs.271721	Homo sapiens, clone IMAGE:4179986, mRNA,		7.80		
	105667	AA767526	Hs.22030	paired box gene 5 (B-cell lineage specif	4.12			
	105743	BE246502	Hs.9598	sema domain, immunoglobulin domain (Ig),	3.82			
30	105782	H09748	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro		27.00		
	105848	AW954064	Hs.24951	ESTs		7.60		
	105891	U55984	Hs.289088	heat shock 90kD protein 1, alpha			4.14	
	106019	AF221993	Hs.46743	McKusick-Kaufman syndrome		16.80		
	106069	BE566623	Hs.29899	ESTs, Weakly similar to G02075 transcrip		23.40		
35	106073	AL157441	Hs.17834	downstream neighbor of SON	9.50			
	106126	AA576953	Hs.22972	hypothetical protein FLJ13352	6.00			
	106159	AK001301	Hs.3487	hypothetical protein FLJ10439			3.95	
	106220	D61329	Hs.32196	mitochondrial ribosomal protein L36			6.04	
40	106260	AI097144	Hs.5260	ESTs, Weakly similar to ALU1_HUMAN ALU S		13.20		
	106300	Y10043	Hs.19114	high-mobility group (nonhistone chromoso			5.02	
	106307	AA436174	Hs.37751	ESTs, Weakly similar to putative p150 [6.60			
	106318	AA025610	Hs.9605	cleavage and polyadenylation specific fa			5.04	
	106341	AF191020	Hs.5243	hypothetical protein, estradiol-induced			7.25	
	106440	AA449563	Hs.151393	glutamate-cysteine ligase, catalytic sub		13.80		
45	106481	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	4.75			
	106586	AA243837	Hs.57787	ESTs			10.84	
	106605	AW772298	Hs.21103	Homo sapiens mRNA: cDNA DKFZp564B076 (fr			45.60	
	106654	AW075485	Hs.286049	phosphoserine aminotransferase	28.00			
	106785	Y15227	Hs.20149	deleted in lymphocytic leukemia, 1	3.00			
50	106813	C05766	Hs.181022	CGI-07 protein		11.40		
	106895	AK001826	Hs.25245	hypothetical protein FLJ11269		6.00		
	106913	AI219346	Hs.86178	M-phase phosphoprotein 9	6.56			
	106919	AW043637	Hs.21766	ESTs, Weakly similar to ALU5_HUMAN ALU S			4.27	
	107054	AI076459	Hs.15978	KIAA1272 protein			34.80	
55	107059	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	4.71			
	107098	AI823593	Hs.27688	ESTs			24.80	
	107104	AU076640	Hs.15243	nucleolar protein 1 (120kD)			7.05	
	107129	AC004770	Hs.4756	flap structure-specific endonuclease 1	2.60			
	107198	AV657225	Hs.9846	KIAA1040 protein		19.20		
60	107203	D20426	Hs.41639	programmed cell death 2		7.60		
	107217	AL080235	Hs.35861	DKFZP586E1621 protein	9.50			
	107284	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitte	2.71			
	107318	T74445	Hs.5957	Homo sapiens clone 24416 mRNA sequence		8.71		
	107516	X57152	Hs.99853	fibrillarin			4.33	
65	107529	BE515065	Hs.296585	nucleolar protein (KKE/D repeat)			4.00	
	107728	AA019551	Hs.294151	Homo sapiens, clone IMAGE:3603836, mRNA,	10.80			
	107851	AA022953	Hs.61172	EST		8.00		
	107901	L42612	Hs.335952	keratin 6B	3.40			
	107922	BE153855	Hs.61460	Ig superfamily receptor LNIR	2.88			
70	107932	AW392555	Hs.18878	hypothetical protein FLJ21620	7.50			
	108015	AW298357	Hs.49927	protein kinase NYD-SP15			23.40	
	108056	AA043675	Hs.62633	ESTs			12.80	
	108075	AI867370	Hs.139709	hypothetical protein FLJ12572			12.80	
	108187	BE245374	Hs.27842	hypothetical protein FLJ11210	7.00			
75	108296	N31256	Hs.161623	ESTs	6.60			
	108305	AA071391		gb:zm61e06.r1 Stratagene fibroblast (937			11.80	
	108393	AA075211		gb:zm86a08.r1 Stratagene ovarian cancer			11.80	
	108480	AL133092	Hs.68055	hypothetical protein DKFZp434I0428			20.80	
	108554	AA084948		gb:zn13b09.s1 Stratagene hNT neuron (937	6.40			
80	108573	AA086005		gb:zi84c04.s1 Stratagene colon (937204)			25.40	
	108584	AA088326	Hs.120905	Homo sapiens cDNA FLJ11448 fis, clone HE	9.60			
	108597	AK000292	Hs.278732	hypothetical protein FLJ20285			14.60	
	108695	AB029000	Hs.70823	KIAA1077 protein	3.00			
	108699	AA121514	Hs.70832	ESTs			10.00	
85	108700	AA121518	Hs.193540	ESTs, Moderately similar to 2109260A B c		11.00		
	108780	AU076442	Hs.117938	collagen, type XVII, alpha 1	11.21			

	108810	AW295647	Hs.71331	hypothetical protein MGC5350	8.50			
	108816	AA130884	Hs.270501	ESTs, Moderately similar to ALU2_HUMAN		7.40		
	108857	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	4.00			
5	108860	AA133334	Hs.129911	ESTs	6.09			
	108937	AL050107	Hs.24341	transcriptional co-activator with PDZ-bi	3.00			
	109010	NM_007240	Hs.44229	dual specificity phosphatase 12	2.69			
	109121	BE389387	Hs.49767	NADH dehydrogenase (ubiquinone) Fe-S pro			4.53	
	109166	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rakines	10.58			
10	109227	AA766998	Hs.85874	Human DNA sequence from clone RP11-16L21		9.00		
	109415	U80736	Hs.110826	trinucleotide repeat containing 9		51.40		
	109418	AJ866946	Hs.161707	ESTs			11.00	
	109454	AA232255	Hs.295232	ESTs, Moderately similar to A46010 X-li		17.60		
	109502	AW967069	Hs.211556	hypothetical protein MGC5487		9.49		
15	109543	AA564994	Hs.222851	ESTs	12.67			
	109548	H17800	Hs.71154	ESTs			10.40	
	109680	AB037734	Hs.4993	KIAA1313 protein		33.20		
	109700	F09609		gb:HSC33H092 normalized infant brain cDN			16.00	
	109704	AI743880	Hs.12876	ESTs		11.00		
20	109792	R49625		gb:yg61f03.s1 Soares infant brain 1N1B H			12.60	
	109981	BE546208	Hs.26090	hypothetical protein FLJ20272	4.00			
	109998	AL042201	Hs.21273	transcription factor NYD-sp10		7.80		
	110039	H11938	Hs.21907	histone acetyltransferase		7.00		
	110156	AA581322	Hs.4213	hypothetical protein MGC16207			4.24	
25	110500	AA907723	Hs.36962	ESTs	4.50			
	110551	AW450381	Hs.14529	ESTs		8.60		
	110561	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	3.06			
	110854	BE612992	Hs.27931	hypothetical protein FLJ10607 similar to		6.80		
	110886	AW274992	Hs.72249	three-PDZ containing protein similar to		8.80		
30	110916	BE178102	Hs.24349	ESTs		6.80		
	111003	N52980	Hs.83765	dihydrofolate reductase			16.80	
	111337	AA837396	Hs.263925	LIS1-Interacting protein NUDE1, rat homo	2.54			
	111434	R01608	Hs.142736	ESTs			9.80	
	111439	AI476429	Hs.19238	ESTs			10.40	
35	111540	U82670	Hs.9786	zinc finger protein 275		15.40		
	111597	R11499	Hs.189716	ESTs			9.20	
	111895	T80581	Hs.12723	Homo sapiens clone 25153 mRNA sequence	6.80			
	111929	AF027208	Hs.112360	prominin (mouse)-like 1			14.67	
	112054	R43590		gb:yc85g02.s1 Soares infant brain 1N1B H	10.80			
40	112210	R49645	Hs.7004	ESTs			10.20	
	112244	AB029000	Hs.70823	KIAA1077 protein	2.99			
	112382	R59904		gb:yh07g12.s1 Soares infant brain 1N1B H		6.60		
	112392	R60763	Hs.193274	ESTs, Moderately similar to I57588 HSrel		7.10		
	112442	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	3.00			
45	112539	R70318	Hs.339730	ESTs			37.20	
	112772	AI992283	Hs.35437	ESTs, Moderately similar to I38026 MLN 6			14.60	
	112869	BE261750	Hs.4747	dyskeratosis congenita 1, dyskerin			4.83	
	112935	R71449	Hs.268760	ESTs	2.73			
	112970	AA694010	Hs.6932	Homo sapiens clone 23809 mRNA sequence			12.00	
50	112973	AB033023	Hs.318127	hypothetical protein FLJ10201	11.50			
	112992	AL157425	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (f		10.89		
	113063	W15573	Hs.5027	ESTs, Weakly similar to A47582 B-cell gr	15.00			
	113073	N39342	Hs.103042	microtubule-associated protein 1B		15.31		
	113078	T40444	Hs.118354	CAT56 protein		7.00		
55	113238	R45467	Hs.189813	ESTs			41.20	
	113591	T91881	Hs.200597	KIAA0563 gene product			9.40	
	113702	T97307		gb:ye53h05.s1 Soares fetal liver spleen	25.00			
	113844	AI369275	Hs.243010	Homo sapiens cDNA FLJ14445 fis, clone HE			13.91	
60	113984	R96696	Hs.35598	ESTs		7.80		
	114073	R44953	Hs.22908	Homo sapiens mRNA; cDNA DKFZp434J1027 (f		7.20		
	114162	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	3.42			
	114208	AL049466	Hs.7859	ESTs		6.74		
	114251	H15261	Hs.21948	ESTs			33.20	
	114285	R44338	Hs.22974	ESTs			13.20	
65	114313	H18456	Hs.27946	ESTs			10.00	
	114339	AA782845	Hs.22790	ESTs		7.80		
	114407	BE539976	Hs.103305	Homo sapiens mRNA; cDNA DKFZp434B0425 (f			4.14	
	114560	AI452469	Hs.165221	ESTs			9.80	
	114699	AA127386		gb:zn90d09.r1 Stratagene lung carcinoma		7.60		
70	114767	AI859865	Hs.154443	minichromosome maintenance deficient (S	3.21			
	114793	AA158245		gb:zo76c03.s1 Stratagene pancreas (93720		6.00		
	114833	AI417215	Hs.87159	hypothetical protein FLJ12577			11.40	
	115047	BE270930	Hs.82916	chaperonin containing TCP1, subunit 6A (4.31	
	115060	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3			4.03	
75	115097	AA256213	Hs.72010	ESTs			35.40	
	115113	AA256460		gb:zr81a04.s1 Soares_NhHMPu_S1 Homo sapi			15.20	
	115123	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m			4.19	
	115134	AW968073	Hs.194331	ESTs, Highly similar to A55713 inositol			12.40	
	115291	BE545072	Hs.122579	hypothetical protein FLJ10461	25.00			
80	115347	AA356792	Hs.334824	hypothetical protein FLJ14825		7.00		
	115414	AA662240	Hs.283099	AF15q14 protein	3.25			
	115522	BE614387	Hs.333893	c-Myc target JPO1	3.68			
	115536	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	10.50			
	115566	AI142336	Hs.43977	Human DNA sequence from clone RP11-196N1			24.40	
85	115645	AI207410	Hs.69280	Homo sapiens, clone IMAGE:3636299, mRNA,	4.17			
	115648	AW016811	Hs.234478	Homo sapiens cDNA: FLJ22648 fis, clone H		6.00		

	115652	BE093589	Hs.38178	hypothetical protein FLJ23468	3.81			
	115697	D31382	Hs.63325	transmembrane protease, serine 4	62.14			
	115793	AA424883	Hs.70333	hypothetical protein MGC10753			11.80	
	115816	BE042915	Hs.287588	Homo sapiens cDNA FLJ13675 fis, clone PL			9.71	
5	115892	AA291377	Hs.50831	ESTs		27.40		
	115906	AI767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	2.53			
	115909	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	11.82			
	115965	AA001732	Hs.173233	hypothetical protein FLJ10970			34.29	
10	115978	AL035864	Hs.69517	cDNA for differentially expressed CO16 g				8.23
	115985	AA447709	Hs.268115	ESTs, Weakly similar to T08599 probable	3.00			
	116090	AI591147	Hs.61232	ESTs	5.17			
	116096	AA682382	Hs.59982	ESTs		8.20		
	116127	AF126743	Hs.279884	DNAJ domain-containing		10.60		
15	116157	BE439838	Hs.44298	mitochondrial ribosomal protein S17				5.82
	116190	AI949095	Hs.67776	ESTs, Weakly similar to T22341 hypothe				4.08
	116278	NM_003686	Hs.47504	exonuclease 1	9.50			
	116335	AK001100	Hs.41690	desmocollin 3	3.67			
	116486	AW450694	Hs.21433	hypothetical protein DKFZp547J036		7.00		
20	116503	AI925316	Hs.212617	ESTs			12.60	
	116674	AI768015	Hs.92127	ESTs		32.00		
	116929	AA586922	Hs.80475	polymerase (RNA) II (DNA directed) polyp		7.60		
	116973	AI702054	Hs.166982	phosphatidylinositol glycan, class F	9.80			
	116993	AI417023	Hs.40478	ESTs			10.20	
25	117079	H92325		gb:ys85f05.s1 Soares retina N2b4HR Homo			15.20	
	117317	AI263517	Hs.43322	ESTs			13.40	
	117326	N23629	Hs.241420	Homo sapiens mRNA for KIAA1756 protein,			20.60	
	117396	W20128	Hs.296039	ESTs			10.60	
	117412	N32536	Hs.42645	ESTs			16.00	
	117519	N32528	Hs.146286	kinesin family member 13A			9.11	
30	117693	AW179019	Hs.112110	mitochondrial ribosomal protein L42				4.01
	117721	N46100	Hs.93939	EST			19.80	
	117881	AF161470	Hs.260622	butyrate-induced transcript 1	2.71			
	117903	AA768283	Hs.47111	ESTs			17.80	
35	117992	AI015709	Hs.172089	Homo sapiens mRNA; cDNA DKFZp586I2022 (f				4.17
	118013	AI674126	Hs.94031	ESTs			10.60	
	118017	AI813444	Hs.42197	ESTs		8.82		
	118186	N22886	Hs.42380	ESTs		7.00		
	118325	AI868065	Hs.166184	Intersectin 2			13.80	
40	118367	N64269	Hs.48946	EST		6.14		
	118368	N64339	Hs.48956	gap junction protein, beta 6 (connexin 3	3.14			
	118472	AL157545	Hs.42179	bromodomain and PHD finger containing, 3		12.40		
	118709	AA232970	Hs.293774	ESTs			12.20	
	119025	BE003760	Hs.55209	Homo sapiens mRNA; cDNA DKFZp434K0514 (f	4.50			
45	119027	AF086161	Hs.114611	hypothetical protein FLJ11808	3.22			
	119052	R10889		gb:rf38d02.s1 Soares fetal liver spleen		9.60		
	119164	AF221993	Hs.46743	McKusick-Kaufman syndrome		6.60		
	119186	AI979147	Hs.101265	hypothetical protein FLJ22593			10.80	
	119243	T12603		gb:CHR90123 Chromosome 9 exon II Homo sa			9.44	
50	119490	AA195276	Hs.263858	ESTs, Moderately similar to B34087 hypot			11.80	
	119499	AI918906	Hs.55080	ESTs		14.80		
	119599	W45552		gb:zc26d03.s1 Soares_senescent_fibroblas		12.60		
	119780	NM_016625	Hs.191381	hypothetical protein	17.00			
	119845	W79123	Hs.58561	G protein-coupled receptor 87	13.50			
55	119941	AA699485	Hs.58896	ESTs		8.00		
	119994	AA642402	Hs.59142	ESTs	7.73			
	120102	W67353	Hs.170218	KIAA0251 protein		39.60		
	120104	AK000123	Hs.180479	hypothetical protein FLJ20116	2.91			
	120294	AK000059	Hs.153881	Homo sapiens NY-REN-62 antigen mRNA, par		8.20		
60	120486	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	8.73			
	120599	AA804448	Hs.104463	ESTs		7.00		
	120699	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribos			10.00	
	120715	AA292700		gb:zs59a06.s1 NCI_CGAP_GCB1 Homo sapiens		9.40		
	120821	Y19062	Hs.96870	staufer (Drosophila, RNA-binding protein			13.80	
65	120859	AA826434	Hs.1619	achaete-scute complex (Drosophila) homol		9.00		
	120880	AA360240	Hs.97019	EST		15.60		
	120983	AA398209	Hs.97587	EST		27.66		
	121034	AL389951	Hs.271623	nucleoporin 50kD		20.80		
	121121	AA399371	Hs.189095	similar to SALL1 (sal (Drosophila)-like		22.80		
70	121313	AA402713	Hs.97872	ESTs			10.00	
	121369	AW450737	Hs.128791	CGI-09 protein	25.71			
	121376	AA448103	Hs.187958	solute carrier family 6 (neurotransmitte			5.42	
	121476	AA412311	Hs.97903	ESTs		8.30		
	121509	AA868939	Hs.97888	ESTs		8.59		
75	121553	AA412488	Hs.48820	TATA box binding protein (TBP)-associat	18.50			
	121753	AK000552	Hs.323518	WD repeat domain 5	7.00			
	121838	AA425680	Hs.98441	ESTs			10.40	
	121857	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	6.00			
	121991	AA430058	Hs.98649	EST			12.20	
80	122089	AW016543	Hs.98682	hypothetical protein FKSG32		8.60		
	122105	AW241685	Hs.98699	ESTs		6.14		
	122163	AA435702	Hs.98829	EST			10.40	
	122318	AA429743		gb:zv60b05.r1 Soares_testis_NHT Homo sap			18.20	
	122335	AA443258	Hs.241551	chloride channel, calcium activated, fam	13.50			
	122338	AA443311	Hs.98998	ESTs	4.80			
85	122414	AI313473	Hs.99087	ESTs, Weakly similar to S47073 finger pr		8.00		

	122512	AF053305	Hs.98658	budding uninhibited by benzimidazoles 1	8.80		
	122516	AA449352	Hs.99217	ESTs		9.40	
	122702	AI220089	Hs.99439	ESTs	9.20		
5	122852	AI580056	Hs.98992	ESTs		10.40	
	122925	AW268962	Hs.111335	ESTs	6.80		
	123005	AW369771	Hs.52620	integrin, beta 8	12.60		
	123044	AK001035	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro		5.35	
	123160	AA488687	Hs.284235	ESTs, Weakly similar to I38022 hypotheti	6.06		
10	123315	AA496369		gb:zv37d10.s1 Soares ovary tumor NbHOT H	12.40		
	123329	Z47542	Hs.179312	small nuclear RNA activating complex, po	11.80		
	123497	AA765256	Hs.135191	ESTs, Weakly similar to unnamed protein	12.00		
	123518	AL035414	Hs.21068	hypothetical protein	13.00		
	123519	AW015887	Hs.112574	ESTs	12.20		
15	123614	AK000492	Hs.98806	hypothetical protein	7.80		
	123616	AA680003	Hs.109363	Homo sapiens cDNA: FLJ23603 fis, clone L		10.60	
	123673	BE550112	Hs.158549	ESTs, Weakly similar to T2D3_HUMAN TRANS	23.00		
	123727	AI083986	Hs.282977	hypothetical protein FLJ13490	7.00		
	123731	AA609839		gb:ae62f01.s1 Stratagene lung carcinoma	9.80		
20	123752	AA227714	Hs.179703	KIAA0129 gene product	3.50		
	123900	AA621223	Hs.112953	EST		12.80	
	124006	AI147155	Hs.270016	ESTs	97.00		
	124059	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	3.02		
	124069	AF134160	Hs.7327	claudin 1	27.80		
25	124191	T96509	Hs.248549	ESTs, Moderately similar to S65657 alpha		35.80	
	124273	AA457211	Hs.8858	bromodomain adjacent to zinc finger doma	7.20		
	124297	AL080215	Hs.102301	Homo sapiens mRNA; cDNA DKFZp586J0323 (f		11.00	
	124305	AW963221		gb:EST375294 MAGE resequences, MAGH Homo		16.00	
	124676	AI360119.comp	Hs.181013	phosphoglycerate mutase 1 (brain)		6.08	
30	124874	BE550182	Hs.127826	RaiGEF-like protein 3, mouse homolog		21.00	
	124904	AK000483	Hs.93872	KIAA1682 protein	9.40		
	124969	AI650360	Hs.100256	ESTs		10.80	
	125000	T58615	Hs.110640	ESTs		9.80	
	125201	AA693960	Hs.103158	ESTs, Weakly similar to T33296 hypotheti	7.60		
35	125266	W90022	Hs.186809	ESTs, Highly similar to LCT2_HUMAN LEUKO	6.59		
	125299	T32982	Hs.102720	ESTs		9.57	
	125356	AI057052	Hs.133554	ESTs, Weakly similar to Z195_HUMAN ZINC		14.00	
	125370	AA256743	Hs.134158	Homo sapiens, Similar to KIAA0092 gene p	8.20		
	125418	AA777690	Hs.188501	ESTs		13.20	
40	125433	AL162066	Hs.54320	hypothetical protein DKFZp762D096	21.40		
	125437	AI609449	Hs.140197	ESTs	6.96		
	125446	BE219987	Hs.166982	phosphatidylinositol glycan, class F	8.80		
	125711	AA305800	Hs.5672	hypothetical protein AF140225		11.20	
	125756	BE174587	Hs.289721	growth arrest specific transcript 5		4.31	
45	125757	AI274906	Hs.166835	ESTs, Highly similar to 1814460A p53-ass		15.60	
	125769	BE270266	Hs.82128	ST4 oncofetal trophoblast glycoprotein	3.20		
	125839	AW836261	Hs.337717	ESTs	8.20		
	125850	W85858	Hs.99804	ESTs	2.65		
	125875	H14480		gb:ym18b09.r1 Soares infant brain 1NIB H	7.40		
50	125924	BE272506	Hs.82109	syndecan 1		4.23	
	125972	AI927475	Hs.35406	ESTs, Highly similar to unnamed protein		3.98	
	126034	H60340		gb:yr39b04.r1 Soares fetal liver spleen		10.60	
	126327	AA432266	Hs.44648	ESTs	11.60		
	126345	N49713		gb:yv23f06.s1 Soares fetal liver spleen	6.67		
55	126435	AW614529	Hs.285847	CGI-19 protein		10.60	
	126487	AA283809	Hs.184601	solute carrier family 7 (cationic amino		4.38	
	126521	AI475110	Hs.203933	ESTs	6.60		
	126522	W31912		gb:zc76d03.s1 Pancreatic Islet Homo sapi		14.80	
60	126543	AL035864	Hs.69517	cDNA for differentially expressed CO16 g		4.01	
	126567	AA058394	Hs.57887	ESTs, Weakly similar to KIAA0758 protein	7.80		
	126605	AA676910		gb:zj65h07.s1 Soares_fetal_liver_spleen_		11.60	
	126627	AA497044	Hs.20887	hypothetical protein FLJ10392		14.60	
	126628	N49776	Hs.170994	hypothetical protein MGC10946	8.00		
	126737	AW976516	Hs.283707	Homo sapiens cDNA: FLJ21354 fis, clone C	2.92		
65	126795	AW975076	Hs.172589	nuclear phosphoprotein similar to S. cer	7.50		
	126802	AW805510	Hs.97056	hypothetical protein FLJ21634	11.60		
	126892	AF121856	Hs.284291	sorting nexin 6	3.50		
	126928	AA480902	Hs.137401	ESTs		22.83	
	126979	AA210954		gb:zq89h10.r1 Stratagene hNT neuron (937		11.80	
70	126986	AI279892	Hs.46801	sorting nexin 14		11.60	
	126992	AI809521		gb:wf30e03.x1 Soares_NFL_T_GBC_S1 Homo s		20.80	
	127066	R25066		gb:yq42c07.r1 Soares infant brain 1NIB H		27.60	
	127099	AA347668		gb:EST54026 Fetal heart II Homo sapiens		21.60	
	127139	AA830233	Hs.293585	ESTs		11.20	
75	127209	AA305023	Hs.81964	SEC24 (S. cerevisiae) related gene famil	3.10		
	127221	BE062109	Hs.241551	chloride channel, calcium activated, fam	2.76		
	127225	AA315933	Hs.120879	ESTs		16.80	
	127313	AK002014	Hs.47546	Homo sapiens cDNA FLJ11458 fis, clone HE	14.00		
	127444	AW978474	Hs.7560	Homo sapiens mRNA for KIAA1729 protein,		13.60	
80	127500	AW971353	Hs.162115	ESTs	11.20		
	127524	AI243596	Hs.94830	ESTs, Moderately similar to T03094 A-kin	7.80		
	127540	N45572	Hs.105362	Homo sapiens, clone MGC:18257, mRNA, com	3.53		
	127599	AA613204	Hs.150399	ESTs		13.80	
	127609	X80031	Hs.530	collagen, type IV, alpha 3 (Goodpasture		28.00	
85	127662	W80755	Hs.8294	KIAA0195 gene product		19.80	
	127668	AI343257	Hs.139993	ESTs		11.20	

	127746	AI239495	Hs.120189	ESTs			14.18
	127812	AA741368	Hs.291434	ESTs	4.50		
	127817	AA836641	Hs.163085	ESTs			24.60
5	127959	AI302471	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L			9.20
	127960	AI613226	Hs.41569	phosphatidic acid phosphatase type 2A			16.83
	127969	F06458	Hs.93748	Homo sapiens cDNA FLJ14676 fis, clone NT	13.60		
	128015	Z21169	Hs.334659	hypothetical protein MGC14139	7.00		
	128027	AI433721	Hs.164153	ESTs			37.40
10	128077	AI310330	Hs.128720	ESTs			9.60
	128166	NM_006147	Hs.11801	interferon regulatory factor 6			9.24
	128226	AI284940	Hs.289082	GM2 ganglioside activator protein	19.00		
	128305	AI954968	Hs.279009	matrix Gla protein			10.40
	128341	AA191420	Hs.185030	ESTs	9.00		
15	128527	AA504583	Hs.101047	transcription factor 3 (E2A immunoglobul			4.30
	128539	R46163	Hs.258618	ESTs	12.60		
	128568	H12912	Hs.274691	adenylate kinase 3			4.56
	128572	AA933022	Hs.256583	interleukin enhancer binding factor 3, 9		10.00	
	128777	AI878918	Hs.10526	cysteine and glycine-rich protein 2	16.80		
20	128781	N71826	Hs.105465	small nuclear ribonucleoprotein polypept			4.48
	128796	AJ000152	Hs.105924	defensin, beta 2	8.12		
	128920	AA622037	Hs.166468	programmed cell death 5			4.62
	128924	BE279383	Hs.26557	plakophilin 3			4.04
	128971	H05132	Hs.107510	ESTs	12.60		
25	129008	AL079648	Hs.301088	ESTs	8.80		
	129041	BE382756	Hs.169902	solute carrier family 2 (facilitated glu			6.05
	129075	BE250162	Hs.83765	dihydrofolate reductase	2.59		
	129105	AI769160	Hs.108681	Homo sapiens brain tumor associated prot		6.67	
	129189	AB023179	Hs.9059	KIAA0962 protein	8.00		
30	129229	AF013758	Hs.109643	polyadenylate binding protein-interactin	4.00		
	129241	AI878857	Hs.109706	hematological and neurological expressed			4.06
	129300	W94197	Hs.110165	ribosomal protein L26 homolog	2.55		
	129404	AI267700	Hs.317584	ESTs	18.00		
	129457	X61959	Hs.207776	aspartylglucosaminidase	6.50		
35	129466	L42583	Hs.334309	keratin 6A	12.94		
	129494	AI148976	Hs.112062	ESTs		11.00	
	129605	AF061812	Hs.115947	keratin 16 (focal non-epidermolytic palm			4.46
	129541	AI911527	Hs.11805	ESTs		12.00	
	129655	AW163331	Hs.118778	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic			4.70
40	129703	BE388665	Hs.179999	Homo sapiens, clone IMAGE:3457003, mRNA			4.02
	129720	AA156214	Hs.12152	APMCF1 protein			5.71
	129748	M16707	Hs.123053	H4 histone, family 2	3.50		
	129890	AI868872	Hs.282804	hypothetical protein FLJ22704			4.21
	129896	BE295568	Hs.13225	UDP-Gal:betaGlcNAc beta 1,4- galactosylt	2.56		
45	129945	BE514376	Hs.165998	PAI-1 mRNA-binding protein			4.03
	130010	AA301116	Hs.142838	nucleolar phosphoprotein Nopp34		7.00	
	130026	T40480	Hs.332112	EST	6.40		
	130080	X14850	Hs.147097	H2A histone family, member X			4.65
50	130149	AW067805	Hs.172665	methylentetrahydrofolate dehydrogenase	2.74		
	130285	AA063546	Hs.75981	ubiquitin specific protease 14 (tRNA-gua		7.40	
	130441	U63630	Hs.155637	protein kinase, DNA-activated, catalytic			3.91
	130482	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	4.87		
	130500	AB007913	Hs.158291	KIAA0444 protein		9.60	
	130524	U89995	Hs.159234	forkhead box E1 (thyroid transcription f		13.40	
55	130541	X05608	Hs.211584	neurofilament, light polypeptide (68kD)		8.20	
	130553	AF062649	Hs.252587	pituitary tumor-transforming 1			6.06
	130567	AA383092	Hs.1608	replication protein A3 (14kD)		7.00	
	130577	M69241	Hs.162	insulin-like growth factor binding prote	3.04		
	130627	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	3.87		
60	130648	AI458165	Hs.17296	hypothetical protein MGC2376			16.20
	130697	L29472	Hs.1802	major histocompatibility complex, class			17.80
	130744	H59696	Hs.18747	POP7 (processing of precursor, S. cerevi			5.28
	130800	AI187292	Hs.19574	hypothetical protein MGC5469			4.43
	130867	NM_001072	Hs.284239	UDP glycosyltransferase 1 family, polype	16.84		
65	130869	J03626	Hs.2057	uridine monophosphate synthetase (orotat			4.92
	130925	AF093419	Hs.169378	multiple PDZ domain protein		9.60	
	130994	W17044	Hs.327337	ESTs	12.40		
	131028	AI879165	Hs.2227	CCAAT/enhancer binding protein (C/EBP),	10.21		
	131031	NM_001650	Hs.288650	aquaporin 4			9.80
70	131041	T15767	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,			9.60
	131058	W28545	Hs.101514	hypothetical protein FLJ10342			17.00
	131090	AI143139	Hs.2288	visinin-like 1	2.74		
	131112	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f		8.80	
	131148	AW953575	Hs.303125	p53-induced protein PIGPC1	3.12		
75	131185	BE280074	Hs.23960	cyclin B1	3.07		
	131200	BE540516	Hs.293732	hypothetical protein MGC3195	3.07		
	131219	W25005	Hs.24395	small inducible cytokine subfamily B (Cy	2.87		
	131257	AW339037	Hs.24908	ESTs			14.67
	131375	AW293165	Hs.143134	ESTs		19.20	
80	131460	NM_003729	Hs.27076	RNA 3'-terminal phosphate cyclase	3.50		
	131476	AI521663	Hs.334644	hypothetical protein FLJ14668	15.00		
	131510	BE245374	Hs.27842	hypothetical protein FLJ11210		7.80	
	131646	BE302464	Hs.30057	MRS2 (S. cerevisiae)-like, magnesium hom		7.00	
	131786	BE000971	Hs.306083	Novel human gene mapping to chromosome 22	2.65		
85	131839	AB014533	Hs.33010	KIAA0633 protein			35.20
	131843	AA192315	Hs.184062	putative Rab5-interacting protein			4.11

	131877	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	19.00		
	131885	BE502341	Hs.3402	ESTs	6.48		
	131921	AA456093	Hs.34720	ESTs		8.40	
5	131945	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	56.00		
	131958	NM_014062	Hs.3566	ART-4 protein			3.82
	131965	W79283	Hs.35962	ESTs	3.03		
	132000	AW247017	Hs.36978	melanoma antigen, family A, 3		9.80	
	132040	NM_001196	Hs.315689	Homo sapiens cDNA: FLJ22373 fis, clone H	3.30		
10	132109	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	21.00		
	132114	NM_006152	Hs.40202	lymphoid-restricted membrane protein		8.40	
	132162	AA315805	Hs.94560	desmoglein 2			12.25
	132164	AI752235	Hs.41270	procollagen-lysine, 2-oxoglutarate 5-dio	2.70		
	132180	NM_004460	Hs.418	fibroblast activation protein, alpha	2.71		
	132181	AW961231	Hs.16773	Homo sapiens clone TCCCA00427 mRNA sequ	3.83		
15	132182	NM_014210	Hs.70499	ecotropic viral integration site 2A			13.20
	132231	AA662910	Hs.42635	hypothetical protein DKFZp434K2435	9.50		
	132277	AK001745	Hs.184628	hypothetical protein FLJ10883	4.50		
	132328	NM_014787	Hs.44896	DnaJ (Hsp40) homolog, subfamily B, membe			9.20
	132394	AK001680	Hs.30488	DKFZP434F091 protein			19.80
20	132424	AA417878	Hs.48401	ESTs, Moderately similar to ALU8_HUMAN A		8.60	
	132528	T78736	Hs.50758	SMC4 (structural maintenance of chromoso		27.40	
	132543	BE568452	Hs.5101	protein regulator of cytokinesis 1	4.38		
	132544	L19778	Hs.51011	H2A histone family, member P		7.00	
	132550	AW969253	Hs.170195	bone morphogenetic protein 7 (osteogenic	2.64		
25	132552	BE621985	Hs.296922	thiopurine S-methyltransferase			15.83
	132581	AK000631	Hs.52256	hypothetical protein FLJ20624		6.60	
	132617	AF037335	Hs.5338	carbonic anhydrase XII	4.95		
	132638	AI796870	Hs.54277	DNA segment on chromosome X (unique) 992		8.20	
30	132653	Z15008	Hs.54451	laminin, gamma 2 (nicotin (100kD), kallini	4.38		
	132669	W38586	Hs.293981	guanine nucleotide binding protein (G pr			4.36
	132710	W74001	Hs.55279	serine (or cysteine) proteinase inhibitor	4.60		
	132771	Y10275	Hs.56407	phosphoserine phosphatase	3.71		
	132799	W73311	Hs.169407	SAC2 (suppressor of actin mutations 2,			9.48
35	132833	U78525	Hs.57783	eukaryotic translation initiation factor			5.83
	132892	AW834050	Hs.9973	tensin			12.00
	132906	BE613337	Hs.234896	geminin	3.09		
	132959	AW014195	Hs.61472	ESTs, Weakly similar to YAE6_YEAST HYPOT			3.87
	132962	AA576635	Hs.6153	CGI-48 protein	3.50		
40	132990	X77343	Hs.334334	transcription factor AP-2 alpha (activat	6.18		
	132994	AA112748	Hs.279905	clone HQ0310 PRO0310p1	3.19		
	133000	AL042444	Hs.62402	p21/Cdc42/Rac1-activated kinase 1 (yeast	2.96		
	133050	X73424	Hs.63788	propionyl Coenzyme A carboxylase, beta p	2.55		
	133083	BE244588	Hs.6456	chaperonin containing TCP1, subunit 2 (b			4.00
	133086	L17131	Hs.139800	high-mobility group (nonhistone chromoso			8.96
45	133134	AF198620	Hs.65648	RNA binding motif protein 8A			4.28
	133155	M58583	Hs.662	cerebellin 1 precursor			10.80
	133181	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	3.00		
	133204	BE267696	Hs.254105	enolase 1, (alpha)			4.63
50	133412	U41493	Hs.73112	guanine nucleotide binding protein (G pr		12.50	
	133421	AF134160	Hs.7327	claudin 1	2.85		
	133451	AW970026	Hs.73818	ubiquinol-cytochrome c reductase hinge p			4.66
	133453	AI659306	Hs.73826	protein tyrosine phosphatase, non-recept		6.80	
	133504	NM_004415	Hs.74316	desmoplakin (DPI, DPII)	6.14		
55	133506	BE562958	Hs.74346	hypothetical protein MGC14353			4.55
	133615	M62843	Hs.75236	ELAV (embryonic lethal, abnormal vision,			17.80
	133627	NM_002047	Hs.75280	glycyl-tRNA synthetase			4.85
	133649	U25849	Hs.75393	acid phosphatase 1, soluble			6.34
	133669	NM_006925	Hs.166975	splicing factor, arginine/serine-rich 5			14.00
60	133749	L20852	Hs.10018	solute carrier family 20 (phosphate tran		6.11	
	133776	BE268649	Hs.177766	ADP-ribosyltransferase (NAD+; poly (ADP-			4.91
	133865	AB011155	Hs.170290	discs, large (Drosophila) homolog 5	3.07		
	133946	AJ001258	Hs.173878	NIPSNAP, C. elegans, homolog 1			4.60
	133973	N55540	Hs.78026	ESTs, Weakly similar to similar to ankyr			13.00
65	134047	BE262529	Hs.78771	phosphoglycerate kinase 1			3.85
	134098	BE513171	Hs.79086	mitochondrial ribosomal protein L3	2.56		
	134107	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitte		8.20	
	134112	AW449809	Hs.79150	chaperonin containing TCP1, subunit 4 (d			4.08
	134158	U15174	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	31.00		
70	134160	T98152	Hs.79432	fibrillin 2 (congenital contractural ara		24.60	
	134168	AA398908	Hs.181634	Homo sapiens cDNA: FLJ23602 fis, clone L			6.71
	134185	AA285136	Hs.301914	neuronal specific transcription factor D			14.74
	134201	L35035	Hs.79886	ribose 5-phosphate isomerase A (ribose 5		8.40	
	134272	X76040	Hs.278614	protease, serine, 15	4.50		
75	134276	BE083936	Hs.80976	antigen identified by monoclonal antibod		9.00	
	134353	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, m			16.40
	134367	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	2.80		
	134380	AU077143	Hs.179565	minichromosome maintenance deficient (S.	4.68		
	134423	H53497	Hs.83006	CGI-139 protein			3.84
	134469	AA279661	Hs.83753	small nuclear ribonucleoprotein polypept			5.81
80	134470	X54942	Hs.83758	CDC28 protein kinase 2			4.21
	134498	AW246273	Hs.84131	threonyl-tRNA synthetase			7.30
	134502	BE148534	Hs.84168	UV-B repressed sequence, HUR 7		13.60	
	134510	NM_002757	Hs.250870	mitogen-activated protein kinase kinase			9.70
	134548	N95406	Hs.333495	Deleted in split-hand/split-foot 1 regio			4.63
85	134654	AK001741	Hs.8739	hypothetical protein FLJ10879	6.00		

	134724	AF045239	Hs.321576	ring finger protein 22		12.00	
	134743	AA044163	Hs.89463	potassium large conductance calcium-acti	4.00		
	134781	AA374372	Hs.89626	parathyroid hormone-like hormone		25.20	
5	134806	AD001528	Hs.89718	spermine synthase			4.58
	134853	BE268326	Hs.90280	5-aminimidazole-4-carboxamide ribonucle			4.79
	134859	D26488	Hs.90315	KIAA0007 protein		6.20	
	134891	R51083	Hs.90787	ESTs		7.40	
	134960	BE246400	Hs.285176	acetyl-Coenzyme A transporter	4.00		
10	134993	BE409809	Hs.301005	purine-rich element binding protein B			4.48
	135047	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	9.50		
	135080	AI761180	Hs.94211	rdc1 (required for cell differentiation,	5.00		
	135103	NM_003428	Hs.9450	zinc finger protein 84 (HPF2)		11.00	
	135145	AW014729	Hs.95262	nuclear factor related to kappa B bindin			4.01
15	135184	U13222	Hs.96028	forkhead box D1		7.00	
	135242	AI583187	Hs.9700	cyclin E1	13.50		
	135286	AW023482	Hs.97849	ESTs	6.46		
	135289	AW372569	Hs.9788	hypothetical protein MGC10924 similar to		8.80	
	135355	AK001652	Hs.99423	ATP-dependent RNA helicase	10.00		
20	135371	NM_008025	Hs.997	protease, serine, 22	8.00		
	135393	L11244	Hs.99886	complement component 4-binding protein,		14.60	

TABLE 5B shows the accession numbers for those primekeys lacking unigenelD's for Table 5A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

Pkey	CAT number	Accessions
35	117079	1621717_1 H92325 T97125
	124305	242183_1 AW963221 AA344870 AA344871 H93331
	101502	18202_6 M26958
	109792	754958_1 R49625 F10674
	126034	1598157_1 H60340 N91637
40	102768	44641_1 U82321 H66077
	126345	1653833_1 N49713 N49819 W03810
	127066	1703458_1 R25066 R20144 R20145 Z43845
	127099	244301_1 AA347668 AW956810 Z44271 F07065 F07064 R13506
	119243	1774795_1 T12603 T12604
45	125875	1566433_1 H14480 N98295
	112054	1538292_1 R43590 F10439
	126979	171411_1 AA210954 AA211007
	126992	880655_1 AI809521 H12174 Z42556
	122318	292419_1 AA429743 AA442754
50	114699	135322_1 AA127386 R15644 AA127404
	114793	150742_1 AA158245 AA158235
	108305	111550_1 AA071391 AA069892 AA069891
	108393	113411_1 AA075211 AA075245 AA075126 AA074946
	100867	tigr_HT4586 U14622
55	123731	genbank_AA609839 AA609839
	109700	genbank_F09609 F09609
	120715	genbank_AA292700 AA292700
	113702	genbank_T97307 T97307
	115113	genbank_AA256460 AA256460
60	101045	entrez_J05614 J05614
	108554	genbank_AA084948 AA084948
	108573	genbank_AA086005 AA086005
	119052	149538_1 R10889 R10888
	126522	416020_1 W31912 AI167491
65	126605	439280_1 AA676910 AA778853 AA778865 W86800
	103768	46922_1 W42667 AI580740 AI690440 AI561350 AW467906 AW151450 AI825927 AL041716 AI885600 AI742213 AW248624 AI955498 AA033947
		AA845593 AI623711 N68583 C00064 AA193567 AW083868 AW163216 AA191595 AA522778 AI628008 AI915518 AA843508 AI926195
		AA176265 AW167963 AA992115 W93647 AW103572 AI862994 AI342059 AA911719 AA176155 AA024712 AA069988 AA205591 AI591107
70		AI199673 AI811766 AI275832 AI422233 AI191852 AI096682 AI580124 AI683612 AA582453 AA927559 AA486415 T32414 AI084978 H44849
		H44848 H20477 T91695 W47039 AA070055 AA024795 AA328855 AA379248 AA379330 AA385580 W25920 W03688 AA448359 AA093881
		AW362477 AA089997 AI350265 W93479 N99688 AA932257 AW351459 H68590 AA663402 AA069771 AW087986 AI858420 AA600214
		AI970774 AI857712 AI683081 AI885584 AW131150 AI567981 AW002714 AW189973 AW075495 AW168303 AA953714 AW516881 AI357375
		AI566663 AW512676 AI570580 AI023690 AA448216 AI079853 AI422707 AA779516 AW026972 AW130082 AW162307 AW438646 AA709332
		AW192394 AI167350 AI217879 AI129152 AA719509 AI350480 AA663418 AI003634 AW118546 AA180261 AA442833 AI268625 AA888881
75		AI038759 AA846723 AI248770 AA993694 AI280335 AI885107 AW518649 AA641563 AA995835 AA582521 AI276744 AA436478 AI017360
		AI620763 AI859887 N73926 AI076327 AI741615 AI160617 AW172819 AI492005 AA677429 AA996334 AI693771 AI950039 AI245629 AI288515
		AI866186 T93293 AA173262 AA599779 AI680092 AW439316 AI084555 AI272672 AI583507 AW473219 AA738132 AW473283 AI367492
		AA995410 AI689624 AA206353 AI033095 AI040382 AA873630 AI221074 AI934840 AI418680 AA844306 R94503 AA773520 AA843169
		AA219425 AA629658 AI811719 AW411275 AI590981 W37907 AI591178 AI864051 AA983238 AA669347 AA976239 AA704570 AI628339
80		AI884391 AI241580 AI003539 AW176687 AA009650 N34566 AI333493 AI186070 AA070827 AA411683 AI280884 AA872023 AA207255
		AA021576 N71953 AI885888 AW076039 T15777 AI537673 AW248048 H09554 W93480 W47001 AW079114 AA063160 AA757453 R60788
		AI859431 H20478 AA218882 AA757465 AA100995 AI864135 AI934209 AA070503 H47008 AA219646 W61039 W93907 AW385050 W37967
		W78028 AA189007 AA479136 R93650 AA442312 T30287 AA847628 AA180262 AA009549 C03892 AW149464 AA310963 AA219693
		AA069747 R29207 AA094784 AA293615 AA447848 AI984167 N90393 C05097 N56499 AW292351 AW149681 AW473258 AA629322 AI004409
85		AW105577 AI954937 AI811070 AA902422 AW514437 AA535460 AA916877 AW517122 AA974657 AA975649 AW517130 AW517129 F31737
		W07688 AA193645 AA378994 AA489273 F32267 W39303 AA021181 N86810 AA406524 AA062553 AA436801 H08985 H15979 N40310

AA436789 AA232172 AW360778 W25862 R60282 AA436530 AA378894 AA187461 AI940535 AA604210 AA089514 AA360421 N88243 N84281
 AA209340 N56174 N88374 AA191088 AW247691 AA249013 AA093111 AA972535 AW298594 AA375893 T12139 W28186 AW243849
 AI288629 AA843996 W15260 AI188286 AW248079 R15836

119599 genbank_W45552 W45552
 112382 genbank_R59904 R59904
 105264 genbank_AA227934 AA227934
 100071 entrez_A28102 A28102
 123315 714071_1 AA495369 AA496646

Table 6A shows 99 genes up-regulated nonsmokers with lung cancer relative to smokers with lung cancer. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: average of AI for samples from non-smokers with adenocarcinoma divided by the 90th percentile of AI for samples from smokers with adenocarcinoma
 R2: average of AI for samples from non-smokers with squamous cell carcinoma divided by the 90th percentile of AI for samples from smokers with squamous cell carcinoma

Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2
100971	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte		3.64
101174	L17330	Hs.280	pre-T/NK cell associated protein	15.00	
101296	Y12490	Hs.85092	thyroid hormone receptor interactor 11		2.46
101304	AA001021	Hs.6685	thyroid hormone receptor interactor 8		12.00
101806	AA586894	Hs.112408	S100 calcium-binding protein A7 (psoriasis)		2.68
101972	S82472		gb:beta-pol-DNA polymerase beta (exon a		2.11
102274	U30930	Hs.158540	UDP glycosyltransferase 8 (UDP-galactose	7.50	
102394	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	7.50	
102832	U92015		gb:Human clone 143789 defective mariner	13.50	
103010	X52509	Hs.161640	tyrosine aminotransferase	9.50	
103439	X98266		gb:H.sapiens mRNA for ligase like protei		2.50
103563	L02911	Hs.150402	activin A receptor, type I	9.00	
103857	AJ076795	Hs.45033	lacrimal proline rich protein		3.94
104239	AB002367	Hs.21355	doublecortin and CaM kinase-like 1	13.50	
104590	AW373062	Hs.83623	nuclear receptor subfamily 1, group I, m		12.66
104907	AA055829	Hs.196701	ESTs, Weakly similar to ALU1_HUMAN ALU	16.50	
106131	BE514788	Hs.296244	SNARE protein		2.17
106672	H47233	Hs.30643	ESTs	7.00	
106872	T56887	Hs.18282	KIAA1134 protein	11.50	
106960	AA156238	Hs.32501	ESTs		2.38
106971	Z43846	Hs.194478	Homo sapiens mRNA; cDNA DKFZp434O1572 (f	9.50	
107982	AA035375	Hs.57887	ESTs, Weakly similar to KIAA0758 protei		2.95
108562	AA100796		gb:zm26c06.s1 Stratagene pancreas (93720	16.50	
108599	AB018549	Hs.69328	MD-2 protein	13.00	
108663	BE219231	Hs.292653	ESTs, Weakly similar to T26845 hypotheti		2.40
109247	AA314907	Hs.85950	ESTs	7.00	
109630	R44607	Hs.22672	ESTs		5.00
110193	AJ004874	Hs.310764	Homo sapiens mRNA; cDNA DKFZp434M082 (fr	12.50	
110234	H24458	Hs.32085	EST	16.50	
110644	R94207	Hs.268989	ESTs, Highly similar to type II CALM/AF1	8.00	
110886	AW274992	Hs.72249	three-PDZ containing protein similar to	17.00	
111057	T79639	Hs.14629	ESTs	16.50	
111950	AF071594	Hs.110457	Wolf-Hirschhorn syndrome candidate 1	11.00	
112291	R53972	Hs.25026	ESTs		3.00
112956	Z43784	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)		2.79
113009	T23699	Hs.7246	ESTs		4.50
113060	BE564162	Hs.250820	hypothetical protein FLJ14827	9.79	
113073	N39342	Hs.103042	microtubule-associated protein 1B	32.50	
113074	AK001335	Hs.31137	protein tyrosine phosphatase, receptor t		3.82
113121	T48011	Hs.8764	EST		2.21
113125	AA968672	Hs.8929	hypothetical protein FLJ11362	19.50	
113757	AA703095	Hs.18631	ESTs		2.65
113848	W52854	Hs.27099	hypothetical protein FLJ23293 similar to	6.00	
113884	AI333076	Hs.28529	chromosome 12 open reading frame 2		6.00
113936	W17056	Hs.83623	nuclear receptor subfamily 1, group I, m		4.63
114875	AA235609	Hs.236443	Homo sapiens mRNA; cDNA DKFZp564N1063 (7.00
114987	AA251016	Hs.87808	EST		6.00
115460	AW958439	Hs.38613	ESTs		2.27
115722	W91892	Hs.59609	ESTs		9.00
116261	AA481788	Hs.190150	ESTs	9.50	
116830	H61037	Hs.70404	ESTs, Weakly similar to ALU2_HUMAN ALU	8.50	
116970	AB023179	Hs.9059	KIAA0962 protein	7.50	
117178	H98675	Hs.269034	ESTs		2.68
117757	AF088019	Hs.46732	EST	7.50	
118283	AA287747	Hs.173012	ESTs, Weakly similar to A46010 X-linked	16.50	
118384	AF217525	Hs.49002	Down syndrome cell adhesion molecule		2.50
118657	AI822106	Hs.49902	ESTs		2.39
120328	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi		3.50
120404	AB023230	Hs.96427	KIAA1013 protein	7.00	
120524	AA261852	Hs.192905	ESTs	6.00	
120688	AW207555	Hs.97093	Homo sapiens cDNA: FLJ23004 fis, clone L	17.92	

	121558	AA412497	gb:z195g12.s1 Soares_testis_NHT Homo sap		2.95
	121676	H56037	Hs.108146 ESTs	10.00	
	121936	AI024600	Hs.98612 ESTs	15.00	
5	121938	AA428659	Hs.98610 ESTs	14.00	
	122177	AA435789	Hs.98833 EST	8.93	
	123442	AA299652	Hs.111496 Homo sapiens cDNA FLJ11643 fis, clone HE	13.04	
	123551	AA608837	gb:af03h12.s1 Soares_testis_NHT Homo sap	11.50	
	123756	AA609971	Hs.112795 EST	11.00	
10	123861	AA620840	gb:af89g01.s1 Soares_testis_NHT Homo sap		2.50
	124371	N24924	Hs.188601 ESTs	6.50	
	127477	BE328720	Hs.280651 ESTs		4.33
	127591	AI190540	Hs.131092 ESTs		3.02
	128252	AA455924	Hs.192228 ESTs	7.00	
	128426	AI265784	Hs.145197 ESTs		2.08
15	128925	R67419	Hs.21851 Homo sapiens cDNA FLJ12900 fis, clone NT		2.11
	128945	AI990506	Hs.8077 Homo sapiens mRNA; cDNA DKFZp547E184 (fr	10.00	
	129105	AI769160	Hs.108681 Homo sapiens brain tumor associated prot	15.50	
	129235	AW977238	Hs.126084 KIAA1055 protein		4.25
	129506	AB020684	Hs.11217 KIAA0877 protein	6.50	
20	129595	U09550	Hs.1154 oviductal glycoprotein 1, 120kD (mucin 9		10.00
	130160	AA305688	Hs.267695 UDP-Gal:betaGlcNAc beta 1,3-galactosyltr	20.00	
	130340	D82326	Hs.239106 solute carrier family 3 (cystine, dibasi	11.50	
	131220	AB023194	Hs.300855 KIAA0977 protein	17.50	
	131430	AI879148	Hs.26770 fatty acid binding protein 7, brain	6.10	
25	132114	NM_006152	Hs.40202 lymphoid-restricted membrane protein		6.15
	132458	AA935315	Hs.48965 Homo sapiens cDNA: FLJ21693 fis, clone C		5.58
	132647	NM_006927	Hs.54432 sialyltransferase 4B (beta-galactosidase	7.50	
	132655	D49372	Hs.54460 small inducible cytokine subfamily A (Cy		2.53
	132682	AI077500	Hs.54900 serologically defined colon cancer antig		2.50
30	132747	AA345241	Hs.55950 ESTs, Weakly similar to KIAA1330 protein		2.83
	132812	R50333	Hs.92186 Leman coiled-coil protein		3.82
	133337	AF085983	Hs.293676 ESTs		5.00
	133876	AL134906	Hs.771 phosphorylase, glycogen; liver (Hers dis		3.00
	134119	AW157837	Hs.79226 fasciculation and elongation protein zet		2.06
35	134464	AA302983	Hs.239720 CCR4-NOT transcription complex, subunit		2.27
	134542	M14156	Hs.85112 insulin-like growth factor 1 (somatomedi		11.50
	135002	AA448542	Hs.251677 G antigen 7B	87.00	
	135305	AA203555	Hs.98288 Homo sapiens cDNA FLJ14903 fis, clone PL		6.50

TABLE 6B show the accession numbers for those primekeys lacking unigeneID's for Table 6A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accessions
108562	36375_1	AA100796 AF020589 AA074629 AA075946 AA100849 AA085347 AA126309 AA079311 AA079323 AA085274
103439	35330_1	X98266 N41124
123551	genbank_AA608837	AA608837
123861	genbank_AA620840	AA620840
102832	entrez_U92015	U92015
101972	entrez_S82472	S82472
60	121558	genbank_AA412497 AA412497

Table 7A shows 98 genes down-regulated in non-smokers with lung cancer relative to smokers with lung cancer. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

5	Pkey:	Unique Eos probeset identifier number				
	ExAccn:	Exemplar Accession number, Genbank accession number				
	UnigeneID:	Unigene number				
	Unigene Title:	Unigene gene title				
10	R1:	90th percentile of AI for samples from smokers with adenocarcinoma divided by the average of AI for samples from non-smokers with adenocarcinoma.				
	R2:	90th percentile of AI for samples from smokers with squamous cell carcinoma divided by the average of AI for samples from non-smokers with squamous cell carcinoma.				
	Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2
15	100187	D17793	Hs.78183	aldo-keto reductase family 1, member C3		164.10
	100380	D82343	Hs.18551	neuroblastoma (nerve tissue) protein		77.40
	100576	X00356	Hs.37058	calcitonin/calcitonin-related polypeptid	102.40	
	100971	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	463.80	
	101046	K01160		(NONE)	672.00	
20	101066	AW970254	Hs.889	Charot-Layden crystal protein	66.00	
	101175	U82671	Hs.36980	melanoma antigen, family A, 2		77.20
	101497	W05150	Hs.37034	homeo box A5	62.80	
	101663	NM_003528	Hs.2178	H2B histone family, member Q	78.00	
	101677	NM_000715	Hs.1012	complement component 4-binding protein,	186.20	
25	101745	M88700	Hs.150403	dopa decarboxylase (aromatic L-amino aci	80.08	
	101941	S77583		gb:HERV10/HUMMTV reverse transcriptase	99.20	
	102125	NM_006456	Hs.288215	sialyltransferase		103.10
	102242	U27185	Hs.82547	retinoic acid receptor responder (lazarol	67.00	
	102340	U37055	Hs.278657	macrophage stimulating 1 (hepatocyte gro	71.60	
30	102369	U39840	Hs.299867	hepatocyte nuclear factor 3, alpha		69.70
	102457	NM_001394	Hs.2359	dual specificity phosphatase 4	153.00	
	102669	U71207	Hs.29279	eyes absent (Drosophila) homolog 2		65.70
	102796	AL079646	Hs.107019	sympleskin; Huntingtin interacting protei		58.80
	102829	NM_006183	Hs.80962	neurotensin		268.80
35	103207	X72790		gb:Human endogenous retrovirus mRNA for	70.00	
	103242	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o		212.10
	103260	X78416	Hs.3155	casein, alpha		130.70
	103351	X89211		gb:H.sapiens DNA for endogenous retrovir	64.60	
	104212	AB002298	Hs.173035	KIAA0300 protein	66.80	
40	104252	AF002246	Hs.210863	cell adhesion molecule with homology to	63.80	
	104258	AF007216	Hs.5462	solute carrier family 4, sodium bicarbon	94.40	
	105024	AA126311	Hs.9879	ESTs	68.20	
	106260	AI097144	Hs.5250	ESTs, Weakly similar to ALU1_HUMAN ALU S		74.60
	106440	AA449563	Hs.151393	glutamate-cysteine ligase, catalytic sub		71.10
45	106566	BE298210		gb:601118016F1 NIH_MGC_17 Homo sapiens c	73.20	
	106605	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (fr	83.80	
	106614	AA648459	Hs.335951	hypothetical protein AF301222		62.30
	106654	AW075485	Hs.286049	phosphoserine aminotransferase		202.40
	106999	H93281	Hs.10710	hypothetical protein FLJ20417		89.60
50	108700	AA121518	Hs.193540	ESTs, Moderately similar to 2109260A B c		66.40
	108810	AW295647	Hs.71331	hypothetical protein MGC5350		95.50
	108857	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act		63.40
	109597	AA989362	Hs.293780	ESTs	85.00	
	109691	T65568	Hs.12860	ESTs		58.70
55	109704	AI743880	Hs.12876	ESTs		60.60
	110942	R63503	Hs.28419	ESTs	76.40	
	111722	R23924	Hs.23596	EST	74.60	
	112891	T03927	Hs.293147	ESTs, Moderately similar to A46010 X-li	64.80	
60	112992	AL157425	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (f		76.70
	113073	N39342	Hs.103042	microtubule-associated protein 1B		120.20
	114251	H15261	Hs.21948	ESTs	127.20	
	115230	AA278300	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	174.00	
	115291	BE545072	Hs.122579	hypothetical protein FLJ10461		91.00
	115815	AW905328	Hs.180842	ribosomal protein L13	66.40	
65	115909	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH		226.60
	115965	AA001732	Hs.173233	hypothetical protein FLJ10970	82.80	
	116107	AL133916	Hs.172572	hypothetical protein FLJ20093		361.60
	116552	D20508	Hs.164649	hypothetical protein DKFZp434H247	69.00	
	116571	D45652		gb:HUMGS02848 Human adult lung 3' direct	64.20	
70	118466	N66741		gb:yz33g08.s1 Morton Fetal Cochlea Homo		63.50
	120484	AA253170	Hs.96473	EST	81.60	
	120983	AA398209	Hs.97587	EST		81.10
	121034	AL389951	Hs.271623	nucleoporin 50kD		66.20
	121423	AW973352	Hs.290585	ESTs	64.40	
75	122553	AA451884	Hs.190121	ESTs		60.40
	122946	AI718702	Hs.308026	major histocompatibility complex, class	188.60	
	123130	AA487200		gb:ab19f02.s1 Stratagene lung (937210) H		80.20
	124472	N52517	Hs.102670	EST	71.00	
	124526	N62096	Hs.293185	ESTs, Weakly similar to JC7328 antino aci		104.90
80	125489	H49193	Hs.124984	ESTs, Moderately similar to ALU7_HUMAN A		72.00
	125731	R61771	Hs.26912	ESTs		69.90
	125747	NM_002884	Hs.865	RAP1A, member of RAS oncogene family	69.00	
	126020	H79863	Hs.114243	ESTs		62.40
	126547	U47732	Hs.84072	transmembrane 4 superfamily member 3		62.80
85	126966	R38438	Hs.182575	solute carrier family 15 (H+/peptide tra		60.10

	127472	AA761378	Hs.192013	ESTs	70.20	
	127610	AA960867	Hs.150271	ESTs, Highly similar to unnamed protein	64.00	
	127742	AW293496	Hs.180138	ESTs	85.20	
5	127987	AI022103	Hs.124511	ESTs	96.60	
	128233	AW889132	Hs.11916	ribokinase		78.90
	128420	AA650274	Hs.41296	fibronectin leucine rich transmembrane p		106.90
	128766	AW160432	Hs.296460	craniofacial development protein 1	66.80	
	129014	AW935187	Hs.170162	KIAA1357 protein		58.53
10	129215	AB040930	Hs.126085	KIAA1497 protein	64.20	
	130090	H97878	Hs.132390	zinc finger protein 36 (KOX 18)	63.80	
	130385	AW067800	Hs.155223	stanniocalcin 2		139.60
	130732	AW890487	Hs.63984	cadherin 13, H-cadherin (heart)		64.60
	131025	AB040900	Hs.6189	KIAA1467 protein	64.40	
15	131241	BE501914	Hs.24654	Homo sapiens cDNA FLJ11640 fis, clone HE	76.20	
	131775	AB014548	Hs.31921	KIAA0648 protein	97.80	
	132240	AB018324	Hs.42676	KIAA0781 protein		71.00
	132856	NM_001448	Hs.58367	glypican 4		88.40
	132977	AA093322	Hs.301404	RNA binding motif protein 3	133.20	
20	133749	L20852	Hs.10018	solute carrier family 20 (phosphate tran		59.30
	133818	AI110684	Hs.7645	fibrinogen, B beta polypeptide	341.00	
	134264	AF149297	Hs.8087	NAG-5 protein		64.30
	134265	M83772	Hs.80876	flavin containing monooxygenase 3		232.53
	134346	X84002	Hs.82037	TATA box binding protein (TBP)-associate	66.00	
25	134395	AA456539	Hs.8262	lysosomal-associated membrane protein 2		75.80
	135047	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su		108.30
	135056	N75765	Hs.93765	lipoma HMGIC fusion partner	71.40	
	135309	AI564123	Hs.42500	ADP-ribosylation factor-like 5	70.40	

30 TABLE 7B shows the accession numbers for those primkeys lacking unigenelD's for Table 7A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

35 Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

	Pkey	CAT number	Accessions
40	103207	30635_4	X72790
	106566	120358_1	BE298210 AI672315 AW086489 BE298417 AA455921 AA902537 BE327124 R14963 AA085210 AW274273 AI333584 AI369742 AI039658 AI885095 AI476470 AI287650 AI885299 AI985381 AW592624 AW340136 AI266556 AA456390 AI310815 AA484951
45	116571	genbank_D45652	D45652
	118466	genbank_N66741	N66741
	101046	entrez_K01160 K01160	
	101941	entrez_S77583 S77583	
	103351	entrez_X89211 X89211	
50	123130	genbank_AA487200	AA487200

Table 8A shows 1720 genes either up or down-regulated in lung tumors or chronically diseased lung relative to a broad collection of over 40 distinct normal body tissues. Chronically diseased lung samples represent chronic non-malignant lung diseases such as fibrosis, emphysema, and bronchitis. These genes were selected from 39494 probesets on the Eos/Affymetrix Hu02 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 R1: 70th percentile of AI for lung tumors divided by 90th percentile of AI for normal lung
 R2: 70th percentile of AI for chronically diseased lung divided by 90th percentile of AI for normal lung

	Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2
15	300097	AI916973	Hs.213603	ESTs	5.46	4.69
	300117	AW189787	Hs.147474	ESTs	0.58	0.56
	300197	AI686661	Hs.218286	ESTs	4.26	5.44
	300201	AI308300		gb:ta90c06.x1 NCI_CGAP_Bm20 Homo sapien	0.62	0.83
	300225	AI989963	Hs.197505	ESTs	1.68	1.75
20	300247	AW274682	Hs.161394	ESTs	1.08	2.28
	300256	AI469095	Hs.298241	Transmembrane protease, serine 3	0.86	1.00
	300337	AI707881	Hs.202090	ESTs	5.80	9.09
	300362	Z42308		gb:HSC0FB121 normalized infant brain cDN	4.18	12.78
	300374	AI859947	Hs.314158	ESTs	2.99	4.38
25	300387	AW270150	Hs.254516	ESTs	1.50	2.53
	300440	AI421541	Hs.146164	ESTs	3.98	5.25
	300441	R10367	Hs.307921	EST, Weakly similar to Z232_HUMAN ZINC F	3.18	6.80
	300449	AI362967	Hs.132221	hypothetical protein FLJ12401	0.43	0.62
	300469	AW135830	Hs.233955	hypothetical protein FLJ20401	0.16	0.83
30	300552	X85711	Hs.21838	hypothetical protein FLJ11191	4.10	9.75
	300627	W27363		gb:ab37d01.r1 Stratagene HeLa cell s3 93	4.60	12.60
	300630	AW118822	Hs.128757	ESTs	2.91	5.86
	300716	AI216113	Hs.126280	hypothetical protein FLJ23393	1.00	0.92
	300738	AI623332	Hs.130541	KIAA1542 protein	1.82	1.71
35	300777	AA235361	Hs.96840	KIAA1527 protein	4.48	8.22
	300790	AI492471	Hs.188270	ESTs	1.29	1.18
	300832	AI688147	Hs.220615	ESTs, Weakly similar to T03829 transcrip	5.51	8.56
	300836	Z44942	Hs.22958	calcium channel alpha2-delta3 subunit	4.90	6.34
	300838	AI582897	Hs.192570	hypothetical protein FLJ22028	1.70	2.81
40	300878	AW449802	Hs.285901	Homo sapiens cDNA FLJ20428 fis, clone KA	4.56	7.91
	300897	AI890356	Hs.127804	ESTs, Weakly similar to T17233 hypotheti	2.23	1.58
	300926	AA504860		gb:ab03a10.s1 Stratagene fetal retina 93	2.13	3.50
	300960	AI041019	Hs.152454	ESTs	2.74	4.46
	300961	AW204069	Hs.312716	ESTs, Weakly similar to unnamed protein	1.00	1.00
45	300962	AA593373	Hs.293744	ESTs	1.46	1.51
	300967	AA565209	Hs.269439	ESTs	0.39	1.30
	300987	AW450840	Hs.148590	ESTs, Weakly similar to AF208846 1 BM-00	1.49	1.08
	300988	AI927208	Hs.208952	ESTs	0.16	0.37
	301050	AW136973	Hs.288516	ESTs, Weakly similar to S69890 mitogen i	3.23	1.94
50	301098	AA677570	Hs.185918	ESTs	6.76	14.28
	301157	AA729905	Hs.231916	ESTs	3.16	8.85
	301162	AI142118	Hs.129004	ESTs	1.68	7.18
	301170	AA737594	Hs.247606	ESTs	4.40	6.42
	301192	AI808751	Hs.121188	ESTs	6.38	11.59
55	301193	AA758115	Hs.128350	ESTs, Weakly similar to JC5423 2-hydroxy	4.35	7.78
	301267	AW297762	Hs.255690	ESTs	1.56	1.61
	301281	AA843986	Hs.190586	ESTs	2.19	1.78
	301341	AI819198	Hs.208229	ESTs	0.76	0.76
	301382	AA912839	Hs.163369	ESTs	1.00	1.81
60	301407	AW450466	Hs.126830	ESTs	1.48	1.51
	301452	AA975688	Hs.159955	ESTs	0.51	1.46
	301483	AW272467	Hs.254655	Untitled	2.40	5.02
	301494	AI678034	Hs.131099	ESTs	2.79	3.41
	301521	AI733621	Hs.133011	zinc finger protein 117 (HPF9)	0.67	0.67
65	301531	AI077462	Hs.134084	ESTs	2.52	3.76
	301580	AI878959	Hs.73737	splicing factor, arginine/serine-rich 1	7.41	11.92
	301676	Z43570	Hs.27453	ESTs, Moderately similar to G01251 Rar p	8.31	10.70
	301690	F05865	Hs.108323	ubiquitin-conjugating enzyme E2E 2 (homo	2.70	4.22
	301718	F07744	Hs.7987	DKFZP434F162 protein	4.20	8.78
70	301799	AA384252	Hs.286132	D15F37 (pseudogene)	5.93	7.04
	301804	AA581004	Hs.62180	anillin (Drosophila Scraps homolog), act	1.70	0.76
	301822	X17033	Hs.271986	Integrin, alpha 2 (CD49B, alpha 2 subuni	1.58	1.36
	301846	R20002	Hs.6823	hypothetical protein FLJ10430	1.00	1.00
	301868	T71508	Hs.13861	ESTs, Weakly similar to pH sensitive max	2.88	5.49
75	301882	T78054		gb:yc97g09.r1 Soares infant brain 1N18 H	2.28	3.80
	301905	AI991127	Hs.117202	ESTs	1.00	1.00
	301948	AA344647	Hs.116724	aldo-keto reductase family 1, member B11	5.28	2.28
	301960	AW070252	Hs.27973	KIAA0874 protein	5.38	6.48
	302011	T91418	Hs.125156	transcriptional adaptor 2 (ADA2, yeast,	3.03	3.42
80	302016	N40834	Hs.23495	hypothetical protein FLJ11252	1.00	1.25
	302041	NM_001501	Hs.129715	gonadotropin-releasing hormone 2	0.71	0.99
	302072	AJ238381	Hs.132576	paired box gene 9	1.60	1.71
	302094	AI286176	Hs.6786	ESTs	0.52	1.20
	302095	AW044300	Hs.137506	Homo sapiens BAC clone RP11-120J2 from 7	2.75	4.93
85	302148	AW269618	Hs.23244	ESTs	3.04	3.87

	302155	AI088485	Hs.144759	ESTs	0.45	1.15
	302201	AJ006276	Hs.159003	transient receptor potential channel 6	0.33	0.84
	302202	AF097159	Hs.159140	UDP-Gal:betaGlcNAc beta 1,4- galactosylt	0.52	0.94
5	302206	AI937193	Hs.41143	phosphoinositide-specific phospholipase	2.76	3.65
	302209	AF047445	Hs.159297	killer cell lectin-like receptor subfam1	1.00	1.00
	302235	AL049987	Hs.166361	Homo sapiens mRNA; cDNA DKFZp564F112 (fr	1.68	1.50
	302290	AL117607	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	1.00	2.11
	302328	AA354849	Hs.23240	Homo sapiens cDNA FLJ13496 fis, clone PL	9.38	13.08
10	302346	AL039101	Hs.194625	dynein, cytoplasmic, light intermediate	3.27	7.24
	302360	AJ010901	Hs.198267	mucin 4, tracheobronchial	2.54	1.88
	302384	Y08982	Hs.202676	synaptonemal complex protein 2	1.00	0.91
	302406	U86751	Hs.211956	CD3-epsilon-associated protein; antisens	2.63	2.67
	302409	AF155156	Hs.218028	adaptor-related protein complex 4, epsil	5.82	9.34
	302423	AB028977	Hs.225974	KIAA1054 protein	3.66	3.18
15	302432	AL080068	Hs.272534	Homo sapiens mRNA; cDNA DKFZp564J062 (fr	2.44	6.77
	302435	AF092047	Hs.227277	sine oculis homeobox (Drosophila) homolo	0.44	0.84
	302437	AB024730	Hs.227473	UDP-N-acetylglucosamine:alpha-1,3-D-mannosid	4.18	5.64
	302455	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	1.85	0.92
	302472	AA317451	Hs.6335	SWI/SNF related, matrix associated, acti	2.04	2.13
20	302476	AF182294	Hs.241578	U6 snRNA-associated Sm-like protein LSm8	1.44	1.89
	302489	T80660	Hs.230424	Homo sapiens cDNA FLJ13540 fis, clone PL	0.51	1.10
	302490	AA885502	Hs.187032	ESTs	2.64	4.87
	302562	AJ005585	Hs.48956	gap junction protein, beta 6 (connexin 3	5.34	2.68
25	302566	AA085996	Hs.248572	hypothetical protein FLJ22965	1.00	1.21
	302630	AB029488	Hs.272100	SMS3 protein	0.52	1.24
	302634	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	1.00	1.00
	302638	AA463798	Hs.102696	MCT-1 protein	1.58	1.02
	302647	X57723	Hs.198273	NADH dehydrogenase (ubiquinone) 1 beta s	2.72	6.85
30	302655	AJ227892	Hs.146274	ESTs	1.00	4.32
	302656	AW293005	Hs.70704	Homo sapiens, clone IMAGE:2823731, mRNA,	2.97	0.93
	302668	AA580691	Hs.180789	S164 protein	0.80	0.95
	302679	H65022		gb:yu66g11.1 r1 Weizmann Olfactory Epithel	1.68	5.04
	302680	AW192334	Hs.38218	ESTs	2.70	7.98
35	302697	AJ001408		gb:Homo sapiens mRNA for immunoglobulin	4.25	8.13
	302705	U09060		gb:Human immunoglobulin heavy chain, V-r	3.91	8.68
	302711	L08442		gb:Human autonomously replicating sequen	2.20	2.73
	302719	W69724	Hs.288959	hypothetical protein FLJ20920	0.54	1.02
	302742	L12069		gb:Homo sapiens (clone WR4.10VH) anti-th	4.28	11.57
40	302755	AW384815	Hs.149208	KIAA1555 protein	1.57	2.38
	302771	H98476	Hs.42522	ESTs	2.94	4.68
	302789	AJ245067		gb:Homo sapiens mRNA for immunoglobulin	3.49	6.31
	302795	AJ245313	Hs.272838	hypothetical protein FLJ10494	0.80	2.74
	302802	Y08250		gb:H.sapiens mRNA for variable region of	1.13	0.77
45	302803	AA442824	Hs.293961	ESTs, Moderately similar to putative DNA	3.14	10.68
	302812	N31301	Hs.152664	hypothetical protein FLJ20051	3.04	8.24
	302847	X98940		gb:H.sapiens rearranged Ig heavy chain (1.80	1.92
	302885	AL137763	Hs.132127	hypothetical protein LOC57822	1.00	1.00
	302943	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypothi	0.53	0.67
50	302977	AW263124	Hs.315111	hypothetical protein FLJ12894	2.45	2.62
	303006	AF078950	Hs.24139	Homo sapiens cDNA: FLJ23137 fis, clone L	4.88	8.61
	303011	AF090405		gb:Homo sapiens clone 2A1 scFV antibody	1.41	1.86
	303013	F07898	Hs.288968	RAB22A, member RAS oncogene family	1.51	1.19
	303061	AF151882	Hs.27693	peptidylprolyl isomerase (cyclophilin)-I	0.72	0.76
55	303077	AF163305		gb:H.sapiens T-cell receptor mRNA	1.17	3.90
	303090	AA443259	Hs.146286	kinesin family member 13A	4.08	6.46
	303091	AF192913	Hs.130683	zinc finger protein 180 (HHZ168)	2.50	4.37
	303094	AF195513	Hs.278953	Pur-gamma	5.38	8.38
	303095	AF202051	Hs.134079	NM23-H8	3.26	4.08
60	303131	AW081061	Hs.103180	DC2 protein	2.02	1.83
	303195	AA082211	Hs.233936	myosin, light polypeptide, regulatory, n	1.32	3.95
	303196	AA082298	Hs.59710	ESTs	0.77	0.53
	303216	AA581439	Hs.152328	ESTs	0.24	0.63
	303222	AA333538	Hs.204501	hypothetical protein FLJ10534	3.56	6.22
65	303234	AA132255	Hs.143951	ESTs	2.28	3.17
	303251	AW340037	Hs.115897	protocadherin 12	0.38	1.02
	303295	AA205625	Hs.208067	ESTs	2.30	1.00
	303297	T80072	Hs.13423	Homo sapiens clone 24468 mRNA sequence	1.86	4.48
	303316	AF033122	Hs.14125	p53 regulated PA26 nuclear protein	0.10	0.80
70	303467	AA398801	Hs.323397	ESTs	4.54	9.65
	303506	AA340605	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	0.09	0.04
	303552	AA359799	Hs.224652	ESTs, Weakly similar to unnamed protein	1.00	1.72
	303598	AA382814		gb:EST96097 Testis I Homo sapiens cDNA 5	4.96	9.14
	303637	AF056083	Hs.24879	phosphatidic acid phosphatase type 2C	2.06	2.02
75	303655	AA504702	Hs.258802	ATPase, (Na+)/K+ transporting, beta 4 po	1.00	1.24
	303756	AI738488	Hs.115838	ESTs	1.08	1.43
	303856	AA968589	Hs.180532	glucose phosphate isomerase	1.76	1.31
	303893	N88597	Hs.113503	karyopherin (importin) beta 3	2.30	2.57
	303907	AW467774	Hs.171880	polymerase (RNA) II (DNA directed) polyp	3.10	5.79
80	303946	AW474196	Hs.306637	Homo sapiens cDNA FLJ12363 fis, clone MA	5.06	11.86
	303978	AW513315		gb:xa043c12.x1 NCI_CGAP_Ut1 Homo sapiens	5.14	7.31
	303981	AW513804	Hs.278834	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.83	4.06
	303990	AW515465		gb:xu71a11.x1 NCI_CGAP_Kd8 Homo sapiens	1.15	2.35
	303998	AW516449		gb:xt68f05.x1 NCI_CGAP_Ut2 Homo sapiens	2.20	9.35
	303999	AW516611		gb:xp70b11.x1 NCI_CGAP_Ov39 Homo sapiens	4.85	6.28
85	304006	AW517947		gb:xt66h02.x1 NCI_CGAP_Ut2 Homo sapiens	3.21	4.07

	304008	AW518198	Hs.3297	ribosomal protein S27a	6.50	11.08
	304009	AW518206	Hs.181165	eukaryotic translation elongation factor	1.88	3.27
	304024	T03036		gb:FB2187 Fetal brain, Stratagene Homo s	2.15	3.55
5	304026	T03160		gb:FB26F2 Fetal brain, Stratagene Homo s	5.88	11.80
	304028	T03266		gb:FB7C1 Fetal brain, Stratagene Homo sa	5.59	13.46
	304036	T16855	Hs.244621	ribosomal protein S14	6.55	14.43
	304046	T54803		gb:yb42d06.s1 Stratagene fetal spleen (9	6.18	12.19
	304061	T61521		gb:yb73g01.s1 Stratagene ovary (937217)	2.64	8.23
10	304063	T62536		gb:yc04c12.s1 Stratagene lung (937210) H	0.53	1.61
	304097	R25376	Hs.177592	ribosomal protein, large, P1	6.49	11.67
	304114	R78946		gb:yi87g02.s1 Soares placenta Nb2HP Homo	2.90	4.18
	304122	H28966		gb:ym31a06.s1 Soares infant brain 1NIB H	1.00	2.76
	304155	H68696		gb:yr78b06.s1 Soares fetal liver spleen	0.79	1.18
15	304203	N56929		gb:yy82d08.s1 Soares_multiple_sclerosis_	4.28	11.34
	304234	W81608		gb:zd88h06.s1 Soares_fetal_heart_NbHH19W	6.47	11.03
	304267	AA064862	Hs.73742	ribosomal protein, large, P0	1.34	1.16
	304270	AA069711	Hs.297753	vimentin	3.40	5.40
	304287	AA079286	Hs.78466	proteasome (prosome, macropain) 26S sub	2.93	4.42
20	304348	AA179868		gb:zp38g12.s1 Stratagene muscle 937209 H	3.98	10.96
	304415	AA290747	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	3.32	5.99
	304430	AA347682		gb:EST54044 Fetal heart II Homo sapiens	1.00	1.00
	304456	AA411240		gb:zv26g05.s1 Soares_NhHMPu_S1 Homo sapi	1.42	3.33
	304521	AA464716		gb:zx82c11.s1 Soares ovary tumor NbHOT H	2.18	1.15
25	304526	AA476427		gb:zx02c05.s1 Soares_total_fetus_Nb2HF8_	5.38	14.11
	304542	AA482602	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	4.16	8.23
	304546	AA486074	Hs.297681	serine (or cysteine) proteinase inhibitor	0.55	1.20
	304607	AA513322		gb:nh85e08.s1 NCI_CGAP_Br1.1 Homo sapien	1.95	2.10
	304640	AA524440	Hs.111334	ferritin, light polypeptide	2.10	2.83
30	304650	AA527489	Hs.3463	ribosomal protein S23	3.33	12.62
	304735	AA576453		gb:nm75h11.s1 NCI_CGAP_Co9 Homo sapiens	1.33	0.88
	304760	AA580401		gb:nn13g09.s1 NCI_CGAP_Co12 Homo sapiens	3.68	8.14
	304849	AA588157	Hs.13801	KIAA1685 protein	2.77	3.70
	304917	AA602685	Hs.284136	PRO2047 protein	7.16	11.01
35	304921	AA603092	Hs.297753	vimentin	2.47	4.24
	304966	AA613893	Hs.282435	ESTs	6.78	11.66
	304987	AA618044	Hs.300697	immunoglobulin heavy constant gamma 3 (G	0.90	1.23
	305016	AA626876		gb:zu89h06.s1 Soares_testis_NHT Homo sap	6.46	10.17
	305034	AA630128		gb:ab99c04.s1 Stratagene lung (937210) H	1.00	1.00
40	305072	AA641012		gb:nr72a12.s1 NCI_CGAP_Pr24 Homo sapiens	5.68	11.59
	305111	AA644187	Hs.303405	ESTs	1.48	1.37
	305148	AA654070		gb:nl01g08.s1 NCI_CGAP_Lym3 Homo sapiens	1.76	4.61
	305159	AA659166	Hs.275668	EST, Weakly similar to EF1D_HUMAN ELONG	1.00	2.15
	305190	AA665955		gb:ag57d12.s1 Gessler Wilms tumor Homo s	5.31	8.14
45	305232	AA670052	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	0.78	1.18
	305235	AA670480		gb:ag37e01.s1 Jia bone marrow stroma Hom	3.11	8.66
	305245	AA676695	Hs.81328	nuclear factor of kappa light polypeptid	4.38	7.53
	305312	AA700201		gb:zj44f07.s1 Soares_fetal_liver_spleen_	2.13	2.66
	305322	AA701597	Hs.163019	EST	1.20	1.40
50	305394	AA720942	Hs.300697	immunoglobulin heavy constant gamma 3 (G	1.16	0.68
	305413	AA724659		gb:al10f08.s1 Soares_parathyroid_tumor_N	5.86	9.87
	305447	AA737856		gb:nx10c08.s1 NCI_CGAP_GC3 Homo sapiens	2.21	2.86
	305476	AA745664	Hs.287445	hypothetical protein FLJ11726	3.36	6.54
	305483	AA748030	Hs.303512	EST	1.00	2.02
55	305528	AA769156		gb:nz12e05.s1 NCI_CGAP_GCB1 Homo sapiens	6.44	9.10
	305612	AA782347	Hs.272572	hemoglobin, alpha 2	0.19	0.79
	305614	AA782866		gb:aj09h02.s1 Soares_parathyroid_tumor_N	1.00	1.00
	305616	AA782884	Hs.275865	ribosomal protein S18	7.57	10.20
	305637	AA806124		gb:oe29a12.s1 NCI_CGAP_Pr25 Homo sapiens	4.78	12.42
60	305639	AA806138		gb:oe29c12.s1 NCI_CGAP_Pr25 Homo sapiens	0.89	0.70
	305650	AA807709		gb:nw31e04.s1 NCI_CGAP_GCB0 Homo sapiens	4.49	8.71
	305690	AA813477		gb:ai67a05.s1 Soares_testis_NHT Homo sap	4.91	9.40
	305726	AA828156	Hs.73742	ribosomal protein, large, P0	0.19	0.81
	305728	AA828209		gb:of34a02.s1 NCI_CGAP_Kid6 Homo sapiens	5.12	9.29
65	305759	AA835353		gb:ak72b06.s1 Barstead spleen HPLRB2 Hom	1.66	4.11
	305792	AA845256		gb:ak84a08.s1 Barstead spleen HPLRB2 Hom	2.34	4.25
	305864	AA864374	Hs.73742	ribosomal protein, large, P0	0.30	1.40
	305901	AA872958		gb:oh63h08.s1 NCI_CGAP_Kid5 Homo sapiens	2.10	5.21
	305910	AA875981		gb:nx21h02.s1 NCI_CGAP_GC3 Homo sapiens	0.32	1.01
70	306015	AA897116		gb:am08b07.s1 Soares_NFL_T_GBC_S1 Homo s	1.56	1.12
	306017	AA897221	Hs.109058	ribosomal protein S6 kinase, 90kD, polyp	5.21	7.90
	306020	AA897630	Hs.130027	EST	1.96	6.59
	306063	AA906316		gb:ok03g03.s1 Soares_NFL_T_GBC_S1 Homo s	7.38	20.69
	306065	AA906725		gb:ok78g02.s1 NCI_CGAP_GC4 Homo sapiens	7.19	13.48
75	306104	AA910956		gb:ok85h11.s1 NCI_CGAP_Kid3 Homo sapiens	6.50	9.13
	306109	AA911861		gb:og21a07.s1 NCI_CGAP_PNS1 Homo sapiens	4.21	5.25
	306148	AA917409	Hs.288036	tRNA isopentenylpyrophosphate transferas	2.20	2.70
	306242	AA932805		gb:oo60g04.s1 NCI_CGAP_Lu5 Homo sapiens	2.84	5.35
	306288	AA936900		gb:oi53h05.s1 NCI_CGAP_HN3 Homo sapiens	1.60	1.12
80	306325	AA953072	Hs.210546	interleukin 21 receptor	1.65	2.26
	306353	AA961382	Hs.275865	ribosomal protein S18	3.78	6.32
	306375	AA966650	Hs.276018	EST, Moderately similar to JC4662 ribos	4.30	5.74
	306396	AA970223		gb:op09d05.s1 NCI_CGAP_Kid6 Homo sapiens	0.95	2.45
	306428	AA975110	Hs.191228	hypothetical protein FLJ20284	3.19	4.10
85	306442	AA976899		gb:ooq35e09.s1 NCI_CGAP_GC4 Homo sapiens	4.67	7.44
	306446	AA977348		gb:ooq72e12.s1 NCI_CGAP_Kid6 Homo sapiens	3.92	6.27

	306458	AA978186		gb:op33c06.s1 Soares_NFL_T_GBC_S1 Homo s	3.35	5.77
	306467	AA983508	Hs.163593	ribosomal protein L18a	3.72	5.37
	306510	AA988546		gb:or84d07.s1 NCI_CGAP_Lu5 Homo sapiens	1.00	1.00
5	306555	AA994304	Hs.276083	EST, Weakly similar to RL23_HUMAN 60S R	6.61	10.91
	306557	AA994530		gb:ou57e08.s1 NCI_CGAP_Br2 Homo sapiens	16.20	31.83
	306572	AA995686		gb:os25c12.s1 NCI_CGAP_Kid5 Homo sapiens	2.51	6.52
	306582	AA996248		gb:os18c10.s1 NCI_CGAP_Kid5 Homo sapiens	1.42	3.13
	306598	AI000320	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	4.91	8.68
10	306605	AI000497	Hs.119500	ribosomal protein, large P2	1.96	8.60
	306656	AI004024		gb:ou11b07.x1 Soares_NFL_T_GBC_S1 Homo s	0.11	0.45
	306676	AI005603	Hs.284136	PRO2047 protein	9.56	17.28
	306686	AI015615		gb:ov29f10.x1 Soares_testis_NHT Homo sap	1.86	3.60
	306702	AI022565	Hs.307670	EST	1.47	1.19
	306728	AI027359	Hs.272572	hemoglobin, alpha 2	1.28	2.83
15	306751	AI032589		gb:ow70h12.s1 Soares_fetal_liver_spleen_	3.91	5.21
	306767	AI038963	Hs.249118	ESTs	3.33	6.06
	306892	AI092465		gb:qa75h12.x1 Soares_fetal_heart_NbHH19W	3.77	7.46
	306897	AI093967		gb:qa33c06.s1 Soares_NhHMPu_S1 Homo sapi	2.12	2.85
20	306956	AI125111		gb:am66f03.s1 Barstead spleen HPLRB2 Hom	6.10	10.52
	306958	AI125152		gb:am55e09.x1 Johnston frontal cortex Ho	1.72	1.56
	307035	AI142774	Hs.119122	ribosomal protein L13a	2.00	4.70
	307041	AI144243		gb:qb85b12.x1 Soares_fetal_heart_NbHH19W	9.12	12.56
	307091	AI167439		gb:ox70h06.s1 Soares_NhHMPu_S1 Homo sapi	4.88	8.52
	307181	AI189251		gb:qc99g06.x1 Soares_pregnan uterus_NbH	3.55	6.44
25	307297	AI205798	Hs.111334	ferritin, light polypeptide	2.46	4.65
	307317	AI208303	Hs.147333	EST	5.64	10.13
	307327	AI214142	Hs.246381	CD68 antigen	3.18	5.15
	307382	AI223158	Hs.147885	ESTs	2.02	3.73
30	307410	AI241715	Hs.77039	ribosomal protein S3A	0.72	0.48
	307415	AI242118		gb:qh92b02.x1 Soares_NFL_T_GBC_S1 Homo s	2.38	3.51
	307423	AI243206	Hs.179573	collagen, type I, alpha 2	2.60	5.44
	307426	AI243364		gb:qh30g11.x1 Soares_NFL_T_GBC_S1 Homo s	3.18	7.67
	307517	AI275055		gb:ql72d03.x1 Soares_NhHMPu_S1 Homo sapi	1.00	1.00
35	307551	AI281556		gb:qu52f11.x1 NCI_CGAP_Lym6 Homo sapiens	3.40	11.20
	307561	AI282207		gb:qp65a12.x1 Soares_fetal_lung_NbHL19W	4.74	15.51
	307608	AI290295		gb:qm01f02.x1 Soares_NhHMPu_S1 Homo sapi	3.50	7.19
	307657	AI306428	Hs.298262	ribosomal protein S19	1.76	2.44
	307691	AI318285		gb:tb17b01.x1 NCI_CGAP_Ov37 Homo sapiens	1.59	1.31
40	307701	AI318583	Hs.276672	EST, Weakly similar to RL6_HUMAN 60S RI	1.90	2.13
	307718	AI333406	Hs.83753	small nuclear ribonucleoprotein polypept	0.45	0.99
	307730	AI336092		gb:ql43b07.x1 Soares_fetal_lung_NbHL19W	1.51	0.99
	307760	AI342387		gb:ql27f07.x1 Soares_pregnan uterus_NbH	1.00	1.00
	307764	AI342731		gb:qp26a07.x1 NCI_CGAP_Lu5 Homo sapiens	4.52	12.58
45	307783	AI347274		gb:lc05d02.x1 NCI_CGAP_Co16 Homo sapiens	1.42	1.00
	307796	AI350556		gb:ql18f09.x1 NCI_CGAP_GC4 Homo sapiens	6.57	9.61
	307807	AI351799		gb:ql09d02.x1 NCI_CGAP_GC4 Homo sapiens	3.38	7.68
	307808	AI351826		gb:ql09g03.x1 NCI_CGAP_GC4 Homo sapiens	0.33	0.86
	307820	AI355761		gb:ql94a11.x1 NCI_CGAP_Co14 Homo sapiens	7.94	21.57
50	307830	AI358722	Hs.276737	EST, Weakly similar to R5HU22 ribosomal	2.05	3.32
	307852	AI365541		gb:qp08g05.x1 NCI_CGAP_CLL1 Homo sapiens	3.18	5.21
	307902	AI380462		gb:lg02h05.x1 NCI_CGAP_CLL1 Homo sapiens	3.13	4.99
	307997	AI434512	Hs.181165	eukaryotic translation elongation factor	1.00	3.01
	308002	AI435240	Hs.283442	ESTs	5.86	12.64
55	308011	AI439473		gb:ti60a08.x1 NCI_CGAP_Lym12 Homo sapien	3.79	5.83
	308023	AI452732	Hs.251577	hemoglobin, alpha 1	0.38	0.88
	308041	AI458824	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	4.36	6.06
	308059	AI468938	Hs.276877	EST, Weakly similar to RL10_HUMAN 60S R	1.80	1.98
	308085	AI474135	Hs.181165	eukaryotic translation elongation factor	3.38	4.14
60	308101	AI475950	Hs.181165	eukaryotic translation elongation factor	1.30	3.87
	308106	AI476803		gb:ij77e12.x1 Soares_NSF_F8_9W_OT_PA_P_S2.38		8.72
	308122	AI480123	Hs.309411	EST	2.70	3.86
	308154	AI500600		gb:tn93d08.x1 NCI_CGAP_Ut2 Homo sapiens	0.66	1.33
	308171	AI523632	Hs.298766	ESTs, Weakly similar to schlafen4 [M.mu	2.48	4.86
65	308211	AI557029	Hs.278572	anaplastic lymphoma kinase (K1-1)	2.43	2.14
	308213	AI557041		gb:PT2.1_12_E04.r tumor2 Homo sapiens cD	3.34	3.79
	308216	AI557135		gb:PT2.1_13_H06.r tumor2 Homo sapiens cD	4.61	4.78
	308219	AI557246		gb:PT2.1_15_D07.r tumor2 Homo sapiens cD	4.87	7.94
	308271	AI567844	Hs.252259	ribosomal protein S3	2.40	6.35
70	308319	AI583983	Hs.181165	eukaryotic translation elongation factor	2.45	3.33
	308362	AI613519	Hs.105749	KIAA0553 protein	1.24	1.41
	308413	AI636253	Hs.196511	ESTs	3.16	4.82
	308450	AI660860	Hs.96840	KIAA1527 protein	1.79	2.68
	308464	AI672425	Hs.277117	EST, Moderately similar to I38055 myosi	4.87	8.27
75	308588	AI718299		gb:as51g12.x1 Barstead aorta HPLRB6 Homo	3.90	5.64
	308599	AI719893		gb:as47d07.x1 Barstead aorta HPLRB6 Homo	3.32	5.12
	308615	AI738593	Hs.101774	hypothetical protein FLJ23045	3.11	2.36
	308643	AI745040		gb:tr19a12.x1 NCI_CGAP_Ov23 Homo sapiens	3.98	3.69
	308673	AI760864		gb:wi09c10.x1 NCI_CGAP_CLL1 Homo sapiens	0.82	0.99
80	308697	AI767143		gb:wi97a07.x1 NCI_CGAP_Kid12 Homo sapien	2.76	5.59
	308762	AI807405	Hs.259408	ESTs	3.17	6.30
	308778	AI811109		gb:tr04c11.x1 NCI_CGAP_Ov23 Homo sapiens	1.00	1.00
	308782	AI811767	Hs.2186	eukaryotic translation elongation factor	2.94	5.15
	308808	AI818289		gb:wk52c01.x1 NCI_CGAP_Pr22 Homo sapiens	4.41	8.34
	308823	AI824118	Hs.217493	annexin A2	1.85	1.92
85	308875	AI832332		gb:al48g03.x1 Barstead colon HPLRB7 Homo	2.52	3.80

	308879	AI832763	Hs.75968	thymosin, beta 4, X chromosome	3.38	7.96
	308886	AI833240		gb:al76d10.x1 Barstead colon HPLRB7 Homo	3.06	2.65
	308898	AI858845		gb:wl32d10.x1 NCI_CGAP_U11 Homo sapiens	2.45	3.44
5	308934	AI865023	Hs.177	phosphatidylinositol glycan, class H	4.14	6.76
	308966	AI870704		gb:wl47h01.x1 NCI_CGAP_U11 Homo sapiens	1.00	1.00
	308979	AI873111		gb:wl52h05.x1 NCI_CGAP_Bm25 Homo sapien	7.15	11.10
	309045	AI910902		gb:tg39f01.x1 NCI_CGAP_U11 Homo sapiens	0.61	0.59
	309051	AI911975		gb:wd78d01.x1 NCI_CGAP_Lu24 Homo sapiens	1.78	4.42
10	309069	AI917366	Hs.78202	SWI/SNF related, matrix associated, act	3.27	5.88
	309083	AI922426	Hs.119598	ribosomal protein L3	2.39	3.34
	309105	AI925503	Hs.265884	ESTs	5.54	17.78
	309122	AI928178		gb:wo95a11.x1 NCI_CGAP_Kid11 Homo saplen	1.00	2.92
	309128	AI928816	Hs.180842	ribosomal protein L13	1.38	5.55
15	309164	AI937761		gb:wp84b09.x1 NCI_CGAP_Bm25 Homo sapien	2.43	3.11
	309177	AI951118		gb:wx63g05.x1 NCI_CGAP_Br18 Homo sapiens	0.81	0.97
	309288	AI991525	Hs.299426	ESTs	4.86	7.46
	309299	AW003478		gb:wx66c06.x1 NCI_CGAP_GC6 Homo sapiens	4.36	9.43
	309303	AW004823		gb:ws93a08.x1 NCI_CGAP_Co3 Homo sapiens	2.88	7.54
20	309411	AW085201	Hs.244144	EST	4.30	7.14
	309437	AW090702	Hs.278242	tubulin, alpha, ubiquitous	2.49	3.11
	309459	AW117645	Hs.65114	keratin 18	2.88	4.55
	309476	AW129368		gb:xe14b05.x1 NCI_CGAP_U14 Homo sapiens	2.08	6.60
	309499	AW136325	Hs.279771	Homo sapiens clone PP1596 unknown mRNA	2.82	3.55
25	309529	AW150807	Hs.181357	laminin receptor 1 (67kD, ribosomal pro	4.78	3.95
	309532	AW151119		gb:xg33e10.x1 NCI_CGAP_U11 Homo sapiens	1.18	4.40
	309626	AW192004	Hs.297681	serine (or cysteine) proteinase inhibit	4.46	12.06
	309641	AW194230	Hs.253100	EST, Moderately similar to GHU Ig gamm	1.47	1.39
	309675	AW205681	Hs.253506	EST, Moderately similar to ATPN_HUMAN A	5.68	15.20
30	309693	AW237221	Hs.181357	laminin receptor 1 (67kD, ribosomal prot	1.00	1.00
	309695	AW238011	Hs.295605	mannosidase, alpha, class 2A, member 2	5.45	9.61
	309700	AW241170	Hs.179661	tubulin, beta polypeptide	1.41	1.25
	309747	AW264889		gb:xq36h02.x1 NCI_CGAP_Lu28 Homo sapiens	5.00	8.35
	309769	AW272346		gb:xs13c10.x1 NCI_CGAP_Kid11 Homo sapien	5.76	11.90
35	309782	AW275156	Hs.156110	immunoglobulin kappa constant	0.42	0.69
	309783	AW275401	Hs.254798	EST	1.00	4.11
	309799	AW276964		gb:xp58h01.x1 NCI_CGAP_Ov39 Homo sapiens	1.68	1.44
	309866	AW299916		gb:xs44c01.x1 NCI_CGAP_Kid11 Homo sapien	3.02	5.04
40	309903	AW339071	Hs.300697	immunoglobulin heavy constant gamma 3 (G	1.05	1.18
	309923	AW340684		gb:hd05g08.x1 Soares_NFL_T_GBC_S1 Homo s	2.30	3.67
	309928	AW341418		gb:hd08c03.x1 Soares_NFL_T_GBC_S1 Homo s	7.41	13.71
	309931	AW341683		gb:hd13d01.x1 Soares_NFL_T_GBC_S1 Homo s	1.20	12.70
	309933	AW341936		gb:hb73f10.x1 NCI_CGAP_U12 Homo sapiens	4.90	18.29
	309964	AW449111	Hs.257111	hypothetical protein MGC3265	1.99	3.07
45	310002	AI439096	Hs.323079	Homo sapiens mRNA; cDNA DKFZp564P116 (fr	0.20	0.47
	310096	AW136822	Hs.172824	ESTs, Weakly similar to B48013 proline-r	1.51	1.22
	310098	AI685841	Hs.161354	ESTs	0.31	0.76
	310109	AI203094	Hs.148633	ESTs	2.06	5.83
	310112	AW197233	Hs.147253	ESTs	2.92	3.55
50	310115	AI611317	Hs.223796	ESTs	1.25	0.84
	310121	AW195642	Hs.148901	ESTs	1.00	2.71
	310146	AI206614	Hs.197422	ESTs	9.50	15.31
	310193	AI627653	Hs.147562	ESTs	2.85	4.18
	310255	AW450439	Hs.153378	ESTs	4.26	10.63
55	310261	AI240483	Hs.201217	ESTs	3.28	4.40
	310264	AI915771	Hs.74170	metallothionein 1E (functional)	0.26	0.86
	310275	AI242102	Hs.213636	ESTs	5.43	8.19
	310282	AI243332	Hs.156055	ESTs	3.15	8.06
	310290	AW013815	Hs.149103	ESTs	2.19	3.12
60	310333	AI253200	Hs.145402	ESTs	1.17	1.91
	310346	AI261340	Hs.145517	ESTs	4.81	9.95
	310385	AI263392	Hs.156151	ESTs	5.96	7.79
	310443	AW119018	Hs.164231	ESTs	2.90	4.63
	310444	AW196632	Hs.252956	ESTs	0.85	1.01
65	310446	AI275715	Hs.145926	ESTs	2.18	3.85
	310468	AI984074	Hs.196398	ESTs	3.39	5.19
	310477	AI948801	Hs.171073	ESTs	1.00	1.00
	310512	AW275603	Hs.200712	ESTs	3.87	8.12
	310514	AI681145	Hs.160724	ESTs	3.30	7.33
70	310524	AW082270	Hs.12496	ESTs, Highly similar to AC004836 1 simil	0.72	1.44
	310547	AI302654	Hs.208024	ESTs	3.26	3.46
	310584	AI653007	Hs.156304	ESTs	2.39	4.08
	310608	AI962234	Hs.196102	ESTs	5.60	6.49
	310624	AI341594		gb:Human endogenous retrovirus H proteas	4.91	9.09
75	310636	AI814373	Hs.164175	ESTs	1.85	1.71
	310648	AI347863	Hs.156672	ESTs	0.17	0.69
	310694	AI654370	Hs.157752	Homo sapiens mRNA full length insert cDN	5.40	13.22
	310695	AI472124	Hs.157757	ESTs	4.82	6.27
	310714	AI418446	Hs.157882	ESTs	1.76	3.51
80	310722	AI989803	Hs.157289	ESTs	1.14	6.85
	310756	AI916560	Hs.158707	ESTs	8.46	13.01
	310764	AI376769	Hs.167172	ESTs	4.76	7.37
	310848	AI459554	Hs.161286	ESTs	2.84	1.96
	310851	AW291714	Hs.221703	ESTs	1.00	2.32
85	310854	AI421677	Hs.161332	ESTs	6.37	7.94
	310858	AI871000	Hs.161330	ESTs	6.07	9.84

	310864	AJ924558	Hs.161399	ESTs	0.87	0.78
	310875	T47764	Hs.132917	ESTs	1.00	3.63
	310896	AW157731	Hs.270982	ESTs, Moderately similar to ALU7_HUMAN A	7.07	16.68
5	310922	AW195634	Hs.170401	ESTs	1.00	1.00
	310955	AJ560210	Hs.263912	ESTs	10.08	17.66
	310957	AW190974	Hs.196918	ESTs	2.18	3.18
	311000	AJ521830	Hs.171050	ESTs	3.06	6.64
	311012	AW298070	Hs.241097	ESTs	1.23	3.77
10	311034	AJ564023	Hs.311389	ESTs, Moderately similar to PT0375 natur	2.44	2.09
	311074	AW290922	Hs.199848	ESTs	6.04	14.19
	311134	AJ990849	Hs.196971	ESTs	3.54	6.96
	311174	AW450552	Hs.205457	periaxin	0.65	0.95
	311187	AJ638374	Hs.224189	ESTs	2.46	2.78
15	311220	AJ56040	Hs.196532	ESTs	1.10	2.52
	311230	AJ989808	Hs.197663	ESTs	1.41	1.75
	311236	AJ653378	Hs.197674	ESTs	2.18	2.11
	311242	AW016812	Hs.200266	ESTs	0.63	5.11
	311258	AJ671221	Hs.199887	ESTs	1.00	1.41
20	311277	AW072813	Hs.270868	ESTs, Moderately similar to ALU4_HUMAN A	2.56	1.94
	311294	AA826425	Hs.291829	ESTs	1.04	2.69
	311308	F12664	Hs.49000	ESTs	1.96	6.70
	311351	AJ682303	Hs.201274	ESTs	4.77	9.38
	311390	AW392997	Hs.202280	ESTs	2.80	6.06
25	311405	AW290961	Hs.201815	ESTs	3.80	11.66
	311409	AJ698839	gb:wd31f02.x1 Soares_NFL_T_GBC_S1 Homo s	3.84	6.94	
	311420	AJ936291	Hs.209867	ESTs	5.30	12.56
	311443	AJ791521	Hs.192206	ESTs	4.39	6.09
	311467	AJ934909	Hs.175377	ESTs	1.00	1.04
30	311479	AJ933672	Hs.211399	ESTs	2.76	5.61
	311488	R57390	Hs.301064	arfaplin 1	2.50	5.73
	311495	AW300077	Hs.221358	ESTs	3.63	6.09
	311511	AW444568	Hs.210303	ESTs	2.00	2.87
	311534	AW130351	Hs.243549	ESTs	0.31	1.33
35	311537	AJ805121	Hs.211828	ESTs	3.69	5.85
	311543	AJ681360	Hs.201259	ESTs	1.73	1.34
	311551	AW449774	Hs.296380	POM (POM121 rat homolog) and ZP3 fusion	3.31	6.12
	311557	AJ819230	Hs.211238	interleukin-1 homolog 1	1.00	1.00
	311558	Z44432	Hs.63128	KIAA1292 protein	2.25	3.41
40	311559	AW008271	Hs.265848	similar to rat myomegalin	2.68	5.90
	311563	AJ922143	Hs.211334	ESTs	2.39	3.32
	311586	AJ827834	Hs.211227	ESTs	2.47	3.85
	311616	AW450675	Hs.212709	ESTs	1.00	1.00
	311621	AJ924307	Hs.213464	ESTs	4.16	6.74
45	311635	AJ928456	Hs.213081	ESTs	2.17	3.76
	311668	AW193674	Hs.240044	ESTs	2.60	3.12
	311672	R11807	Hs.20914	hypothetical protein FLJ23056	2.79	5.18
	311683	AW183738	Hs.232644	ESTs	0.19	0.96
	311700	R49601	Hs.171495	retinoic acid receptor, beta	6.28	8.83
50	311714	AW131785	Hs.246831	ESTs, Weakly similar to CIKG_HUMAN VOLTA	5.00	8.17
	311735	AW294416	Hs.144687	Homo sapiens cDNA FLJ12981 fis, clone NT	0.96	0.72
	311743	T99079	Hs.191194	ESTs	1.00	1.95
	311783	AJ682478	Hs.13528	hypothetical protein FLJ14054	0.16	0.77
	311785	AJ056769	Hs.133512	ESTs	1.34	3.97
55	311799	AA780791	Hs.14014	ESTs, Weakly similar to KIAA0973 protein	8.52	13.32
	311819	AW265275	Hs.254325	ESTs	3.58	3.91
	311823	AJ089422	Hs.131297	ESTs	1.40	1.72
	311877	AA349893	Hs.85339	G protein-coupled receptor 39	0.95	0.91
	311886	AA522738	Hs.132554	ESTs	0.88	0.87
60	311896	AW206447	gb:U1-H-B11-afg-g-02-D-U1.s1 NCI_CGAP_Su	1.66	1.13	
	311910	N28365	Hs.22579	Homo sapiens clone CDABP0036 mRNA sequen	1.66	2.30
	311923	T60843	Hs.189679	ESTs	0.42	2.63
	311933	AJ597963	Hs.118726	ESTs	1.88	3.02
	311959	T67262	Hs.124733	ESTs	2.02	2.33
65	311960	AW440133	Hs.189690	ESTs	3.87	6.62
	311967	AJ382726	Hs.182434	ESTs	5.80	8.14
	311975	AA804374	Hs.272203	Homo sapiens cDNA FLJ20843 fis, clone AD	0.98	3.26
	312005	T78450	Hs.13941	ESTs	0.12	1.39
	312028	T78886	Hs.284450	ESTs	3.78	4.92
70	312046	AJ580018	Hs.268591	ESTs	4.11	7.32
	312056	T83748	Hs.268594	ESTs	2.36	3.08
	312064	AA676713	Hs.191155	ESTs	3.34	5.28
	312088	AW303760	Hs.13685	ESTs	1.60	1.15
	312093	T91809	Hs.121296	ESTs	0.68	0.85
75	312094	Z78390	gb:HSZ78390 Human fetal brain S. Meier-E	3.05	4.48	
	312097	AJ352096	Hs.112180	zinc finger protein 148 (pH2-52)	4.52	9.70
	312118	T85332	Hs.178294	ESTs	2.40	2.60
	312128	AJ052609	Hs.17631	Homo sapiens cDNA FLJ20118 fis, clone CO	2.39	3.53
	312147	T89855	Hs.195648	ESTs	0.67	1.03
80	312175	AA953383	Hs.127554	ESTs	5.85	10.60
	312179	AJ052572	Hs.269864	ESTs	2.41	3.32
	312201	AJ928365	Hs.91139	solute carrier family 1 (neuronal)/epithe	0.24	0.89
	312207	H90213	Hs.191330	ESTs	2.20	4.55
	312220	N74613	gb:za55a07.s1 Soares fetal liver spleen	4.28	11.13	
85	312252	AJ128388	Hs.143655	ESTs	1.64	1.57
	312304	AA491949	Hs.269392	ESTs	0.12	2.47

	312318	AW235092	Hs.143981	ESTs	3.46	5.69
	312319	AA216698	Hs.180780	TERA protein	5.78	4.46
	312321	R66210	Hs.186937	ESTs	0.44	1.74
5	312331	AA825512	Hs.289101	glucose regulated protein, 58kD	3.73	5.96
	312339	AA524394	Hs.165544	ESTs	3.07	0.95
	312363	AI675558	Hs.181867	ESTs	10.08	16.73
	312375	AI375096	Hs.172405	cell division cycle 27	2.78	3.71
	312376	R52089	Hs.172717	ESTs	1.00	1.00
10	312389	AI863140		gb:tz43h12.x1 NCI_CGAP_Bm52 Homo sapien	2.37	3.98
	312437	AA995028		gb:RC4-BT0629-120200-011-b10 BT0629 Homo	4.06	5.41
	312440	AI051133	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (f	1.00	1.00
	312451	R59989	Hs.176539	ESTs	4.96	10.04
	312458	AI167637	Hs.146924	ESTs	1.11	1.00
	312507	AI168177	Hs.143653	ESTs	5.89	8.24
15	312520	AI742591	Hs.205392	ESTs	3.30	8.92
	312548	AI566228	Hs.159426	hypothetical protein PRO2121	1.38	1.65
	312564	H21520	Hs.35088	ESTs	0.40	0.77
	312583	AI193122	Hs.124141	ESTs	0.13	0.94
	312599	AI865073	Hs.125720	ESTs	3.75	5.29
20	312602	AA046451	Hs.165200	ESTs	6.78	12.93
	312645	H52121	Hs.193007	ESTs	0.38	1.13
	312666	AI240582	Hs.214678	ESTs	0.98	2.03
	312689	AW450461	Hs.203965	ESTs	0.21	0.61
	312817	H75459	Hs.233425	ESTs	1.51	0.85
25	312846	AW152104	Hs.200879	ESTs	8.93	13.78
	312873	AI690071	Hs.283552	ESTs, Weakly similar to unnamed protein	4.20	6.23
	312893	AI016204	Hs.172922	ESTs	2.67	3.15
	312902	AW292797	Hs.130316	ESTs, Weakly similar to T2D3_HUMAN TRANS	1.19	0.71
	312925	N90868	Hs.271695	ESTs	2.50	4.25
30	312936	AI681581	Hs.121525	ESTs	1.00	1.17
	312975	AI640506	Hs.293119	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.30	4.80
	312978	N24887	Hs.292500	ESTs	0.80	1.05
	312980	AA497043	Hs.115685	ESTs	3.12	3.60
	312984	N25871	Hs.177337	ESTs	2.03	2.13
35	313000	AI147412	Hs.146657	ESTs	5.52	8.42
	313029	AA731520	Hs.170504	ESTs	0.96	1.39
	313039	AI419290	Hs.149990	ESTs, Weakly similar to unnamed protein	6.48	13.20
	313049	AW293055	Hs.119357	ESTs	6.44	10.73
	313056	AI651930	Hs.135684	ESTs	1.51	2.04
40	313058	D81015	Hs.125382	ESTs	0.25	1.50
	313070	AI422023	Hs.161338	ESTs	8.56	11.60
	313097	AI676164	Hs.204339	ESTs	3.72	4.56
	313130	AW449171	Hs.168677	ESTs	3.28	5.06
	313136	N59284	Hs.288010	ESTs	0.49	1.36
45	313153	AI240838	Hs.132750	ESTs	5.36	5.52
	313210	N74077	Hs.197043	ESTs	0.30	0.66
	313236	AW238169	Hs.83513	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.16	8.76
	313239	W19632	Hs.124170	ESTs	1.00	3.87
50	313265	N93466	Hs.121764	ESTs, Weakly similar to testicular tekt1	0.74	2.06
	313267	AI770008	Hs.129583	ESTs	0.23	1.30
	313275	AI027604	Hs.159650	ESTs	6.68	9.57
	313290	AI753247	Hs.29543	Homo sapiens cDNA FLJ13103 fis, clone NT	1.34	1.07
	313292	AI362991	Hs.202121	ESTs, Weakly similar to env protein [H.s	2.00	4.32
55	313325	AI420611	Hs.127832	ESTs	1.20	2.27
	313357	AW074848	Hs.201501	ESTs	4.02	5.33
	313393	AI674685	Hs.200141	ESTs	1.36	2.84
	313399	AW376889	Hs.194097	ESTs	2.58	5.26
	313414	AI241540	Hs.132933	ESTs	6.57	15.07
60	313417	AA741151	Hs.137323	ESTs	0.63	3.01
	313457	AA576052	Hs.193223	Homo sapiens cDNA FLJ11646 fis, clone HE	2.78	4.70
	313499	AI261390	Hs.146085	KIAA1345 protein	0.91	2.37
	313516	AA029058	Hs.135145	ESTs	3.41	7.08
	313556	AA628517	Hs.118502	ESTs	0.23	0.70
65	313569	AI273419	Hs.135146	hypothetical protein FLJ13984	1.88	1.00
	313570	AA041455	Hs.209312	ESTs	0.73	2.27
	313638	AI753075	Hs.104627	Homo sapiens cDNA FLJ10158 fis, clone HE	1.00	1.72
	313662	AA740151	Hs.130425	ESTs	0.20	1.42
	313671	W49823	Hs.104613	RP42 homolog	1.00	1.00
70	313672	AW468891	Hs.122948	ESTs	3.46	5.80
	313690	AI493591	Hs.78146	platelet/endothelial cell adhesion molec	0.51	0.97
	313711	AA398070	Hs.133471	ESTs	0.18	1.01
	313723	AA070412		gb:zm68c10.s1 Stralagene neuroepithelium	1.08	1.03
	313726	AI744687	Hs.257806	ESTs	2.13	2.99
75	313774	AW136836	Hs.144583	ESTs	1.38	1.19
	313784	AA910514	Hs.134905	ESTs	3.88	5.78
	313790	AW078569	Hs.177043	ESTs	0.22	2.06
	313832	AW271022	Hs.133294	ESTs	1.15	0.91
	313834	AW418779	Hs.114889	ESTs	0.68	3.14
80	313835	AI538438	Hs.159087	ESTs	5.74	8.88
	313852	H18633	Hs.123641	protein tyrosine phosphatase, receptor t	0.16	1.14
	313854	AW470806	Hs.275002	ESTs	2.09	4.06
	313865	AA731470	Hs.163839	ESTs	3.41	4.09
	313871	AW471088	Hs.145950	ESTs	5.28	6.83
85	313883	AI949384		gb:nu76d01.s1 NCI_CGAP_Alv1 Homo sapiens	2.90	10.91
	313915	AI969390	Hs.163443	Homo sapiens cDNA FLJ11576 fis, clone HE	1.00	1.00

	313926	AW473830	Hs.171442	ESTs	3.40	4.11
	313948	AW452823	Hs.135268	ESTs	5.77	9.15
	313978	AI870175	Hs.13957	ESTs	0.46	0.75
5	313983	AI829133	Hs.226780	ESTs	4.10	6.40
	314035	AA164199	Hs.270152	ESTs	5.88	7.90
	314037	AW300048	Hs.275272	ESTs	1.00	3.79
	314040	AA166970	Hs.118748	ESTs	7.60	11.33
	314067	AW293538	Hs.51743	KIAA1340 protein	1.86	1.21
10	314103	AI028477	Hs.132775	ESTs	2.90	5.29
	314107	AA806113	Hs.189025	ESTs	2.00	1.66
	314113	AA218986	Hs.118854	ESTs	0.91	4.17
	314124	AW118745	Hs.9460	Homo sapiens mRNA; cDNA DKFZp547C244 (fr	2.53	3.32
	314126	AA226431		gb:nc18b12.s1 NCL_CGAP_Pr1 Homo sapiens	3.13	5.08
	314128	AA935633	Hs.194628	ESTs	2.90	6.35
15	314151	AA236163	Hs.202430	ESTs	4.15	6.45
	314184	AW081795	Hs.233465	ESTs	3.44	4.65
	314192	AW290975	Hs.118923	ESTs	1.00	1.23
	314244	AL036450	Hs.103238	ESTs	2.88	3.67
20	314253	AA278679	Hs.189510	ESTs	4.98	7.16
	314262	AW086215	Hs.246096	ESTs	0.38	1.94
	314320	AA811598	Hs.275809	ESTs	3.34	5.66
	314332	AL037551	Hs.95612	ESTs	2.85	2.09
	314335	AA287443	Hs.142570	Homo sapiens clone 24629 mRNA sequence	4.35	4.78
25	314340	AW304350	Hs.130879	ESTs, Moderately similar to putative p15	0.77	0.86
	314351	AA292275	Hs.193746	ESTs	3.07	3.77
	314376	AI628633	Hs.324679	ESTs	4.10	6.11
	314443	AA827125	Hs.192043	ESTs	6.20	13.67
	314458	AI217440	Hs.143873	ESTs	0.58	2.49
30	314466	AA767818	Hs.122707	ESTs	2.53	2.62
	314478	AI521173	Hs.125507	DEAD-box protein	3.94	5.65
	314482	AL043807	Hs.134182	ESTs	1.30	1.44
	314506	AA833655	Hs.206868	Homo sapiens cDNA FLJ14056 fis, clone HE	3.28	3.47
	314519	R42554	Hs.210862	T-box, brain, 1	3.12	6.16
35	314529	AL046412	Hs.202151	ESTs	3.43	6.87
	314546	AW007211	Hs.16131	hypothetical protein FLJ12876	1.38	1.00
	314562	AI564127	Hs.143493	ESTs	2.29	5.27
	314579	AW197442	Hs.116998	ESTs	3.87	5.75
	314580	AW451832	Hs.255938	ESTs, Moderately similar to KIAA1200 pro	0.10	0.71
40	314585	AA918474	Hs.216363	ESTs	1.08	1.40
	314589	AW384790	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	1.00	1.00
	314592	AA435761	Hs.192148	ESTs	0.90	2.60
	314603	AA418024	Hs.270670	ESTs	4.56	6.29
	314604	AA946582	Hs.8700	deleted in liver cancer 1	3.42	3.92
45	314606	AA418241	Hs.188767	ESTs	2.97	4.55
	314648	AA878419		gb:EST391378 MAGE resequences, MAGP Homo1.42		1.36
	314699	AI038719	Hs.132801	ESTs	3.66	4.97
	314701	AI754634	Hs.131987	ESTs	0.03	0.90
	314710	AI669131	Hs.290989	EST	3.40	7.52
50	314750	AI095005	Hs.135174	ESTs	2.80	6.54
	314767	AW135412	Hs.164002	ESTs	3.20	4.26
	314801	AA481027	Hs.109045	hypothetical protein FLJ10498	1.00	1.00
	314817	AI694139	Hs.192855	ESTs	0.91	0.99
	314835	AI281370	Hs.76064	ribosomal protein L27a	5.75	7.44
55	314852	AI903735		gb:MR-BT035-200199-031 BT035 Homo sapien	1.68	4.34
	314853	AA729232	Hs.153279	ESTs	0.60	1.85
	314940	AW452768	Hs.162045	ESTs	10.10	16.20
	314941	AA515902	Hs.130650	ESTs	0.31	1.02
	314943	AI476797	Hs.184572	cell division cycle 2, G1 to S and G2 to	2.18	0.37
60	314955	AA521382	Hs.192534	ESTs	2.59	3.90
	314973	AW273128	Hs.300268	ESTs	1.05	1.25
	315004	AA527941	Hs.325351	EST	5.64	13.63
	315006	AI538613	Hs.298241	Transmembrane protease, serine 3	0.52	1.78
	315033	AI493046	Hs.146133	ESTs	2.46	1.00
65	315035	AI569476	Hs.177135	ESTs	0.34	1.33
	315056	AI202703	Hs.152414	ESTs	2.10	2.64
	315069	AI821517	Hs.105866	ESTs	1.00	1.30
	315071	AA552690	Hs.152423	Homo sapiens cDNA: FLJ21274 fis, clone C	1.78	1.00
	315073	AW452948	Hs.257631	ESTs	1.17	1.52
70	315078	AA568548	Hs.190616	ESTs	3.00	3.79
	315080	AA744550	Hs.136345	ESTs	1.00	1.00
	315120	AA564991	Hs.269477	ESTs	0.64	1.44
	315175	AI025842	Hs.152530	ESTs	0.61	1.91
	315193	AI241331	Hs.131765	ESTs	1.06	0.97
75	315196	AA972756	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	0.48	1.96
	315200	AI808235	Hs.307686	EST	3.76	9.40
	315254	AI474433	Hs.179556	ESTs	5.37	9.36
	315353	AW452608	Hs.279610	hypothetical protein FLJ10493	1.00	1.30
	315397	AA218940	Hs.137516	fidgulin-like 1	3.38	2.24
80	315403	AW362980	Hs.163924	ESTs	2.04	5.23
	315431	AA622104	Hs.184838	ESTs	2.36	8.04
	315454	AI239473		gb:gh36f02.x1 Soares_NFL_T_GBC_S1 Homo s	3.46	7.64
	315455	AW393391	Hs.156919	ESTs	3.78	5.76
	315473	AI681671	Hs.312671	ESTs, Moderately similar to OVCA1	0.89	2.15
	315483	AW512763	Hs.222024	transcription factor BMAL2	2.32	1.96
85	315526	AI193048	Hs.128685	ESTs	1.67	1.78

	315530	AI200852	Hs.127780	ESTs	1.05	1.01
	315541	AI168233	Hs.123159	sperm associated antigen 4	0.85	0.56
	315552	AW445034	Hs.256578	ESTs	1.00	2.22
	315562	AA737415	Hs.152826	ESTs	2.66	2.48
5	315577	AW513545	Hs.17283	hypothetical protein FLJ10890	2.20	2.25
	315587	AI268399	Hs.140489	ESTs	1.00	1.04
	315589	AW072387	Hs.158258	Homo sapiens mRNA; cDNA DKFZp434B1272 (f	0.14	1.05
	315623	AA364078	Hs.258189	ESTs	7.44	12.56
10	315634	AA837085	Hs.220585	ESTs	0.50	1.40
	315658	AA912347	Hs.136585	ESTs	0.43	1.22
	315677	AI932662	Hs.164073	ESTs	0.60	1.39
	315706	AW440742	Hs.155556	hypothetical protein FLJ20202	2.18	3.77
	315707	AI418055	Hs.161160	ESTs	2.88	2.63
	315730	H25899	Hs.201591	ESTs	0.11	0.60
15	315745	AI821759	Hs.191856	ESTs	3.50	7.25
	315791	AA678177		gbz115a05.s1 Soares_fetal_liver_spleen_	1.78	2.63
	315801	AA827752	Hs.266134	ESTs	4.31	6.23
	315820	AI652022	Hs.258785	ESTs	2.35	3.01
	315878	AA683336	Hs.189046	ESTs	2.12	2.64
20	315905	AI821911	Hs.209452	ESTs	1.03	1.97
	315923	AI052789	Hs.133263	ESTs	2.63	5.06
	315954	AW276810	Hs.254859	ESTs, Moderately similar to ALU5_HUMAN A	1.21	0.85
	315978	AA830893	Hs.119769	ESTs	3.09	3.41
	316001	AI248584	Hs.190745	Homo sapiens cDNA: FLJ21326 fis, clone C	2.20	6.82
25	316011	AW516953	Hs.201372	ESTs	0.35	1.63
	316012	AA764950	Hs.119898	ESTs	6.56	8.13
	316040	AI983409	Hs.189226	ESTs	5.69	10.69
	316048	AI720759	Hs.224971	ESTs	2.84	10.45
30	316076	AW297895	Hs.116424	ESTs	0.30	1.05
	316124	AI308862	Hs.167028	ESTs	1.00	1.43
	316151	AI806016	Hs.156520	ESTs	5.80	9.03
	316187	AW518299	Hs.192253	ESTs	1.20	3.96
	316204	AA731509	Hs.120257	ESTs	4.92	6.94
35	316232	AW297853	Hs.251203	ESTs	1.48	1.60
	316275	AI671041	Hs.292611	ESTs, Moderately similar to ALU1_HUMAN A	5.86	12.14
	316291	AW375974	Hs.156704	ESTs	2.73	2.69
	316303	AA740994	Hs.209609	ESTs	1.53	1.26
	316344	AA744518	Hs.120610	ESTs	3.66	8.34
40	316346	AI028478	Hs.157447	ESTs	3.51	6.69
	316365	AI627845	Hs.210776	ESTs	2.50	4.33
	316380	AI393378	Hs.164496	ESTs	1.16	2.16
	316470	AA809902	Hs.243813	ESTs	5.40	10.34
	316509	AA767310	Hs.291766	ESTs	2.46	2.89
45	316514	AA768037	Hs.291671	ESTs	4.70	6.04
	316519	AI929097		gbxod10c11.s1 NCI_CGAP_GCB1 Homo sapiens	4.41	9.70
	316609	AW292520	Hs.122082	ESTs	1.00	2.89
	316633	AI125586	Hs.127955	ESTs	2.61	3.72
	316700	AW172316	Hs.252961	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.46	4.64
50	316711	AI743721	Hs.285316	ESTs, Moderately similar to ALU7_HUMAN A	4.45	6.95
	316713	AI090671	Hs.134807	hypothetical protein FLJ12057	0.30	2.40
	316715	AI440266	Hs.170673	ESTs, Weakly similar to AF126780 1 retin	0.20	1.45
	316787	AW369770	Hs.130351	ESTs	4.05	5.53
	316809	AA825839	Hs.202238	ESTs	2.25	3.82
55	316811	AA922060	Hs.132471	ESTs	1.00	1.32
	316812	AW135045	Hs.232001	ESTs	3.28	4.70
	316818	AA827176	Hs.124316	ESTs	0.67	1.81
	316824	AA837416	Hs.124299	ESTs	3.53	6.00
	316827	AI380429	Hs.172445	ESTs	0.72	1.56
60	316891	AW298119	Hs.202536	ESTs	1.64	2.97
	316951	AA134365	Hs.57548	ESTs	1.45	1.08
	316970	AA860172	Hs.132406	ESTs	1.00	1.53
	316971	AA860212	Hs.170991	ESTs	1.08	1.96
	316990	AA861611	Hs.130643	ESTs	5.44	10.04
65	317001	AI627917	Hs.233694	hypothetical protein FLJ11350	3.56	4.37
	317008	AW051597	Hs.143707	ESTs	0.69	1.37
	317051	AA873253	Hs.126233	ESTs	6.18	12.72
	317128	AA971374	Hs.125674	ESTs	1.87	2.66
	317129	H12523	Hs.78521	Homo sapiens cDNA: FLJ21193 fis, clone C	4.12	6.64
70	317137	AW341567	Hs.125710	ESTs	2.82	5.12
	317196	AI348258	Hs.153412	ESTs	1.98	2.51
	317212	AI866468	Hs.148294	ESTs	1.86	2.83
	317223	AW297920	Hs.130054	ESTs	0.83	1.57
	317224	D56760	Hs.93029	sparc/osteonectin, cwcv and kazal-like d	2.74	0.86
75	317266	AA906289	Hs.203614	ESTs	1.00	1.00
	317282	AI807444	Hs.176101	ESTs	2.60	4.21
	317285	AW370882	Hs.222080	ESTs	1.96	3.49
	317302	AA908709	Hs.135564	ESTs	7.16	8.32
	317304	AW449899	Hs.130184	ESTs	1.38	2.28
80	317320	AA927151	Hs.130452	ESTs	3.58	8.13
	317413	AW341701	Hs.126622	ESTs	2.08	4.92
	317417	AA918420	Hs.145378	ESTs	3.06	4.79
	317452	AA972965	Hs.135568	ESTs	4.22	9.21
	317519	AI859695	Hs.126860	ESTs	1.88	4.15
85	317521	AI824338	Hs.126891	ESTs	3.12	4.55
	317529	AI916517	Hs.126865	ESTs	2.73	3.34

	317570	AI733361	Hs.127122	ESTs	1.00	2.43
	317571	AA938663	Hs.199828	ESTs	5.20	11.95
	317598	AW206035	Hs.192123	ESTs	0.33	1.56
5	317627	AI346110	Hs.132553	ESTs	1.50	1.39
	317650	AI733310	Hs.127346	ESTs	0.48	1.46
	317659	AA961216	Hs.127785	ESTs	4.18	7.14
	317674	AW294909	Hs.132208	ESTs	2.92	3.20
	317686	AA969051	Hs.187319	ESTs	1.00	1.01
10	317692	AI307659	Hs.174794	ESTs	5.33	9.59
	317701	AI674774	Hs.128014	ESTs	1.00	1.00
	317711	AI733015	Hs.272189	ESTs	5.13	7.81
	317722	AI733373	Hs.128119	ESTs	2.50	6.03
	317756	AA973667	Hs.128320	ESTs	1.59	1.30
15	317777	AI143525	Hs.47313	KIAA0258 gene product	1.00	2.48
	317799	AI498273	Hs.128808	ESTs	1.78	2.11
	317803	AA983251	Hs.128899	ESTs	0.80	1.06
	317821	AI368158	Hs.70983	PTPL1-associated RhoGAP 1	0.17	0.68
	317848	AI820575	Hs.129086	Homo sapiens cDNA FLJ12007 fis, clone HE	5.30	8.16
20	317850	N29974	Hs.152982	hypothetical protein FLJ13117	1.30	2.28
	317861	AW341064	Hs.129119	ESTs	2.18	5.93
	317865	AI298794	Hs.129130	ESTs	4.48	8.20
	317869	AW295184	Hs.129142	deoxynucleonuclease II beta	0.44	0.99
	317881	AI827248	Hs.224399	Homo sapiens cDNA FLJ11469 fis, clone HE	4.06	2.23
25	317890	AI915599	Hs.129225	ESTs	4.68	7.48
	317899	AI952430	Hs.150614	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.14	3.37
	317986	AI005163	Hs.201378	ESTs, Weakly similar to T12545 hypotheti	0.28	1.66
	318001	AW235697	Hs.130980	ESTs	5.12	9.97
	318016	AI016694	Hs.256921	ESTs	1.86	4.50
30	318023	AW243058	Hs.131155	ESTs	2.92	5.22
	318054	AW449270	Hs.232140	ESTs	3.92	6.37
	318068	AI024540	Hs.131574	ESTs	1.21	1.27
	318117	AI208304	Hs.250114	ESTs	0.86	1.17
	318187	AI792585	Hs.133272	ESTs, Weakly similar to ALUC_HUMAN !!!!	5.90	6.98
35	318223	AI077540	Hs.134090	ESTs	1.05	0.90
	318240	AI085377	Hs.143610	ESTs	3.10	2.40
	318255	AI082692	Hs.134662	ESTs	0.02	1.05
	318266	AI554341	Hs.271443	ESTs	6.12	10.55
	318330	AI093840	Hs.143758	ESTs	4.98	7.90
40	318369	AI493501	Hs.170974	ESTs	2.46	5.62
	318428	AI949409	Hs.194591	ESTs	0.77	0.45
	318458	AI149783	Hs.158438	ESTs	3.54	4.92
	318467	AI151395	Hs.144834	ESTs	4.56	5.62
	318473	AI939339	Hs.146883	ESTs	2.08	4.05
45	318476	AI693927	Hs.265165	ESTs	4.22	8.07
	318487	AI167877	Hs.143716	ESTs	1.47	1.05
	318488	AI217431	Hs.144709	ESTs	1.40	4.14
	318491	T26477	Hs.22883	ESTs, Weakly similar to ALU8_HUMAN ALU S	1.84	1.90
	318499	T25451		gb:PTHI188 HTCDL1 Homo sapiens cDNA 5/3	2.58	5.20
50	318537	AA377908	Hs.13254	ESTs	3.26	4.18
	318538	N28625	Hs.74034	Homo sapiens clone 24651 mRNA sequence	0.35	1.07
	318547	R20578	Hs.90431	ESTs	3.22	4.60
	318552	R18364	Hs.90363	ESTs	4.87	9.06
	318575	R55102	Hs.107761	ESTs, Weakly similar to unnamed protein	1.91	1.98
55	318580	T34571	Hs.49007	poly(A) polymerase alpha	2.74	6.22
	318587	AA779704	Hs.168830	Homo sapiens cDNA FLJ12136 fis, clone MA	0.85	2.46
	318596	AI470235	Hs.172698	EST	4.88	4.93
	318622	T48325	Hs.237658	apolipoprotein A-II	4.80	12.51
	318629	N25163	Hs.8861	ESTs	0.39	1.04
60	318637	AA243539	Hs.9196	hypothetical protein	1.72	3.57
	318648	T77141	Hs.184411	albumin	6.27	9.91
	318650	AA393302	Hs.176626	hypothetical protein EDAG-1	3.96	8.84
	318671	AA188823	Hs.299254	Homo sapiens cDNA: FLJ23597 fis, clone L	1.53	0.81
	318679	T58115	Hs.10336	ESTs	1.00	2.19
65	318711	AI936475	Hs.101282	Homo sapiens cDNA: FLJ21238 fis, clone C	3.05	3.18
	318725	AI962487	Hs.242990	ESTs	1.08	2.46
	318728	Z30201	Hs.291289	ESTs, Weakly similar to ALU1_HUMAN ALU S	0.77	1.33
	318740	NM_002543	Hs.77729	oxidised low density lipoprotein (lectin	0.25	1.49
	318776	R24963	Hs.23766	ESTs	1.00	3.01
70	318784	H00148	Hs.5181	proliferation-associated 2G4, 38kD	2.70	3.86
	318816	F07873	Hs.21273	ESTs	3.90	7.13
	318865	H10818		gb:ym04f10.r1 Soares infant brain 1NIB H	2.25	3.56
	318879	R56332	Hs.18268	adenylate kinase 5	1.78	5.00
	318881	Z43224	Hs.124952	ESTs	4.79	14.13
75	318894	F08138	Hs.7387	DKFZP564B116 protein	5.31	7.00
	318901	AW368520	Hs.301528	L-kynurenine/alpha-aminoadipate aminotra	1.03	0.91
	318925	Z43577	Hs.21470	ESTs	2.23	3.80
	318936	AI219221	Hs.308298	ESTs	1.86	7.16
	318982	Z44140	Hs.269622	ESTs	5.84	9.79
80	318986	Z44186	Hs.169161	ESTs, Highly similar to MAON_HUMAN NADP-	1.00	1.00
	319041	Z44720	Hs.98365	ESTs, Weakly similar to weak similarity	3.38	6.11
	319103	H05896	Hs.4993	KIAA1313 protein	1.00	1.07
	319170	R13578	Hs.285306	putative selenocysteine lyase	3.79	5.03
	319196	F07953	Hs.16085	putative G-protein coupled receptor	1.00	2.98
85	319199	F07361	Hs.13306	ESTs	3.53	5.66
	319242	F11472	Hs.12839	ESTs	5.87	7.26

	319263	T65331	Hs.81360	Homo sapiens cDNA: FLJ21927 fis, clone H	1.81	1.57
	319267	F11802	Hs.6818	ESTs	1.10	4.72
	319270	R13474	Hs.290263	ESTs	4.80	10.40
5	319279	T65094	Hs.12677	CGI-147 protein	1.50	2.11
	319282	AA461358	Hs.12876	ESTs	1.00	1.00
	319289	W07304	Hs.79059	transforming growth factor, beta recepto	0.18	0.68
	319291	W86578	Hs.285243	hypothetical protein FLJ22029	0.26	0.62
	319293	F12119	Hs.12583	ESTs	3.13	4.50
10	319312	Z45481		gb:HSC2QE041 normalized infant brain cDN	1.10	1.00
	319370	H54254	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	0.16	0.73
	319391	R06304	Hs.13911	ESTs	1.26	2.43
	319396	H67130	Hs.301743	ESTs	0.70	0.76
	319398	AA359754	Hs.191196	ESTs	2.45	3.59
15	319407	R05329		gb:ye91b04.r1 Soares fetal liver spleen	2.00	3.54
	319425	T82930		gb:yd39f07.r1 Soares fetal liver spleen	4.28	8.81
	319433	R06050	Hs.191198	ESTs	6.15	14.13
	319437	AA282420	Hs.111991	ESTs, Weakly similar to Y48A5A.1 [C.eleg	3.26	5.68
	319466	A1809937	Hs.116417	ESTs	1.76	5.65
20	319471	R06546	Hs.19717	ESTs	4.29	4.84
	319480	R06933	Hs.184221	ESTs	1.00	1.00
	319484	T91772		gb:yd52a10.s1 Soares fetal liver spleen	2.81	4.88
	319486	A1382429	Hs.250799	ESTs	2.08	2.82
	319508	T99898	Hs.270104	ESTs, Moderately similar to ALU8_HUMAN A	2.80	4.39
	319523	T69499	Hs.191184	ESTs	1.55	3.25
25	319545	R83716	Hs.14355	Homo sapiens cDNA FLJ13207 fis, clone NT	1.65	1.19
	319546	R09692		gb:ylf23b12.r1 Soares fetal liver spleen	5.11	8.54
	319552	AA096106	Hs.20403	ESTs	1.89	3.36
	319582	T82998	Hs.250154	hypothetical protein FLJ12973	3.48	4.82
30	319586	D78808	Hs.283683	chromosome 8 open reading frame 4	0.26	0.82
	319604	R11679	Hs.297753	vimentin	1.68	3.41
	319609	AW247514	Hs.12293	hypothetical protein FLJ21103	3.06	4.24
	319611	H14957		gb:ym19c10.r1 Soares infant brain 1NIB H	2.76	4.24
	319653	AA770183	Hs.173515	uncharacterized hypothalamus protein HT0	2.51	3.55
35	319657	R19897	Hs.106604	ESTs	5.32	7.68
	319658	R13432	Hs.167481	syntrophin, gamma 1	3.35	5.00
	319661	H08035	Hs.21398	ESTs, Moderately similar to A Chain A, H	5.18	12.55
	319662	H06382	Hs.21400	ESTs	1.58	1.56
	319708	R15372	Hs.22664	ESTs	1.00	1.22
40	319742	T77668	Hs.21162	ESTs	2.48	3.13
	319748	R18178	Hs.295866	Homo sapiens mRNA; cDNA DKFZp434N1923 (f	3.02	4.85
	319772	R76633	Hs.22646	ESTs	4.36	11.61
	319788	AA321932	Hs.117414	KIAA1320 protein	2.56	3.68
	319805	R92857	Hs.271350	likely ortholog of mouse polydom	4.63	6.56
45	319812	N74880	Hs.264330	N-acylsphingosine amidohydrolase (acid c	0.63	1.32
	319834	AA071267		gb:zm61g01.r1 Stratagene fibroblast (937	0.30	0.94
	319878	T78517	Hs.13941	ESTs	3.99	6.44
	319882	AA258981	Hs.291392	ESTs	5.09	7.36
	319912	T77559	Hs.94109	Homo sapiens cDNA FLJ13634 fis, clone PL	3.24	3.21
50	319935	H79460	Hs.271722	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.40	9.42
	319944	T79248	Hs.133510	ESTs	3.31	5.39
	319947	AA160967	Hs.14479	Homo sapiens cDNA FLJ14199 fis, clone NT	2.90	4.95
	319962	H06350	Hs.135056	Human DNA sequence from clone RP5-850E9	1.81	1.57
55	320007	AA336314		gb:EST40943 Endometrial tumor Homo sapie	3.42	6.29
	320018	T83263		gb:yd40h09.r1 Soares fetal liver spleen	2.77	5.14
	320030	H63789	Hs.296288	ESTs, Weakly similar to KIAA0638 protein	4.10	6.69
	320032	A1699772	Hs.292664	ESTs, Weakly similar to A46010 X-linked	3.27	3.27
	320040	AA233671	Hs.87164	hypothetical protein FLJ14001	1.81	1.64
	320047	T86564	Hs.302256	EST	3.38	7.36
60	320063	AA074108	Hs.120844	FOXJ2 forkhead factor	5.90	16.73
	320096	H58138	Hs.117915	ESTs	2.08	4.47
	320099	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	1.00	1.00
	320112	T92107	Hs.188489	ESTs	2.27	2.06
	320140	H94179	Hs.119023	SMC2 (structural maintenance of chromoso	1.00	1.00
	320188	AW419200	Hs.172318	ESTs	1.26	1.00
65	320193	AA831259	Hs.17132	ESTs	2.58	6.23
	320195	R62203	Hs.24321	Homo sapiens cDNA FLJ12028 fis, clone HE	2.85	4.53
	320199	R78659	Hs.29792	ESTs	0.40	0.94
	320203	AL049227	Hs.124776	Homo sapiens mRNA; cDNA DKFZp564N1116 (f	0.84	1.18
70	320219	AA327564	Hs.127011	tubulointerstitial nephritis antigen	1.00	1.17
	320220	AF054910	Hs.127111	teklin 2 (testicular)	0.18	1.09
	320225	AF058989	Hs.128231	G antigen, family B, 1 (prostate associa	5.26	13.75
	320231	H03139	Hs.24683	ESTs	1.59	1.93
	320260	NM_003608	Hs.131924	G protein-coupled receptor 65	1.38	4.56
75	320267	AL049337	Hs.132571	Homo sapiens mRNA; cDNA DKFZp564P016 (fr	1.00	1.92
	320268	H06019	Hs.151293	Homo sapiens cDNA FLJ10664 fis, clone NT	5.58	5.70
	320322	AF077374	Hs.139322	small proline-rich protein 3	1.41	1.01
	320325	AI167978	Hs.139851	caveolin 2	0.05	0.67
	320330	AF026004	Hs.141660	chloride channel 2	2.17	1.26
80	320339	H10807	Hs.281434	Homo sapiens cDNA FLJ14028 fis, clone HE	1.81	2.32
	320388	H16065	Hs.31286	ESTs	1.00	3.22
	320402	R22291	Hs.23368	Homo sapiens clone FLC0578 PRO2852 mRNA,	1.41	1.36
	320413	AA203711	Hs.173269	ESTs	2.31	3.61
	320432	R62786	Hs.124136	ESTs	11.25	20.78
85	320436	AA253352	Hs.293663	ESTs	2.22	3.49
	320438	W24548	Hs.5669	ESTs	3.53	8.14

	320448	AJ240233	Hs.80887	v-yes-1 Yamaguchi sarcoma viral related	1.42	3.46
	320451	R26944	Hs.180777	Homo sapiens mRNA; cDNA DKFZp564M0264 (f	0.87	0.81
	320484	AA094436	Hs.296267	folistatin-like 1	0.65	1.18
5	320499	R32555	Hs.24321	Homo sapiens cDNA FLJ12028 fis, clone HE	3.44	7.15
	320514	AB007978	Hs.158278	KIAA0509 protein	6.44	13.62
	320521	N31464	Hs.24743	hypothetical protein FLJ20171	1.48	1.04
	320526	AW374205	Hs.111314	ESTs	3.66	7.87
	320527	R34672	Hs.324522	ESTs	3.16	5.63
10	320536	AA331732	Hs.137224	ESTs	2.83	5.83
	320556	AF054177	Hs.14570	hypothetical protein FLJ22530	1.28	1.00
	320564	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxyg	1.22	0.81
	320587	Z44524	Hs.167456	Homo sapiens mRNA full length insert cDN	1.84	2.44
	320635	R54159	Hs.80506	small nuclear ribonucleoprotein polypept	1.00	6.25
	320639	AA243258	Hs.7395	hypothetical protein FLJ23182	2.60	2.30
15	320648	N48521	Hs.26549	Homo sapiens mRNA for KIAA1708 protein,	1.00	1.53
	320651	AA489268	Hs.111334	ferritin, light polypeptide	0.14	0.79
	320664	AI904216	Hs.91251	hypothetical protein FLJ11198	5.02	8.84
	320676	AA132650	Hs.300511	ESTs	3.63	5.37
	320683	R59291	Hs.26638	ESTs, Weakly similar to unnamed protein	0.37	1.31
20	320689	AA334609	Hs.171929	ESTs, Weakly similar to A54849 collagen	1.27	1.02
	320696	AW135016	Hs.172780	ESTs	3.53	4.60
	320714	AI445591		gb:yr04a10.r1 Soares fetal liver spleen	1.06	0.85
	320727	U96044	Hs.181125	immunoglobulin lambda locus	1.35	1.49
	320771	AI793266	Hs.117176	poly(A)-binding protein, nuclear 1	0.04	0.82
25	320794	AA281993	Hs.91226	ESTs	2.96	4.33
	320822	AF100780	Hs.194679	WNT1 Inducible signaling pathway protein	0.10	0.79
	320824	AF120274	Hs.194689	artemin	1.16	1.11
	320830	AJ132445	Hs.266416	claudin 14	1.06	1.75
	320843	AA317372	Hs.34744	Homo sapiens mRNA; cDNA DKFZp547C136 (fr	1.36	1.47
30	320849	D60031	Hs.34771	ESTs	5.30	7.49
	320853	AJ473796	Hs.135904	ESTs	1.00	1.00
	320896	AB002155	Hs.271580	uropod 1B	5.90	2.55
	320921	R94038	Hs.199538	inhibin, beta C	2.20	1.17
	320927	AI205786	Hs.213923	ESTs	0.18	1.46
35	320957	AJ878933	Hs.92023	core histone macroH2A2.2	1.67	2.18
	320997	H22544		gb:yn69f11.r1 Soares adult brain N2b5HB5	3.26	3.62
	321045	W88483	Hs.293650	ESTs	2.25	4.55
	321046	H27794	Hs.269055	ESTs	2.69	4.25
40	321052	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	2.14	2.56
	321059	AI092824	Hs.126465	ESTs	1.69	0.53
	321062	R87955	Hs.241411	Homo sapiens mRNA full length insert cDN	2.76	5.20
	321067	AF131782	Hs.241438	Homo sapiens clone 24941 mRNA sequence	4.79	7.41
	321102	AA018306		gb:ze40d08.r1 Soares retina N2b4HR Homo	1.79	4.27
	321130	H43750	Hs.125494	ESTs	1.00	3.14
45	321142	AI817933	Hs.298351	ASPL protein	8.73	15.36
	321155	AA336635	Hs.99598	hypothetical protein MGC5338	3.04	5.03
	321158	AA700289		gb:yu76f11.r1 Soares fetal liver spleen	4.62	8.39
	321170	N53742	Hs.172982	ESTs	2.21	4.46
	321199	AW385512		gb:yy56d10.s1 Soares_multiple_sclerosis_	5.69	8.01
50	321206	H54178	Hs.226469	Homo sapiens cDNA FLJ12417 fis, clone MA	4.00	7.32
	321225	AL080073	Hs.251414	Homo sapiens mRNA; cDNA DKFZp564B1462 (f	4.17	4.63
	321236	AW371941	Hs.18192	Ser/Arg-related nuclear matrix protein (1.00	1.00
	321244	AF068654		gb:Homo sapiens isolate AN.1 immunoglobu	2.18	9.13
	321270	R83560		gb:yy76c06.s1 Soares fetal liver spleen	3.80	5.26
55	321317	AI937060	Hs.6298	KIAA1151 protein	1.81	1.65
	321318	AB033041	Hs.137507	KIAA1215 protein	1.00	1.00
	321325	AB033100	Hs.300646	KIAA protein (similar to mouse paladin)	0.44	0.93
	321342	AA127984	Hs.222024	transcription factor BMAL2	4.94	4.93
	321356	R93443	Hs.271770	ESTs	3.10	4.66
60	321418	AI739161	Hs.161075	ESTs	2.28	2.54
	321420	AI368667	Hs.132743	ESTs	1.13	0.97
	321430	U05890		gb:H.sapiens (DIG3) mRNA for immunoglobu	2.42	3.35
	321453	N50080	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H	1.60	3.11
	321467	X13075		gb:Human 2a12 mRNA for kappa-immunoglobu	0.42	0.72
65	321468	AA514198	Hs.38540	ESTs	2.46	6.50
	321491	H70665	Hs.292549	ESTs	1.00	1.25
	321498	AW295517	Hs.255436	ESTs	3.19	6.24
	321504	W02356	Hs.268980	ESTs	2.28	3.86
70	321510	AA703650	Hs.255748	ESTs	2.14	3.94
	321513	H84972	Hs.108551	ESTs	2.78	5.37
	321516	AI382803	Hs.159235	ESTs	3.06	7.19
	321565	AI525773	Hs.266514	hypothetical protein FLJ11342	4.89	7.82
	321577	H84260		gb:ys90g04.r1 Soares retina N2b5HR Homo	1.00	1.73
	321581	AA019964	Hs.28803	ESTs	4.88	6.73
75	321582	AA143755	Hs.21858	trinucleotide repeat containing 3	1.00	2.08
	321587	H95531		gb:ys76e02.r1 Soares retina N2b4HR Homo	2.26	4.52
	321626	AA295430	Hs.96322	hypothetical protein FLJ23560	1.95	3.83
	321628	H87064	Hs.161051	ESTs, Moderately similar to ALU6_HUMAN A	0.47	1.02
	321642	AW085917	Hs.247084	ESTs	1.52	1.38
80	321669	H95404	Hs.294110	ESTs	2.17	2.45
	321687	AA625149		gb:af70c12.r1 Soares_NhHMPu_S1 Homo sapi	4.31	6.95
	321688	H97646	Hs.123158	Homo sapiens cDNA FLJ12830 fis, clone NT	2.82	3.28
	321693	AA700017	Hs.173737	ras-related C3 botulinum toxin substrate	0.51	1.08
	321700	N55160	Hs.167260	ESTs	4.57	7.46
85	321701	AW390923	Hs.42568	ESTs	1.00	1.00

	321709	N25847	Hs.108923	RAB38, member RAS oncogene family	1.00	1.00
	321710	N35682	Hs.259743	ESTs	2.97	5.26
	321775	AI694875	Hs.202312	Homo sapiens clone N11 NTera2D1 teratoca	1.00	1.00
5	321777	AI637993	Hs.202312	Homo sapiens clone N11 NTera2D1 teratoca	1.68	0.45
	321779	N42729	Hs.163835	ESTs	0.90	0.90
	321829	D81993	Hs.8966	tumor endothelial marker 8	2.69	3.89
	321846	AA281594	Hs.87902	ESTs	5.11	7.64
	321879	AL109670	Hs.302809	ESTs	6.49	9.58
10	321883	AA426494	Hs.46901	KIAA1462 protein	0.28	0.95
	321899	N55158	Hs.29468	ESTs	0.39	0.95
	321911	AF026944	Hs.293797	ESTs	6.20	10.76
	321949	R49202	Hs.181694	EST	4.62	10.51
	321955	AI651866	Hs.195689	ESTs	2.89	5.47
	321956	AL110177	Hs.132882	ESTs	0.32	1.25
15	321987	AL133612	Hs.272759	KIAA1457 protein	1.00	1.83
	321991	AL133627	Hs.158923	Homo sapiens mRNA; cDNA DKFZp434K0722 (f	4.00	6.47
	322002	AA328801	Hs.84522	ESTs	2.10	3.48
	322035	AL137517	Hs.306201	hypothetical protein DKFZp564O1278	1.00	1.90
20	322044	AW340926		gb:xy51b10.x1 NCI_CGAP_Lu34.1 Homo sapie	3.20	9.67
	322057	N92197	Hs.154679	synaptotagmin 1	1.55	1.07
	322060	AI341937		gb:ql10e03.x1 NCI_CGAP_GC4 Homo sapiens	4.59	7.68
	322070	U80769	Hs.210322	Homo sapiens mRNA for KIAA1766 protein,	2.78	4.52
	322083	AF074982	Hs.226031	ESTs, Highly similar to KIAA0535 protein	3.10	5.52
	322091	AI819863	Hs.106243	ESTs	1.59	1.75
25	322125	R93901		gb:yy16c12.r1 Soares fetal liver spleen	2.06	5.27
	322130	R98978	Hs.117767	ESTs	10.12	16.49
	322147	AF085919	Hs.114176	ESTs	0.94	0.64
	322166	AF085958		gb:yr88b03.r1 Soares fetal liver spleen	4.09	6.67
30	322173	H52567		gb:yl85d04.r1 Soares_pineal_gland_N3HPG	3.46	4.85
	322178	H56535		gb:yl88g03.r1 Soares_pineal_gland_N3HPG	0.44	2.54
	322179	H92891		gb:yl94c02.s1 Soares_pineal_gland_N3HPG	4.52	7.50
	322186	H67346	Hs.269187	ESTs	0.15	0.98
	322196	W87895	Hs.211516	ESTs	2.20	5.04
35	322212	AF087995	Hs.134877	ESTs	3.42	4.84
	322221	AI890619	Hs.179562	nucleosome assembly protein 1-like 1	0.82	2.14
	322277	AI640193	Hs.226389	ESTs	3.62	3.98
	322278	AF086283		gb:zd46f01.r1 Soares_fetal_heart_NbHH19W	1.00	1.00
	322284	AI792140	Hs.49265	ESTs	0.66	2.76
40	322288	AL037273	Hs.7886	pellino (Drosophila) homolog 1	0.71	0.70
	322320	AF086419		gb:zd78d03.r1 Soares_fetal_heart_NbHH19W	2.02	2.76
	322336	AA308526	Hs.76152	decorin	2.92	4.44
	322339	W17348		gb:zb18c07.x5 Soares_fetal_lung_NbHL19W	8.50	11.56
	322366	AW404274	Hs.122492	hypothetical protein	0.61	1.34
45	322372	W25624	Hs.153943	ESTs	7.37	12.07
	322374	AI394663	Hs.122116	ESTs, Moderately similar to Osf2 [M.musc	4.78	10.50
	322378	AF064819	Hs.201877	DESC1 protein	1.00	1.00
	322388	AI815730	Hs.247474	hypothetical protein FLJ21032	7.09	8.49
	322416	AA223183	Hs.298442	adaptor-related protein complex 3, mu 1	3.20	5.80
50	322419	AA248987	Hs.14084	ring finger protein 7	1.64	1.57
	322425	W37943	Hs.34892	KIAA1323 protein	0.83	1.00
	322431	AA069222	Hs.141892	ESTs	3.96	5.22
	322450	AA040131	Hs.25144	ESTs	5.18	12.67
	322465	AA137152	Hs.286049	phosphoserine aminotransferase	3.41	2.23
55	322467	AF116826	Hs.180340	putative protein-tyrosine kinase	1.00	1.30
	322473	AA744286	Hs.266935	IRNA selenocysteine associated protein	1.75	2.03
	322509	T52172	Hs.302213	ESTs	1.00	2.27
	322523	W80398	Hs.193197	ESTs	2.75	5.49
	322527	AF147359		gb:Homo sapiens full length insert cDNA	1.25	1.27
60	322560	AI916847	Hs.270947	ESTs	4.57	8.81
	322566	W87285	Hs.269587	ESTs	1.00	1.42
	322585	AA837622		gb:zh69c01.r1 Soares_fetal_liver_spleen_	4.18	6.94
	322635	AA679084		gb:zh90h08.r1 Soares_fetal_liver_spleen_	2.40	4.85
	322641	AA007352	Hs.256042	ESTs	2.94	4.64
65	322653	AI828854	Hs.258538	striatin, calmodulin-binding protein	0.48	0.38
	322664	AA011522		gb:zi03g07.r1 Soares_fetal_liver_spleen_	1.92	2.18
	322687	AI110759		gb:AF074666 Human fetal liver cDNA libra	4.14	6.75
	322692	AA018117	Hs.60843	potassium voltage-gated channel, shaker-	3.50	5.00
	322694	AI110872	Hs.279812	PRO0327 protein	1.80	1.72
70	322708	AF113674	Hs.283773	clone FLB1727	1.00	3.43
	322712	AA021328	Hs.23607	hypothetical protein FLJ11109	3.28	3.86
	322766	AW068805	Hs.288467	Homo sapiens cDNA FLJ12280 fis, clone MA	1.63	1.53
	322770	AA045796	Hs.122682	ESTs	1.53	1.06
	322794	AI608591	Hs.38991	S100 calcium-binding protein A2	12.06	1.94
75	322810	AI962276	Hs.127444	ESTs	4.09	6.90
	322818	AW043782	Hs.293516	ESTs	1.20	1.63
	322820	AI377755	Hs.120695	ESTs	0.21	1.93
	322872	AA827228	Hs.126943	ESTs	2.04	1.63
	322882	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	5.26	1.22
80	322887	AI986306	Hs.86149	phosphoinositol 3-phosphate-binding prot	2.80	2.24
	322913	AI733737	Hs.68837	ESTs	2.38	6.61
	322926	AI825940	Hs.211192	ESTs	4.02	5.79
	322929	AI365585	Hs.146246	ESTs	0.30	1.14
	322968	AI905228	Hs.83484	SRY (sex determining region Y)-box 4	2.06	1.13
85	322971	C15953	Hs.212760	hypothetical protein FLJ13649	1.18	2.00
	322981	AA493252	Hs.159577	ESTs	2.28	2.61

	322988	C18727	Hs.171941	ESTs	0.39	2.00
	323003	A1733859	Hs.149089	ESTs	3.28	1.00
	323013	AA134042	Hs.191451	ESTs	3.38	5.68
5	323025	AL157565	Hs.315369	Homo sapiens cDNA: FLJ23075 fis, clone L	0.06	1.10
	323032	AW244073	Hs.145946	ESTs	10.18	21.27
	323052	R21124	Hs.85573	Homo sapiens DC29 mRNA, complete cds	1.46	1.90
	323064	AL119341	Hs.49359	Homo sapiens mRNA; cDNA DKFZp547E052 (fr	3.08	5.64
	323098	A1700025	Hs.270471	ESTs	2.31	4.49
10	323102	AL119913	Hs.163615	ESTs	5.38	11.64
	323155	AL135041		gb:DKFZp762K2310_r1 762 (synonym: hmel2)	2.38	5.56
	323176	AW071648	Hs.82101	pleckstrin homology-like domain, family	1.06	1.41
	323191	AA195600	Hs.301570	ESTs	0.73	1.24
	323225	AA205654	Hs.24790	KIAA1573 protein	5.25	11.95
	323232	AA148722	Hs.224680	ESTs	0.45	1.35
15	323266	AW003362	Hs.243886	nuclear autoantigenic sperm protein (his	1.71	1.83
	323281	A1697556	Hs.292659	ESTs	1.24	3.21
	323283	AA256014	Hs.86682	Homo sapiens cDNA: FLJ21578 fis, clone C	12.68	15.05
	323314	AA226310	Hs.191501	ESTs	4.42	9.61
	323316	AL134620	Hs.280175	ESTs	2.98	5.93
20	323334	AJ336501	Hs.77273	ras homolog gene family, member A	1.98	3.30
	323338	R74219	Hs.23348	S-phase kinase-associated protein 2 (p45	1.62	1.00
	323348	AA233056	Hs.191518	ESTs	1.00	1.07
	323351	AA704103	Hs.24049	ESTs	1.43	1.68
	323359	AA234172	Hs.137418	ESTs	0.34	1.18
25	323360	AA716061	Hs.161719	ESTs	3.01	3.71
	323405	AW139550	Hs.115173	ESTs	1.90	8.81
	323420	A1672386	Hs.263780	ESTs	0.29	1.01
	323434	AW081455	Hs.120219	ESTs	2.27	1.92
	323445	AA253103	Hs.135569	ESTs, Weakly similar to NEUROD (H.sapien	0.43	0.80
30	323449	AA282865	Hs.284153	Fanconi anemia, complementation group A	3.19	3.85
	323492	H00978	Hs.20887	hypothetical protein FLJ10392	2.70	3.20
	323501	AA182461	Hs.84520	ESTs	2.04	3.31
	323505	A1652287		gb:EST382593 MAGE resequences, MAGK Homo2.21		3.08
35	323515	AA282274	Hs.256083	ESTs	2.69	3.40
	323541	A185116	Hs.104613	RP42 homolog	1.20	1.09
	323545	A1814405	Hs.224569	ESTs	1.25	1.55
	323635	R63117	Hs.9691	Homo sapiens cDNA: FLJ23249 fis, clone C	0.27	0.72
	323675	AA984759	Hs.272168	tumor differentially expressed 1	3.70	5.80
40	323678	AL042121	Hs.20880	ESTs	3.33	5.10
	323691	AA317561	Hs.145599	ESTs	1.00	1.00
	323693	AW297758	Hs.249721	ESTs	2.01	1.54
	323746	AW298611	Hs.12808	MARK	4.11	5.53
	323774	AA329806	Hs.321056	Homo sapiens mRNA; cDNA DKFZp586F1322 (f	2.06	3.70
	323856	AA355264	Hs.267604	hypothetical protein FLJ10450	3.42	8.13
45	323857	T18988	Hs.293668	ESTs	5.97	12.51
	323870	AA341774	Hs.129212	ESTs	3.17	4.52
	323876	AL042492	Hs.147313	ESTs	0.36	1.00
	323885	AA344308	Hs.128427	Homo sapiens BAC clone RP11-335J18 from	2.31	3.33
50	323911	AL043212	Hs.92550	ESTs	4.38	5.41
	323919	AA862973	Hs.220704	ESTs	5.80	10.20
	323972	A1869964	Hs.182906	ESTs	3.10	5.14
	324005	AA610011	Hs.208021	ESTs	5.34	10.07
	324036	A1472078	Hs.303662	ESTs	1.00	5.03
55	324055	AA528794	Hs.128644	ESTs	0.86	1.00
	324063	AW292740	Hs.272813	dual oxidase 1	0.45	0.91
	324072	AA381829		gb:EST94855 Activated T-cells I Homo sap	2.82	5.12
	324092	AW269931	Hs.202473	Homo sapiens cDNA: FLJ22278 fis, clone H	2.40	2.52
	324095	AW377983	Hs.298140	Homo sapiens cDNA: FLJ22502 fis, clone H	1.32	4.30
60	324129	A1381918	Hs.285833	Homo sapiens cDNA: FLJ22135 fis, clone H	1.40	1.77
	324132	AW504860	Hs.288836	hypothetical protein FLJ12673	4.24	6.21
	324214	AA412395	Hs.225740	ESTs	6.96	10.69
	324227	AA295552	Hs.28631	Homo sapiens cDNA: FLJ22141 fis, clone H	0.81	0.53
	324266	AL047634	Hs.231913	ESTs	2.42	4.05
	324275	AA429088	Hs.98523	ESTs	3.62	5.38
65	324281	AL048026	Hs.124675	ESTs, Weakly similar to T14742 hypotheti	0.14	0.70
	324290	AA432032	Hs.304420	ESTs	3.71	4.34
	324303	AL118754		gb:DKFZp761P1910_r1 761 (synonym: hamy2)	0.95	0.91
	324312	A1198841	Hs.128173	ESTs	4.08	5.91
	324325	AL138153	Hs.300410	ESTs	5.88	8.25
70	324338	AL138357	Hs.145078	regulator of differentiation (in S. pomb	0.87	1.25
	324341	AW197734	Hs.99807	ESTs, Weakly similar to unnamed protein	1.28	1.00
	324343	AW452016	Hs.293232	ESTs	2.54	3.46
	324371	AA452305	Hs.270319	ESTs	5.85	8.36
75	324382	AW502749	Hs.24724	MFH-amplified sequences with leucine-ric	0.76	1.64
	324384	AA453396	Hs.127656	KIAA1349 protein	2.88	5.69
	324385	F28212	Hs.284247	KIAA1491 protein	1.81	1.99
	324388	A1924963	Hs.306206	hypothetical protein FLJ11215	1.00	1.00
	324432	AA464510	Hs.152812	ESTs	2.73	2.17
	324497	AW152624	Hs.136340	ESTs, Weakly similar to unnamed protein	0.71	1.90
80	324510	A1148353	Hs.287425	Homo sapiens cDNA FLJ11569 fis, clone HE	1.00	1.00
	324580	AA492588		gb:ng99c08.s1 NCI_CGAP_Thy1 Homo sapiens	2.18	3.50
	324582	AA506935	Hs.132036	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.96	11.36
	324633	AA572994	Hs.325489	ESTs	2.92	4.22
	324640	AW295832	Hs.134798	ESTs, Moderately similar to TTL MOUSE TU	5.48	11.74
85	324675	AW014734	Hs.157969	ESTs	0.39	0.73

	324699	AW504732	Hs.21275	hypothetical protein FLJ11011	0.93	0.93
	324747	AA603532	Hs.130807	ESTs	1.57	1.81
	324748	AA657457	Hs.292385	ESTs	1.55	1.34
5	324801	AI819924	Hs.14553	sterol O-acyltransferase (acyl-Coenzyme	1.00	6.56
	324804	AI692552		gb:wd73f12.x1 NCI_CGAP_Lu24 Homo sapiens	1.00	7.53
	324828	AA843926	Hs.124434	ESTs	2.00	3.25
	324855	AW152305	Hs.122364	ESTs	2.74	3.43
	324866	AI541214	Hs.46320	Small proline-rich protein SPRK [human,	1.07	0.95
10	324871	AW297755	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	1.68	1.21
	324886	AA806794	Hs.131511	ESTs	2.56	5.61
	324889	D31010		gb:HUML12147 Human fetal lung Homo sapie	2.20	4.65
	324948	AW383618	Hs.265459	ESTs, Moderately similar to ALU2_HUMAN A	5.28	7.05
	324953	AI264628	Hs.125428	ESTs	3.37	5.51
15	324958	AA625076	Hs.132892	protocadherin 20	5.12	9.81
	324988	T06997	Hs.121028	hypothetical protein FLJ10549	2.52	1.08
	325024	F13254	Hs.78672	laminin, alpha 4	5.24	10.22
	325105	H97109	Hs.105421	ESTs	1.00	1.00
	325108	AA401863	Hs.22380	ESTs	1.99	2.14
20	325114	D83901	Hs.315562	ESTs	2.73	3.17
	325146	AI064690	Hs.171176	ESTs	1.86	3.41
	325149	D61117	Hs.187646	ESTs	0.42	0.93
	325187	AI653682	Hs.197812	ESTs	6.50	11.31
	325228				6.18	15.76
25	325235				2.64	4.12
	325328				2.87	4.42
	325340				0.29	0.33
	325367				16.56	24.29
30	325373				0.63	1.22
	325389				0.88	1.05
	325436				5.75	14.14
	325471				8.46	17.82
	325498				3.32	6.42
	325557				5.51	8.28
35	325559				7.48	21.40
	325560				4.08	6.25
	325569				4.20	5.24
	325585				1.10	1.13
	325587				1.00	1.00
40	325597				2.98	13.40
	325639				0.78	0.78
	325685				0.46	0.66
	325686				0.95	1.55
	325735				4.48	9.20
45	325739				0.59	0.88
	325740				2.42	6.61
	325792				7.88	9.83
	325819				4.74	7.18
	325883				2.02	2.64
50	325895				7.78	15.98
	325925				2.04	10.60
	325932				4.18	7.36
	325941				3.66	9.03
	325969				0.61	0.80
55	325971				4.88	7.42
	326025				0.55	1.07
	326046				7.21	14.72
	326099				3.60	5.98
	326108				1.27	1.06
60	326163				3.27	5.70
	326165				0.45	1.11
	326189				0.13	0.45
	326204				5.60	9.00
	326230				7.00	12.01
65	326274				1.00	8.09
	326360				9.86	15.35
	326393				0.52	0.77
	326505				1.00	1.42
	326515				1.24	5.84
70	326589				9.20	13.49
	326592				2.77	4.01
	326605				2.01	2.53
	326692				1.00	1.00
	326693				1.00	1.31
75	326720				0.19	0.65
	326742				2.34	7.20
	326770				0.25	0.83
	326818				3.09	4.56
	326936				2.08	3.45
80	326964				0.41	1.70
	326983				2.02	3.80
	326991				1.09	1.20
	327036				1.00	8.04
	327040				3.05	4.22
85	327053				3.55	6.31
	327075				1.59	1.40

	327085	2.50	12.57
	327130	5.38	8.04
	327156	3.74	6.58
5	327220	1.28	1.54
	327224	6.56	12.91
	327288	2.61	5.40
	327321	2.42	3.11
	327332	6.62	10.58
10	327361	2.69	4.41
	327377	2.04	6.72
	327396	2.61	4.50
	327414	1.00	8.01
	327442	5.91	9.65
15	327467	6.58	18.01
	327473	3.79	7.48
	327483	4.08	8.87
	327562	0.68	2.86
	327568	1.00	2.00
20	327606	2.06	3.61
	327611	5.90	14.26
	327642	4.05	8.74
	327654	1.05	2.08
	327734	1.00	1.00
25	327775	1.46	11.79
	327796	3.47	5.65
	327840	3.26	6.64
	327940	5.84	15.58
	327984	0.36	1.50
30	328004	1.87	1.42
	328021	0.42	0.59
	328068	2.83	4.68
	328100	3.04	5.39
	328101	3.54	5.20
35	328113	0.72	0.91
	328157	5.58	5.16
	328196	5.76	11.13
	328197	5.98	10.58
	328264	3.11	4.88
40	328299	2.20	3.06
	328342	1.49	1.94
	328365	1.00	1.00
	328369	4.40	7.36
	328381	1.86	4.93
45	328451	5.51	7.56
	328481	0.13	0.72
	328500	2.71	3.97
	328530	5.41	7.62
	328600	3.14	10.68
50	328608	4.56	8.17
	328616	2.24	11.91
	328623	3.04	5.46
	328632	0.70	1.19
	328664	3.48	6.80
55	328666	10.42	26.47
	328698	9.68	14.56
	328700	2.74	10.22
	328708	0.15	0.57
	328735	6.23	8.91
60	328743	3.62	6.54
	328806	0.22	0.78
	328861	3.68	10.54
	328908	5.42	16.36
	328933	2.02	5.29
65	328934	1.73	4.45
	328949	3.34	5.41
	329005	2.88	7.26
	329011	2.52	3.72
	329033	1.00	1.03
70	329037	5.07	8.16
	329067	1.98	2.41
	329134	2.24	3.25
	329157	2.30	11.04
	329178	2.64	5.02
75	329192	6.41	15.27
	329194	0.31	0.79
	329204	1.60	3.75
	329224	2.99	6.11
	329228	0.83	0.83
80	329288	0.63	1.01
	329337	1.00	1.00
	329541	0.76	1.68
	329560	1.34	2.02
	329588	1.68	2.22
85	329643	4.18	11.77
	329703	1.00	1.00

	329764			5.78	15.50	
	329816			2.09	5.44	
	329860			3.13	10.77	
	329993			7.83	14.21	
5	330020			5.58	13.12	
	330036			3.32	5.57	
	330052			4.31	7.97	
	330085			1.34	1.76	
	330088			4.70	12.46	
10	330093			0.44	1.06	
	330100			3.47	4.83	
	330106			2.14	3.61	
	330107			3.17	6.87	
	330120			5.61	11.89	
15	330123			4.50	12.74	
	330208			1.55	7.62	
	330263			13.10	23.38	
	330300			2.81	4.98	
	330313			3.00	4.41	
20	330366			0.67	0.76	
	330372			4.76	11.82	
	330385	AA449749	Hs.182971	karyopherin alpha 5 (importin alpha 6)	2.14	2.15
	330397	D14659	Hs.154387	KIAA0103 gene product	0.40	1.15
	330468	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	1.11	0.94
25	330472	L24203	Hs.82237	ataxia-telangiectasia group D-associated	1.67	1.17
	330478	L38486	Hs.296049	microfibrillar-associated protein 4	0.46	1.07
	330493	M27826	Hs.267319	endogenous retroviral protease	1.07	0.95
	330495	M31328	Hs.71642	guanine nucleotide binding protein (G pr	0.97	0.96
	330506	M61906	Hs.6241	phosphoinositide-3-kinase, regulatory su	0.17	3.66
30	330512	M80563	Hs.81256	S100 calcium-binding protein A4 (calcium	0.60	1.06
	330537	U19765	Hs.2110	zinc finger protein 9 (a cellular retrov	2.81	2.07
	330547	U32989	Hs.183671	tryptophan 2,3-dioxygenase	3.91	1.49
	330551	U39840	Hs.299867	hepatocyte nuclear factor 3, alpha	1.15	1.03
	330568	U56244		(NONE)	2.83	4.79
35	330599	U90437		gb:Human RP1 homolog mRNA, 3'UTR region	2.08	1.54
	330601	U90916	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H	0.89	1.35
	330605	X02419	Hs.77274	plasminogen activator, urokinase	1.87	1.55
	330609	X04741	Hs.76118	ubiquitin carboxyl-terminal esterase L1	1.83	1.30
40	330617	X53587	Hs.85266	integrin, beta 4	1.54	1.15
	330630	X78669	Hs.79088	reticulocalbin 2, EF-hand calcium bindin	1.39	1.19
	330644	Y07755	Hs.38991	S100 calcium-binding protein A2	3.83	1.13
	330650	Z68228	Hs.2340	junction plakoglobin	1.25	0.95
	330660	AA347868	Hs.139293	ESTs, Weakly similar to ALU7_HUMAN ALU S	15.50	29.07
	330692	AA017045	Hs.6702	ESTs	1.00	1.00
45	330707	AA133891	Hs.293690	ESTs	0.20	1.35
	330715	AA233707	Hs.11571	Homo sapiens cDNA FLJ11570 fis, clone HE	0.12	1.40
	330717	AA233926	Hs.52620	integrin, beta 8	6.62	5.42
	330722	AA243560	Hs.34382	ESTs	1.40	1.65
50	330740	AA297746	Hs.22654	Homo sapiens voltage-gated sodium channe	0.27	2.04
	330742	AA400979	Hs.25691	receptor (calcitonin) activity modifying	0.44	0.90
	330744	AA406142	Hs.12393	dTDP-D-glucose 4,6-dehydratase	0.71	3.23
	330751	AA428286	Hs.29543	Homo sapiens cDNA FLJ13103 fis, clone NT	1.66	1.52
	330760	AA448663	Hs.30469	ESTs	0.52	0.90
55	330763	AA450200	Hs.274337	hypothetical protein FLJ20666	0.37	0.97
	330786	D60374	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	0.78	0.84
	330790	T48536	Hs.105807	ESTs	0.23	3.17
	330814	AA015730	Hs.265398	ESTs, Weakly similar to transformation-r	0.37	2.07
	330827	AA040332	Hs.12744	ESTs	1.60	1.00
60	330844	AA063037	Hs.66803	ESTs	0.93	1.16
	330901	AA157818	Hs.267319	endogenous retroviral protease	1.02	1.03
	330931	F01443	Hs.284256	hypothetical protein FLJ14033 similar to	0.24	0.88
	330952	H02855	Hs.29567	ESTs	0.08	1.31
	330961	H10998	Hs.7164	a disintegrin and metalloproteinase doma	1.29	1.26
65	330968	H16568	Hs.23748	ESTs	0.48	0.96
	331014	H98597	Hs.30340	hypothetical protein KIAA1165	0.29	0.74
	331046	N66563	Hs.191358	ESTs	0.99	8.56
	331060	N75081	Hs.157148	Homo sapiens cDNA FLJ11883 fis, clone HE	1.24	1.00
	331099	R36671	Hs.83937	hypothetical protein	0.75	1.03
70	331108	R41408	Hs.21983	ESTs	1.00	2.75
	331131	R54797		gb:yg87b07.s1 Soares infant brain 1NIB H	6.04	10.68
	331135	R61398	Hs.4197	ESTs	0.80	0.96
	331170	T23461	Hs.159293	ESTs	2.63	4.29
	331180	T32446	Hs.6640	Human DNA sequence from PAC 75N13 on chr	1.78	2.71
75	331183	T40769	Hs.8469	ESTs	1.00	3.01
	331203	T82310		(NONE)	1.70	3.80
	331271	AA059347	Hs.82226	glycoprotein (transmembrane) nmb	1.20	3.19
	331306	AA252079	Hs.63931	dachshund (Drosophila) homolog	0.31	1.30
	331327	AA281076	Hs.109221	ESTs	2.09	2.41
80	331341	AA303125	Hs.23240	Homo sapiens cDNA FLJ13496 fis, clone PL	0.72	2.43
	331359	AA416979	Hs.46901	KIAA1462 protein	0.09	0.91
	331363	AA421562	Hs.91011	anterior gradient 2 (Xenopus laevis) hom	1.02	0.87
	331378	AA448881	Hs.49282	hypothetical protein FLJ11088	1.03	1.23
	331384	AA456001	Hs.93847	NADPH oxidase 4	1.40	1.00
	331402	AA505135	Hs.44037	ESTs	1.80	3.93
85	331422	F10802	Hs.163528	ESTs, Moderately similar to ALU7_HUMAN	1.65	1.89

	331490	N32912	Hs.26813	CDA14	2.48	1.73
	331531	N51343		gb:yz15g04.s1 Soares_multiple_sclerosis_	0.98	1.68
	331547	N54811		gb:od74f04.s1 NCI_CGAP_Ov2 Homo sapiens	3.80	5.75
5	331578	N67960	Hs.249989	ESTs	0.11	0.67
	331589	N71027	Hs.152618	ESTs	1.09	1.38
	331608	N89861	Hs.112110	PTD007 protein	0.93	0.76
	331614	N92293	Hs.240272	EST	0.17	1.34
	331668	W69707	Hs.58030	EST	2.24	3.82
10	331671	W72033	Hs.194695	ras homolog gene family, member I	1.00	1.24
	331676	W79834	Hs.58559	ESTs, Weakly similar to rhotekin [M.musc	0.08	1.07
	331681	W85712	Hs.119571	collagen, type III, alpha 1 (Ehlers-Danl	8.72	4.27
	331692	W93592	Hs.152213	wingless-type MMTV integration site fami	0.94	0.54
	331717	AA190888	Hs.153881	Homo sapiens NY-REN-62 antigen mRNA, par	1.57	1.34
	331718	AA191404	Hs.104072	ESTs	6.80	11.77
15	331811	AA404500	Hs.301570	ESTs	1.10	1.00
	331820	AA405970	Hs.97996	transcription termination factor, mitoc	0.73	0.59
	331831	AA412031	Hs.97901	EST	2.77	4.08
	331852	AA418988	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (f	0.23	0.93
20	331943	AA453418	Hs.21275	hypothetical protein FLJ11011	0.36	1.88
	331969	AA460702	Hs.82772	collagen, type XI, alpha 1	1.00	1.00
	331990	AA478102	Hs.139531	ESTs	3.04	3.87
	332002	AA482009	Hs.105104	ESTs	1.19	0.78
	332027	AA489671	Hs.65641	hypothetical protein FLJ20073	1.27	1.03
25	332029	AA489697	Hs.145053	ESTs	0.30	1.62
	332033	AA489840	Hs.251014	EST	2.30	3.70
	332048	AA496019	Hs.201591	ESTs	0.17	0.52
	332071	AA598594	Hs.205293	KIAA1211 protein	1.35	1.23
	332074	AA599012		gb:ae41e11.s1 Gessler Wilms tumor Homo s	0.19	2.00
30	332083	AA600200	Hs.155546	KIAA1080 protein; Golgi-associated, gamm	0.31	1.18
	332085	AA600353	Hs.173933	nuclear factor I/A	0.30	1.50
	332125	AA609861	Hs.312447	ESTs	0.22	0.62
	332177	F10812	Hs.101433	ESTs	8.21	18.03
	332180	H03348	Hs.7327	claudin 1	2.27	1.57
35	332185	H10356	Hs.101689	ESTs	0.09	1.18
	332203	H49388	Hs.317769	EST	8.05	5.02
	332232	N48891	Hs.101915	Stargardt disease 3 (autosomal dominant)	0.78	0.85
	332240	N54803	Hs.324267	ESTs, Weakly similar to putative p150 [0.96	1.23
	332261	N70294	Hs.269137	ESTs	2.40	3.74
40	332275	R08838	Hs.26530	serum deprivation response (phosphatidyl	0.27	0.75
	332280	R38100	Hs.146381	RNA binding motif protein, X chromosome	0.39	1.88
	332299	R69250	Hs.21201	necln 3; DKFZP566B0846 protein	5.24	12.76
	332304	R74041	Hs.101539	ESTs	1.44	3.18
	332314	T25862	Hs.101774	hypothetical protein FLJ23045	0.68	1.32
	332384	M11433	Hs.101850	retinol-binding protein 1, cellular	1.71	0.88
45	332434	N75542	Hs.289068	Homo sapiens cDNA FLJ11918 fis, clone HE	0.43	0.86
	332445	T63781	Hs.11112	ESTs	0.68	1.00
	332453	L00205	Hs.111758	keratin 6A	31.54	1.00
	332458	M33493	Hs.250700	trypsin beta 1	0.51	1.00
50	332504	AA053917	Hs.15106	chromosome 14 open reading frame 1	0.79	1.24
	332525	M17252	Hs.278430	cytochrome P450, subfamily XXIA (steroid	0.98	1.70
	332530	M31682	Hs.1735	inhibin, beta B (activin AB beta polypep	0.88	0.66
	332535	N20284	Hs.19280	cysteine-rich motor neuron 1	0.22	1.46
	332539	AA412528	Hs.20183	ESTs, Weakly similar to AF164793 1 prote	0.93	1.49
55	332559	M13955	Hs.166189	cytokeratin 2	0.35	1.13
	332563	N92924	Hs.274407	protease, serine, 16 (thymus)	1.00	1.00
	332565	AA234896	Hs.25272	E1A binding protein p300	0.36	1.05
	332594	AA279313	Hs.3239	methyl CpG binding protein 2 (Rett syndr	0.53	0.59
	332634	S38953	Hs.283750	tenascin XA	0.38	1.16
60	332638	AA283034	Hs.50640	JAK binding protein	1.00	1.70
	332640	AA417152	Hs.5101	protein regulator of cytokinesis 1	6.15	1.16
	332654	AA001296	Hs.288217	hypothetical protein MGC2941	1.50	2.73
	332665	AA223335	Hs.63788	propionyl Coenzyme A carboxylase, beta p	1.20	0.91
	332692	AA496035	Hs.247926	gap junction protein, alpha 5, 40kD (con	0.17	1.12
65	332716	L00058	Hs.79070	v-myc avian myelocytomatosis viral oncog	1.00	1.44
	332736	L13773	Hs.114765	myeloid/lymphoid or mixed-lineage leukem	1.00	1.81
	332758	X93921	Hs.296938	dual specificity phosphatase 7	0.53	0.78
	332781	AA233258	Hs.247112	hypothetical protein FLJ10902	1.44	1.56
	332792				1.70	1.19
70	332816				1.85	2.47
	332858				1.04	1.57
	332906				3.48	8.04
	332911				1.00	1.00
	332912				1.06	4.40
75	332922				1.00	1.00
	332956				0.42	0.88
	332959				1.96	6.34
	332982				0.56	0.99
	332984				0.30	0.78
80	332998				1.47	2.01
	333058				0.47	1.38
	333097				2.14	3.19
	333121				2.76	3.70
	333122				1.92	1.21
85	333123				1.85	1.39
	333138				0.47	0.52

	333139	1.88	0.84
	333140	0.21	0.64
	333221	1.51	1.11
5	333260	0.75	1.01
	333380	6.68	15.75
	333387	4.56	12.61
	333512	5.05	8.01
	333524	2.28	3.98
10	333585	2.31	1.53
	333603	2.23	1.17
	333604	2.51	1.58
	333618	0.52	0.98
	333627	1.44	1.36
	333628	1.90	1.90
15	333650	1.85	2.10
	333678	1.85	2.35
	333750	2.18	5.67
	333763	1.99	2.60
20	333767	1.02	0.96
	333768	1.78	1.65
	333769	2.15	2.13
	333772	1.46	2.53
	333777	1.00	1.42
25	333846	2.99	4.50
	333884	0.47	0.94
	333887	0.50	1.00
	333891	0.43	0.89
	333892	0.51	0.91
30	333904	0.26	1.13
	333906	0.55	0.98
	333948	1.70	2.15
	333954	0.37	1.09
35	333966	8.10	14.30
	333968	0.63	1.38
	334061	4.24	12.30
	334094	1.30	12.03
	334113	4.55	8.63
	334161	0.82	1.59
40	334183	0.47	0.76
	334187	1.36	3.70
	334219	0.69	1.04
	334222	1.88	1.70
	334223	4.72	3.14
45	334239	0.79	0.62
	334255	0.45	1.10
	334333	1.00	3.56
	334378	3.98	5.76
	334382	1.50	1.31
50	334492	3.59	4.75
	334562	5.94	15.40
	334588	8.14	19.53
	334616	1.55	1.56
	334633	5.16	8.07
55	334648	0.59	2.13
	334787	3.70	7.15
	334866	8.13	10.60
	334891	0.32	1.14
	334933	1.00	3.84
60	334934	4.01	7.43
	334945	1.04	2.96
	334967	0.29	1.14
	334990	1.50	1.39
	335015	5.88	18.65
65	335093	0.55	1.75
	335120	4.31	8.01
	335125	0.38	1.97
	335179	1.24	1.98
	335188	0.46	1.47
70	335211	1.61	1.42
	335288	0.73	0.97
	335289	0.20	0.26
	335361	2.18	1.58
	335379	0.50	0.71
75	335414	3.64	14.94
	335416	2.93	3.98
	335496	0.96	0.91
	335497	1.71	1.92
	335548	1.15	2.40
80	335551	3.22	10.54
	335558	3.42	4.89
	335586	5.50	12.75
	335619	2.99	3.07
	335620	3.80	8.29
85	335621	0.28	0.57
	335682	0.46	1.17

	335686	2.55	3.81
	335755	2.24	1.07
	335784	0.20	0.97
5	335814	1.13	1.48
	335815	2.45	3.51
	335823	1.00	4.16
	335835	0.49	1.70
	335851	1.66	1.39
10	335868	2.98	6.43
	335896	0.98	0.99
	335936	12.10	21.93
	335948	1.00	1.64
	335983	1.00	4.21
15	335995	0.37	1.17
	336021	1.04	0.84
	336034	11.40	23.54
	336038	1.19	1.21
	336066	0.54	1.63
20	336107	0.95	0.70
	336205	3.13	6.29
	336275	3.20	10.10
	336292	2.34	3.09
	336331	1.00	1.00
	336419	0.65	0.79
25	336632	2.33	2.16
	336633	2.55	2.23
	336634	2.19	2.03
	336635	2.69	2.48
30	336636	2.13	1.83
	336637	2.43	2.24
	336638	2.31	2.03
	336659	0.60	1.31
	336675	0.31	1.18
35	336684	1.50	1.14
	336694	4.74	7.10
	336716	4.43	6.37
	336721	2.20	0.74
	336798	1.64	2.14
40	336900	6.14	12.73
	336948	1.00	1.00
	337028	1.30	2.09
	337043	4.01	11.53
	337046	1.67	1.84
45	337054	2.78	7.35
	337128	7.20	16.14
	337162	3.45	5.34
	337183	5.72	11.41
	337184	3.72	5.90
50	337192	1.27	1.06
	337194	1.88	1.68
	337229	0.22	1.03
	337268	1.00	3.31
	337299	3.23	5.14
55	337325	2.76	3.72
	337389	5.80	10.42
	337493	2.06	6.30
	337497	7.88	20.29
	337500	3.80	4.48
60	337549	1.66	2.31
	337603	1.27	8.54
	337605	5.76	7.16
	337671	0.73	0.97
	337755	1.54	0.92
65	337786	5.07	9.73
	337809	6.18	12.87
	337862	3.78	12.97
	337871	2.66	8.16
	337958	0.26	1.34
70	338008	1.48	1.12
	338033	2.38	14.59
	338083	0.65	2.16
	338110	1.00	1.61
	338112	5.86	8.25
75	338145	1.70	1.97
	338148	8.07	18.19
	338158	1.30	4.55
	338161	2.58	3.57
	338179	1.00	1.00
80	338182	3.32	4.63
	338189	1.00	3.34
	338197	0.99	1.69
	338199	4.58	7.62
	338215	6.01	15.85
85	338279	0.53	0.95
	338316	20.58	38.66

	338322	3.23	7.39
	338357	4.10	11.39
	338359	10.12	21.59
5	338366	0.69	1.02
	338374	0.40	1.18
	338414	0.47	1.06
	338418	6.12	13.86
	338469	3.09	5.11
10	338501	6.28	10.32
	338506	6.97	12.41
	338523	3.10	5.84
	338549	1.70	2.70
	338561	0.79	0.81
15	338662	1.72	1.46
	338671	0.17	0.91
	338676	2.10	15.86
	338726	1.20	1.09
	338779	0.12	0.57
20	338804	0.99	1.67
	338836	1.00	1.00
	338871	4.30	9.81
	338872	5.02	12.81
	338879	0.23	1.12
	338937	6.55	12.26
25	338966	1.76	5.42
	338993	1.00	2.40
	339047	5.26	10.81
	339100	5.10	6.88
30	339114	1.00	1.70
	339121	1.00	3.75
	339170	10.35	19.67
	339229	4.08	13.48
	339264	2.64	3.83
35	339293	1.73	1.94

TABLE 8B shows the accession numbers for those Pkeys in Table 8A lacking unigenelD's. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accessions
	322044	187363_1 AW340926 AA249063 N86075
50	322060	44320_1 AI341937 AW003063 U34725 AA904742
	321430	42705_1 X57414 X57415
	321467	43034_1 X13075 X13076
	322125	46779_1 R93901 AF075073 R93902
	322166	46861_1 H69434 AF085958 H69846
55	322173	46873_1 H52567 H52557 AF085970 H52164
	322178	46882_1 H56535 AF085980 H56712
	322179	46885_1 H92891 AF085982 H92777
	321577	1615102_1 H84849 H84252 H84260 H86664 H85320
	321587	1615333_1 H95531 H95521 H84529
60	313723	111953_1 AA070412 AA102346 AA081885
	320997	627492_1 H22544 H46842 AI204929
	322278	47271_1 W69304 AF086283 W69200
	321687	218439_1 AA625149 AA313030 AA313052 H97463
	313883	129439_1 AA665089 AA135130 AA484059 AA102419 AW877765
65	322320	47422_1 W79150 AF086419
	322339	814584_1 AI668646 AJ734214 W17348
	314648	293660_1 AW979268 AA878419 AA431342 AA431628
	300201	682222_1 AI308300 AI308296
	306897	25196_2 AI093967
70	323155	979809_1 AL120701 AL135041 AL121524
	322527	38927_1 AF147359 T58511 T58560
	322585	473768_2 W88919 W89125
	300362	1574395_1 Z42308 H23514
	322635	82296_1 AA005129 AA679084 AA694399
75	322664	85042_1 AA011522 AA702841 AA011691 AA330797
	315454	380580_1 AI239464 AI239473 AA625812 AI208703
	322687	37372_1 AF074666 AI110759 AF090902
	314852	327472_1 AI903735 AA491283 AI694953 AW976903 AA761362
	307783	697809_1 AI347274 AW844024
80	324072	269032_1 AA381722 AA381829 AW963906 AW963902 AA381242
	300627	221345_1 AA488472 W27363 AA317053 BE082689 AW967036 BE079872
	323505	196389_1 AW970512 AA280251 AI652287 BE466438 AI550725 AA551854 AA281574 AW571481
	315791	403558_1 AA678177 AA677034
	324303	233842_1 AL118754 AA333202 H38001
85	316519	442885_1 AA847835 AA768376
	300926	333127_1 AA504860 AA504911

	324580	328264_1	AA492588 AA492498 AA492571
	301882	275087_1	T78054 T79888 AA398185
	324804	398093_1	AI692552 AI393343 AI800510 AI377711 F24263 AA661876
5	324889	1515978_1	D31010 D30991 D31168 D31166 D31465
	302697	43219_1	AJ001409 AJ001410
	302711	45419_1	L08442 D51348
	302742	458_39	L12061
	318499	364430_1	T25451 AA585296 AA585305
10	310624	34624_4	U88896 U88898 AA916056 T03285 AI341594 AI359534 AI634031 U88897
	302847	458_105	X98941 X98942 X98943 X98953 X98949
	304122	77271_5	H28966
	303598	270283_1	AA382814 AA402411 AA412355
	311409	837264_1	AI698839 AI909260 AI909259
	312094	797889_1	Z78390 T97427
15	319312	1540116_1	Z45481 F12393 T74437
	319407	1688823_1	R05329 R01555 R08276
	319425	1689571_1	T82930 R02424 T85145
	320007	229683_1	AA336314 T82938 AA327744 AW967388 AA639967 T10753
20	320018	1815987_1	T83263 T85731 T85730
	319484	1691553_1	T91772 R07257 R07098
	318865	1535937_1	H10818 F07831 Z43072
	312220	1671607_1	N74613 T98756 T98589
	319546	243305_1	R09692 R09414 AA346353
	312389	902067_1	AI863140 W80703 R43474
25	319611	1566863_1	H14957 R56522 R11908
	312437	291472_1	BE080180 AW827313 AW231970 AA995028 AA428584 AW872716 AW892508 AW854593 AA578441 AW975234 AA664937 AA984131 AA528743 AA552874 AA564758 AW063245 AI267534 AW070190 AW893483 AA770330 AA906928 AA906582 AA758746 AA551717 AW063311 AA429538
	311896	579192_1	AW206447 AI248530 AI084433 AI400976 R16553
30	319834	112523_1	AA071267 T65940 T64515 AA071334
	321102	80531_1	AA018306 H38925 AA001221
	321158	410938_1	H79670 H47798 AA700289
	321199	212379_1	N34524 AA305071 AW954803 AA502335 AI433430 AI203597 AW026670 AW265323 AW850787 AA317554 AW993643 AW835572 AW385512 AI334966 W32951 H62656 H53902 R88904 AW835732
35	305528	28832_3	AA769156
	321270	1662057_1	N59537 N78278 R83560
	314126	177666_1	AA226431 AA226569 AA488748
	320714	743644_1	R91883 AI445591
	306442	AA976899	
40	306446	AA977348	
	306458	AA978186	
	306510	AA988546	
	306557	AA994530	
	306572	AA995686	
45	306582	AA996248	
	306656	AI004024	
	306686	AI015615	
	306751	AI032589	
	308011	AI439473	
50	306892	AI092465	
	308106	AI476803	
	308154	AI500600	
	306956	AI125111	
	306958	AI125152	
55	308213	AI557041	
	308216	AI557135	
	308219	AI557246	
	308588	AI718299	
	308599	AI719893	
60	308643	AI745040	
	308673	AI760864	
	308697	AI767143	
	308778	AI811109	
	308808	AI818289	
65	308875	AI832332	
	308886	AI833240	
	308898	AI858845	
	308966	AI870704	
	308979	AI873111	
70	303011	41689_1	AF090405 AF090407 AF090406
	303077	44060_1	AF163305 AF163307 AF163303
	305016	AA626876	
	305034	AA630128	
75	305072	AA641012	
	305148	AA654070	
	305190	AA665955	
	303978	AW513315	
	303990	AW515465	
	303998	AW516449	
80	303999	AW516611	
	305235	AA670480	
	305312	AA700201	
	305413	AA724659	
	305447	AA737856	
85	321244	29327_1	AF068654 AF068656 AF068655

	305614	AA782866	
	305637	AA806124	
	305639	AA806138	
5	305650	AA807709	
	305690	AA813477	
	305728	AA828209	
	305759	AA835353	
	305792	AA845256	
10	307041	AI144243	
	307091	AI167439	
	307181	AI189251	
	305901	AA872968	
	305910	AA875981	
15	307415	AI242118	
	307426	AI243364	
	307517	AI275055	
	307551	AI281556	
	307561	AI282207	
20	307608	AI290295	
	307691	AI318285	
	307730	AI336092	
	307760	AI342387	
	307764	AI342731	
25	307796	AI350556	
	309045	AI910902	
	309051	AI911975	
	307807	AI351799	
	307808	AI351826	
	307820	AI355761	
30	307852	AI365541	
	309122	AI928178	
	309164	AI937761	
	309177	AI951118	
35	307902	AI380462	
	309299	AW003478	
	309303	AW004823	
	309476	AW129368	
	309532	AW151119	
40	309747	AW264889	
	309769	AW272346	
	309799	AW276964	
	309866	AW299916	
	302679	311853_1	H65022 AA186889
45	309923	AW340684	
	309928	AW341418	
	309931	AW341683	
	309933	AW341936	
	302705	31765_1	U09060 U09061
50	302789	34161_1	AJ245067 AJ245070
	304006	AW517947	
	304024	T03036	
	304026	T03160	
	304028	T03266	
55	304046	T54803	
	304061	T61521	
	304063	T62536	
	302802	34487_1	Y08250 Y08245
	304114	R78946	
60	304155	H68696	
	304203	N56929	
	304234	W81608	
	304348	AA179868	
	304430	AA347682	
65	304456	AA411240	
	304521	AA464716	
	304526	AA476427	
	304607	AA513322	
	304735	AA576453	
70	304760	AA580401	
	306015	AA897116	
	306063	AA906316	
	306065	AA906725	
	306104	AA910956	
75	306109	AA911861	
	306242	AA932805	
	306288	AA936900	
	306396	AA970223	
	330568	NOT_FOUND_entrez	U56244
80	330599	15323_-12	U90437
	331131	genbank_R54797	R54797
	331203	NOT_FOUND_entrez	T82310
	331531	genbank_N51343	N51343
	331547	467396_1	AA828597 N54811
85	332074	genbank_AA599012	AA599012

TABLE 8C shows the genomic position for those Pkeys in Table 8A lacking unigene ID's and accession numbers. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

5	Pkey:	Unique number corresponding to an Eos probeset		
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.		
	Strand:	Indicates DNA strand from which exons were predicted.		
10	Nt_position:	Indicates nucleotide positions of predicted exons.		
	Pkey	Ref	Strand	Nt_position
	332792	Dunham, I. et.al.	Plus	73381-73768
	332816	Dunham, I. et.al.	Plus	359844-360030
15	332906	Dunham, I. et.al.	Plus	1923101-1923205
	332911	Dunham, I. et.al.	Plus	1961767-1961858
	332912	Dunham, I. et.al.	Plus	1962120-1962246
	332922	Dunham, I. et.al.	Plus	2009620-2009738
20	332956	Dunham, I. et.al.	Plus	2510528-2510558
	332959	Dunham, I. et.al.	Plus	2518145-2518213
	333138	Dunham, I. et.al.	Plus	3369205-3369323
	333139	Dunham, I. et.al.	Plus	3369495-3369571
	333221	Dunham, I. et.al.	Plus	3978070-3978187
25	333380	Dunham, I. et.al.	Plus	4904775-4904846
	333387	Dunham, I. et.al.	Plus	4910935-4910997
	333512	Dunham, I. et.al.	Plus	5560510-5560564
	333524	Dunham, I. et.al.	Plus	5612620-5612780
	333585	Dunham, I. et.al.	Plus	6234778-6234894
30	333618	Dunham, I. et.al.	Plus	6562391-6562566
	333627	Dunham, I. et.al.	Plus	6620584-6620903
	333628	Dunham, I. et.al.	Plus	6629004-6629233
	333650	Dunham, I. et.al.	Plus	6796852-6797128
	333678	Dunham, I. et.al.	Plus	7068223-7068288
35	333750	Dunham, I. et.al.	Plus	7608165-7608234
	333763	Dunham, I. et.al.	Plus	7692491-7692630
	333767	Dunham, I. et.al.	Plus	7694407-7694623
	333768	Dunham, I. et.al.	Plus	7695440-7695697
	333769	Dunham, I. et.al.	Plus	7696625-7696707
40	333772	Dunham, I. et.al.	Plus	7706773-7706902
	333777	Dunham, I. et.al.	Plus	7746805-7746916
	333846	Dunham, I. et.al.	Plus	8008623-8008757
	333884	Dunham, I. et.al.	Plus	8153960-8154161
	333887	Dunham, I. et.al.	Plus	8154882-8155025
45	333891	Dunham, I. et.al.	Plus	8156437-8156709
	333892	Dunham, I. et.al.	Plus	8156825-8157001
	333948	Dunham, I. et.al.	Plus	8583497-8583627
	333954	Dunham, I. et.al.	Plus	8563186-8563335
	333966	Dunham, I. et.al.	Plus	8655643-8655826
50	333968	Dunham, I. et.al.	Plus	8681004-8681241
	334061	Dunham, I. et.al.	Plus	9686941-9687077
	334094	Dunham, I. et.al.	Plus	9889953-9890105
	334113	Dunham, I. et.al.	Plus	10282459-10282597
	334161	Dunham, I. et.al.	Plus	10599033-10599180
55	334219	Dunham, I. et.al.	Plus	12716160-12716384
	334239	Dunham, I. et.al.	Plus	13056569-13056693
	334333	Dunham, I. et.al.	Plus	13603544-13603657
	334378	Dunham, I. et.al.	Plus	13907239-13907370
	334382	Dunham, I. et.al.	Plus	13915866-13916036
60	334562	Dunham, I. et.al.	Plus	14987847-14987940
	334588	Dunham, I. et.al.	Plus	15032740-15032817
	334616	Dunham, I. et.al.	Plus	15176123-15176470
	334633	Dunham, I. et.al.	Plus	15333206-15333305
	334866	Dunham, I. et.al.	Plus	18872214-18872317
65	334891	Dunham, I. et.al.	Plus	19299770-19299944
	334934	Dunham, I. et.al.	Plus	20103970-20104058
	335015	Dunham, I. et.al.	Plus	20682792-20682945
	335120	Dunham, I. et.al.	Plus	21436286-21436384
	335125	Dunham, I. et.al.	Plus	21441390-21441471
70	335179	Dunham, I. et.al.	Plus	21634405-21634526
	335188	Dunham, I. et.al.	Plus	21669118-21669328
	335211	Dunham, I. et.al.	Plus	21774611-21774680
	335361	Dunham, I. et.al.	Plus	22807292-22807445
	335379	Dunham, I. et.al.	Plus	22899306-22899420
75	335414	Dunham, I. et.al.	Plus	23235546-23235684
	335416	Dunham, I. et.al.	Plus	23237354-23237465
	335496	Dunham, I. et.al.	Plus	24164386-24164545
	335497	Dunham, I. et.al.	Plus	24167666-24167869
	335558	Dunham, I. et.al.	Plus	24740167-24740347
80	335586	Dunham, I. et.al.	Plus	24990333-24990497
	335586	Dunham, I. et.al.	Plus	25439839-25439920
	335784	Dunham, I. et.al.	Plus	25942710-25942792
	335823	Dunham, I. et.al.	Plus	26365925-26366004
	335983	Dunham, I. et.al.	Plus	27938968-27939070
85	335995	Dunham, I. et.al.	Plus	28009044-28009184
	336021	Dunham, I. et.al.	Plus	28686482-28686559

	336034	Dunham, I. et.al.	Plus	29014404-29014590
	336038	Dunham, I. et.al.	Plus	29022963-29023165
	336107	Dunham, I. et.al.	Plus	29987731-29987869
5	336632	Dunham, I. et.al.	Plus	983890-985529
	336633	Dunham, I. et.al.	Plus	985591-986221
	336634	Dunham, I. et.al.	Plus	986296-986670
	336635	Dunham, I. et.al.	Plus	987908-988364
	336636	Dunham, I. et.al.	Plus	988418-989185
10	336637	Dunham, I. et.al.	Plus	989276-990813
	336638	Dunham, I. et.al.	Plus	991906-993240
	336659	Dunham, I. et.al.	Plus	1896402-1896478
	336694	Dunham, I. et.al.	Plus	2420546-2420616
	336721	Dunham, I. et.al.	Plus	3371522-3371586
	336900	Dunham, I. et.al.	Plus	10236423-10236523
15	336948	Dunham, I. et.al.	Plus	12692290-12692381
	337028	Dunham, I. et.al.	Plus	16644817-16644942
	337054	Dunham, I. et.al.	Plus	17821742-17821922
	337162	Dunham, I. et.al.	Plus	23478943-23479145
	337183	Dunham, I. et.al.	Plus	23943606-23943696
20	337184	Dunham, I. et.al.	Plus	23973949-23974016
	337268	Dunham, I. et.al.	Plus	28011979-28012034
	337299	Dunham, I. et.al.	Plus	29022656-29022775
	337389	Dunham, I. et.al.	Plus	31401509-31401579
	337493	Dunham, I. et.al.	Plus	33330760-33330981
25	337549	Dunham, I. et.al.	Plus	34474472-34474531
	337755	Dunham, I. et.al.	Plus	3971764-3971900
	337809	Dunham, I. et.al.	Plus	4449069-4449193
	337871	Dunham, I. et.al.	Plus	5443027-5443101
30	337958	Dunham, I. et.al.	Plus	6969162-6969270
	338008	Dunham, I. et.al.	Plus	7697068-7697236
	338033	Dunham, I. et.al.	Plus	8092128-8092271
	338110	Dunham, I. et.al.	Plus	10384481-10384621
	338112	Dunham, I. et.al.	Plus	10391398-10391600
	338145	Dunham, I. et.al.	Plus	11386629-11386692
35	338148	Dunham, I. et.al.	Plus	11448985-11449085
	338179	Dunham, I. et.al.	Plus	12808775-12808833
	338197	Dunham, I. et.al.	Plus	13638107-13638181
	338279	Dunham, I. et.al.	Plus	16168944-16169091
40	338316	Dunham, I. et.al.	Plus	17089711-17089988
	338322	Dunham, I. et.al.	Plus	17132477-17132547
	338357	Dunham, I. et.al.	Plus	18062184-18062402
	338359	Dunham, I. et.al.	Plus	18074402-18074501
	338366	Dunham, I. et.al.	Plus	18252026-18252189
45	338374	Dunham, I. et.al.	Plus	18371200-18371282
	338414	Dunham, I. et.al.	Plus	19345573-19345660
	338418	Dunham, I. et.al.	Plus	19435506-19435596
	338501	Dunham, I. et.al.	Plus	21244713-21244828
	338506	Dunham, I. et.al.	Plus	21221871-21221953
50	338523	Dunham, I. et.al.	Plus	21509763-21509864
	338662	Dunham, I. et.al.	Plus	24404720-24404899
	338804	Dunham, I. et.al.	Plus	27236005-27236108
	338836	Dunham, I. et.al.	Plus	27792166-27792272
	338879	Dunham, I. et.al.	Plus	28410653-28410734
55	338937	Dunham, I. et.al.	Plus	29160655-29160725
	338993	Dunham, I. et.al.	Plus	30077787-30078184
	339047	Dunham, I. et.al.	Plus	30760793-30760968
	339100	Dunham, I. et.al.	Plus	31141580-31141765
	339114	Dunham, I. et.al.	Plus	31456454-31456519
60	339121	Dunham, I. et.al.	Plus	31583467-31583536
	339170	Dunham, I. et.al.	Plus	32216399-32216527
	339293	Dunham, I. et.al.	Plus	33223571-33223819
	332858	Dunham, I. et.al.	Minus	1339607-1339397
	332982	Dunham, I. et.al.	Minus	2628296-2628109
65	332984	Dunham, I. et.al.	Minus	2632606-2632457
	332998	Dunham, I. et.al.	Minus	2711704-2711565
	333058	Dunham, I. et.al.	Minus	3028925-3028811
	333097	Dunham, I. et.al.	Minus	3204124-3204036
	333121	Dunham, I. et.al.	Minus	3308446-3308358
70	333122	Dunham, I. et.al.	Minus	3309596-3309531
	333123	Dunham, I. et.al.	Minus	3310817-3310749
	333140	Dunham, I. et.al.	Minus	3377220-3376309
	333260	Dunham, I. et.al.	Minus	4308400-4308304
	333603	Dunham, I. et.al.	Minus	6466335-6465727
75	333604	Dunham, I. et.al.	Minus	6467090-6466768
	333904	Dunham, I. et.al.	Minus	8217374-8217261
	333906	Dunham, I. et.al.	Minus	8218238-8218063
	334183	Dunham, I. et.al.	Minus	11832582-11832508
	334187	Dunham, I. et.al.	Minus	11921456-11921205
80	334222	Dunham, I. et.al.	Minus	12732417-12732289
	334223	Dunham, I. et.al.	Minus	12734365-12734269
	334255	Dunham, I. et.al.	Minus	13200776-13200692
	334492	Dunham, I. et.al.	Minus	14478333-14478172
	334648	Dunham, I. et.al.	Minus	15363301-15363222
85	334787	Dunham, I. et.al.	Minus	16299093-16298937
	334933	Dunham, I. et.al.	Minus	20078117-20077991

	334945	Dunham, I. et al.	Minus	20138885-20138637
	334967	Dunham, I. et al.	Minus	20173311-20173218
	334990	Dunham, I. et al.	Minus	20341159-20341087
5	335093	Dunham, I. et al.	Minus	21297367-21297214
	335288	Dunham, I. et al.	Minus	22304275-22303770
	335289	Dunham, I. et al.	Minus	22305950-22305708
	335548	Dunham, I. et al.	Minus	24662773-24662673
	335551	Dunham, I. et al.	Minus	24679828-24678961
10	335619	Dunham, I. et al.	Minus	25082677-25082498
	335620	Dunham, I. et al.	Minus	25092561-25092434
	335621	Dunham, I. et al.	Minus	25098878-25098767
	335682	Dunham, I. et al.	Minus	25421215-25421093
	335755	Dunham, I. et al.	Minus	25763806-25763747
	335814	Dunham, I. et al.	Minus	26320043-26319845
15	335815	Dunham, I. et al.	Minus	26320518-26320421
	335835	Dunham, I. et al.	Minus	26393311-26393245
	335851	Dunham, I. et al.	Minus	26604863-26604742
	335868	Dunham, I. et al.	Minus	26711437-26711300
	335896	Dunham, I. et al.	Minus	26977639-26977558
20	335936	Dunham, I. et al.	Minus	27360474-27360400
	335948	Dunham, I. et al.	Minus	27555924-27555788
	336066	Dunham, I. et al.	Minus	29241080-29240842
	336205	Dunham, I. et al.	Minus	30477456-30477311
25	336275	Dunham, I. et al.	Minus	32086675-32086536
	336292	Dunham, I. et al.	Minus	32818035-32817927
	336331	Dunham, I. et al.	Minus	33594527-33594371
	336419	Dunham, I. et al.	Minus	34052568-34052445
	336675	Dunham, I. et al.	Minus	2020758-2020664
30	336684	Dunham, I. et al.	Minus	2158060-2157993
	336716	Dunham, I. et al.	Minus	3259952-3259862
	336798	Dunham, I. et al.	Minus	5888954-5888757
	337043	Dunham, I. et al.	Minus	17407330-17407251
	337046	Dunham, I. et al.	Minus	17610892-17610821
35	337128	Dunham, I. et al.	Minus	22215251-22215034
	337192	Dunham, I. et al.	Minus	24591853-24591771
	337194	Dunham, I. et al.	Minus	24610510-24610359
	337229	Dunham, I. et al.	Minus	26716579-26716481
	337325	Dunham, I. et al.	Minus	30015948-30015800
40	337497	Dunham, I. et al.	Minus	33371317-33371258
	337500	Dunham, I. et al.	Minus	33376212-33376158
	337603	Dunham, I. et al.	Minus	1299296-1299194
	337605	Dunham, I. et al.	Minus	1346555-1346397
	337671	Dunham, I. et al.	Minus	3260634-3260547
45	337786	Dunham, I. et al.	Minus	4133203-4133081
	337862	Dunham, I. et al.	Minus	5347658-5347550
	338083	Dunham, I. et al.	Minus	9318438-9318301
	338158	Dunham, I. et al.	Minus	11794465-11794343
	338161	Dunham, I. et al.	Minus	12124716-12124658
50	338182	Dunham, I. et al.	Minus	12824919-12824827
	338189	Dunham, I. et al.	Minus	12878594-12878478
	338199	Dunham, I. et al.	Minus	13760865-13760780
	338215	Dunham, I. et al.	Minus	14055447-14055355
	338469	Dunham, I. et al.	Minus	20520387-20520242
55	338549	Dunham, I. et al.	Minus	22049171-22049081
	338561	Dunham, I. et al.	Minus	22311966-22311856
	338671	Dunham, I. et al.	Minus	24508421-24508346
	338676	Dunham, I. et al.	Minus	24637427-24637369
	338726	Dunham, I. et al.	Minus	25926206-25925618
50	338779	Dunham, I. et al.	Minus	27030151-27029795
	338871	Dunham, I. et al.	Minus	28301708-28301611
	338872	Dunham, I. et al.	Minus	28300921-28300790
	338966	Dunham, I. et al.	Minus	29614876-29614749
	339229	Dunham, I. et al.	Minus	32722330-32722199
55	339264	Dunham, I. et al.	Minus	32975145-32975053
	325228	6381940	Plus	2630-2694
	325235	6381943	Minus	162154-162264
	329588	3962484	Plus	1169-1619
	329560	3962491	Plus	2095-2990
70	329541	3983503	Minus	2765-3059
	325328	5866875	Plus	86780-86854
	325340	6017033	Minus	166656-166819
	325373	5866920	Minus	1136686-1136777
	325367	5866920	Minus	922881-922958
75	325389	5866921	Plus	239672-239759
	325436	5866939	Minus	29778-29907
	325498	5866967	Plus	173372-173930
	325471	6017034	Minus	289268-289342
	325557	6056302	Plus	50921-51050
30	325559	6249595	Minus	118590-119172
	325560	6249595	Minus	133794-133981
	325569	6249599	Plus	79927-80217
	325587	6682462	Plus	126724-126967
	325585	6682462	Plus	73476-73574
35	325597	5866992	Plus	1065020-1065089
	325639	5867002	Plus	253525-253608

	325739	5867038	Minus	205138-205269
	325740	5867038	Minus	207533-207690
	325792	6469828	Minus	1018-1176
5	325735	6552447	Minus	269122-269190
	325685	6682468	Plus	117397-117483
	325686	6682468	Plus	118337-118439
	325819	6682490	Minus	130314-130370
	329764	6048195	Minus	109733-109968
10	329703	6065793	Minus	139994-140138
	329643	6448539	Plus	53403-53537
	329816	6624888	Minus	70296-70423
	329860	6687260	Minus	163474-163605
	325883	5867087	Plus	22498-22663
15	325895	5867097	Plus	358317-358476
	325925	5867124	Plus	115749-115962
	325932	5867127	Plus	7369-7441
	325941	5867133	Minus	64228-64402
	325969	5867153	Plus	101911-102081
20	325971	5867153	Plus	105841-106035
	329993	4567166	Minus	101307-101434
	330020	6671887	Plus	172397-172491
	326163	5867168	Minus	7831-8035
	326274	5867171	Minus	410289-410404
25	326025	5867176	Plus	70854-70915
	326046	5867182	Minus	62668-62825
	326099	5867186	Minus	661381-661510
	326108	5867187	Minus	23784-23903
	326165	5867208	Minus	62787-62929
30	326189	5867212	Plus	69288-69413
	326204	5867218	Minus	148088-148200
	326230	5867230	Minus	301868-301972
	330052	4567182	Plus	352560-352963
	330036	6042048	Plus	117120-117216
35	326360	5867293	Plus	13627-13844
	326589	5867320	Plus	22760-22919
	326393	5867341	Plus	41702-41841
	326505	5867435	Minus	8818-8949
	326515	5867439	Plus	36683-36809
40	326592	6138928	Plus	23689-23828
	330107	6015249	Minus	100091-100282
	330106	6015249	Minus	99443-99778
	330100	6015253	Plus	21166-21301
	330093	6015278	Plus	1043-1199
45	330088	6015293	Plus	37517-37638
	330085	6015302	Minus	59613-59770
	330120	6671864	Minus	127553-127656
	330123	6671869	Minus	35311-35406
	326742	5867611	Minus	95187-95248
50	326605	5867637	Plus	24656-24749
	326818	6117831	Minus	15199-15309
	326720	6552456	Plus	84525-84677
	326770	6598307	Minus	513603-513668
	326692	6682502	Plus	117697-117899
55	326693	6682502	Minus	335002-335095
	326983	5867657	Minus	16023-16581
	326991	5867660	Plus	18147-18339
	326936	6004446	Minus	10217-10357
	326964	6469836	Plus	75340-75456
60	327040	6531965	Plus	783670-783817
	327053	6531965	Plus	2247267-2247437
	327075	6531965	Plus	4041318-4041431
	327085	6531965	Plus	4734947-4735069
	327036	6531965	Plus	319951-320040
65	327130	6531976	Plus	20247-22343
	327156	5866841	Minus	2462-2620
	327288	5867481	Plus	48583-48773
	327332	5867516	Minus	56361-56532
	327220	5867525	Minus	65701-65781
70	327224	5867534	Plus	188468-188544
	327321	6249562	Minus	99745-99836
	327361	6552412	Minus	61013-62130
	327396	5867743	Plus	8702-8820
	327414	5867750	Plus	102461-102586
75	327442	5867759	Plus	111483-111618
	327467	5867772	Plus	88030-88151
	327473	5867775	Plus	75101-75181
	327483	5867783	Plus	181573-181662
	327377	5867793	Minus	37610-37676
80	327562	5867804	Minus	343989-344474
	327568	5867811	Minus	46152-46287
	327606	6004463	Plus	200262-200495
	327611	5867868	Minus	175053-175392
	327642	5867891	Minus	2513-2743
85	327654	5867910	Minus	97564-97710
	327734	5867940	Minus	31003-31583

	327775	5867964	Minus	130791-130871
	327796	5867982	Plus	85267-85405
	327840	6249578	Minus	73065-73206
5	330208	6013599	Plus	66517-66931
	330263	6671884	Minus	101503-101634
	328004	5867993	Minus	157407-157887
	328101	5868020	Plus	289920-290014
	328100	5868020	Minus	263545-263635
10	328113	5868024	Minus	80378-80491
	328157	5868064	Plus	73326-73615
	328196	5868080	Minus	16551-16729
	328197	5868081	Minus	42133-42438
	327940	5868197	Minus	95240-95428
15	327984	5868216	Plus	66611-66677
	328021	5902482	Plus	713478-714590
	328068	6117819	Plus	253903-254022
	328264	6381912	Plus	55086-55404
	330300	2905862	Minus	3246-3302
20	328608	5868222	Minus	87770-87953
	328600	5868229	Minus	38889-40010
	328616	5868239	Plus	293920-294224
	328623	5868246	Minus	120020-120126
	328632	5868247	Plus	76734-76853
	328666	5868254	Minus	778-901
25	328698	5868264	Minus	625555-625633
	328700	5868264	Plus	764089-764203
	328708	5868271	Minus	68114-68854
	328735	5868289	Plus	89389-89455
30	328743	5868289	Plus	274638-274726
	328806	5868324	Plus	29408-29684
	328299	5868366	Minus	149708-149889
	328342	5868383	Plus	59955-60094
	328365	5868387	Minus	270724-270798
35	328369	5868388	Plus	75371-75583
	328381	5868392	Plus	662758-662848
	328451	5868425	Minus	217275-217336
	328481	5868449	Minus	8987-9180
	328500	5868464	Plus	59098-59481
40	328530	5868482	Plus	334973-335406
	328664	6004473	Plus	1193739-1193866
	328861	6381928	Minus	108317-108403
	328908	5868493	Plus	117002-117059
	328933	5868500	Plus	771755-771889
	328934	5868500	Plus	846342-846448
45	328949	6456765	Minus	43552-43619
	330313	6042030	Minus	33642-33775
	329005	5868542	Plus	85470-85673
	330366	2944106	Plus	151837-151914
50	330372	6580495	Minus	317461-317688
	329033	5868561	Minus	5390-5479
	329037	5868562	Minus	32466-32562
	329067	5868591	Minus	146417-147652
	329134	5868679	Plus	29959-30018
55	329157	5868687	Minus	145940-146155
	329178	5868704	Plus	179177-179463
	329192	5868716	Plus	166936-167020
	329194	5868716	Minus	304450-304559
	329204	5868720	Minus	3050-3190
60	329224	5868728	Plus	27422-27664
	329228	5868728	Minus	50118-50287
	329288	5868771	Plus	25554-26299
	329337	5868806	Minus	467155-467222
	329011	6682532	Plus	48658-48741

TABLE 9A: Potential Therapeutic, Diagnostic and Prognostic targets for Therapy of Lung Cancer

Table 9A shows about 1312 genes up-regulated in lung tumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatous and carcinoid tumors) relative to normal body tissues. These genes were selected from about 59680 probesets on the Eos/Affymetrix Hu03 Genechip array.

Table 9B show the accession numbers for those Pkey's lacking UnigenelD's for table 9A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Table 9C show the genomic positioning for those Pkey's lacking Unigene ID's and accession numbers in table 9A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Average of lung tumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatous and carcinoid tumors) divided by the average of normal lung samples
 R2: Average of non-malignant lung disease samples (including bronchitis, emphysema, fibrosis, atelectasis, asthma) divided by the average of normal lung samples

Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2
400195			NM_007057*:Homo sapiens ZW10 interactor	1.00	1.00
400205			NM_006265*:Homo sapiens RAD21 (S. pombe)	15.80	396.00
400220			Eos Control	2.28	2.84
400277			Eos Control	7.68	9.72
400285			Eos Control	1.00	1.00
400288	X06256	Hs.149609	integrin, alpha 5 (fibronectin receptor,	1.04	2.24
400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	132.45	4.00
400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	43.86	74.00
400301	X03635	Hs.1657	estrogen receptor 1	1.00	1.00
400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	1.75	1.65
400328	X87344	Hs.180062	transporter 2, ATP-binding cassette, sub	0.87	1.80
400419	AF084545		Target	156.55	253.00
400512			NM_030878*:Homo sapiens cytochrome P450,	1.00	2.00
400517	AF242388		lengsin	3.67	87.00
400560			NM_030878*:Homo sapiens cytochrome P450,	1.00	1.00
400664			NM_002425:Homo sapiens matrix metallopro	20.26	45.00
400665			NM_002425:Homo sapiens matrix metallopro	1.36	1.07
400666			NM_002425:Homo sapiens matrix metallopro	3.26	3.22
400749			NM_003105*:Homo sapiens sortilin-related	1.00	91.00
400763			Target Exon	7.63	24.00
401027			Target Exon	1.00	1.00
401093			C12000586*:gij6330167[dbj]BAA86477.1 (A	1.00	155.00
401203			Target Exon	1.00	86.00
401212			C12000457*:gij7512178[pir]T30337 polypr	1.00	400.00
401411			ENSP00000247172*:HYPOTHETICAL 126.2 kDa	1.00	72.00
401435			C14000397*:gij7499898[pir]T33295 hypo	1.00	64.00
401464	AF039241		histone deacetylase 5	3.82	49.00
401714			ENSP00000241802*:CDNA FLJ11007 FIS, CLON	2.02	40.00
401747			Homo sapiens keratin 17 (KRT17)	128.43	68.00
401760			Target Exon	1.74	35.00
401780			NM_005557*:Homo sapiens keratin 16 (foca	26.47	10.50
401781			Target Exon	10.33	4.61
401785			NM_002275*:Homo sapiens keratin 15 (KRT1	4.13	2.70
401797			Target Exon	1.44	2.10
401961			NM_021626:Homo sapiens serine carboxypep	1.41	1.86
401985	AF053004		class I cytokine receptor	1.00	177.00
401994			Target Exon	61.84	47.00
402075			ENSP00000251056*:Plasma membrane calcium	1.00	1.00
402260			NM_001436*:Homo sapiens fibrillarin (FBL	1.58	1.39
402265			Target Exon	2.09	35.00
402297			Target Exon	1.00	92.00
402408			NM_030920*:Homo sapiens hypothetical pro	28.87	13.00
402420			C1000823*:gij10432400[emb]CAC10290.1 (A	1.00	1.44
402674			Target Exon	7.44	243.00
402802			NM_001397*:Homo sapiens endothelin conver	1.00	70.00
402994			NM_002463*:Homo sapiens myxovirus (influ	1.37	1.43
403137			NM_005381*:Homo sapiens nucleolin (NCL),	1.00	19.00
403306	NM_006825		transmembrane protein (63kD), endoplasmic	1.00	43.00
403329			Target Exon	1.00	61.00
403381			ENSP00000231844*:Ecotropic virus integra	1.00	119.00
403478			NM_022342:Homo sapiens kinesin protein 9	28.13	136.00
403485			C3001813*:gij12737279[ref]XP_012163.1 k	20.23	76.00
403627			Target Exon	6.30	29.33
403715			Target Exon	1.30	35.00
404044			ENSP00000237855*:DJ398G3.2 (NOVEL PROTEI	1.00	54.00
404076			NM_016020*:Homo sapiens CGI-75 protein (14.29	91.00
404101			C8000950:gij423560[pir]A47318 RNA-bindin	1.00	1.00
404140			NM_006510:Homo sapiens ret finger protei	1.42	1.44
404165			ENSP00000244562:NRH dehydrogenase [quino	1.00	54.00
404185			Target Exon	1.00	117.00
404210			NM_005936:Homo sapiens myeloid/lymphoid	5.93	13.77
404253			NM_021058*:Homo sapiens H2B histone fami	1.00	1.00

404287			C6001909:gi704441 dbj BAA18909.1 [D298	29.71	42.00
404298			C6001238*:gi121715 sp P26697 GTA3_CHICK	1.30	1.00
404347			Target Exon	1.00	1.00
404440			NM_021048:Homo sapiens melanoma antigen,	1.00	15.00
404721			NM_005596*:Homo sapiens nuclear factor I	1.00	60.00
404794	NM_000078		cholesteryl ester transfer protein, plas	1.07	1.38
404854			Target Exon	1.61	2.01
404877			NM_005365:Homo sapiens melanoma antigen,	1.00	1.00
404927			Target Exon	1.00	1.00
404996			Target Exon	1.00	1.00
405449			CY000047*:gi11427234 ref XP_009399.1 z	1.00	1.00
405568			NM_031413*:Homo sapiens cat eye syndrome	1.00	78.00
405572			Target Exon	0.76	1.14
405646			C12000200:gi14557225 ref NP_000005.1 al	1.01	1.28
405676	BE336714		cytochrome c-1	1.13	2.89
405770			NM_002362:Homo sapiens melanoma antigen,	45.52	37.00
405932			C15000305:gi13806122 gb AAC69198.1 (AF0	1.99	1.99
406137			NM_000179*:Homo sapiens mutS (E. coli) h	2.77	2.38
406360			Target Exon	1.00	35.00
406399			NM_003122*:Homo sapiens serine protease	1.00	39.00
406467			Target Exon	1.00	1.00
406621	X57809	Hs.181125	immunoglobulin lambda locus	1.41	1.74
406642	AJ245210		gb:Homo sapiens mRNA for immunoglobulin	2.16	3.91
406663	U24683	Hs.293441	immunoglobulin heavy constant mu	2.07	2.93
406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth fa	15.00	51.00
406673	M34996	Hs.198253	major histocompatibility complex, class	0.98	3.09
406676	X58399	Hs.81221	Human L2-9 transcript of unrearranged im,	1.30	1.53
406678	U77534		gb:Human clone 1A11 immunoglobulin varia	1.33	1.45
406685	M18728		gb:Human nonspecific crossreacting antig	1.46	2.85
406687	M31126	Hs.272822	pregnancy specific beta-1-glycoprotein 9	8.61	8.50
406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	226.37	350.00
406698	X03058	Hs.73931	major histocompatibility complex, class	1.01	2.52
406815	AA833930	Hs.288036	tRNA isopentenylpyrophosphate transferas	20.25	32.00
406851	AA609784		major histocompatibility complex, class	0.75	1.91
406964	M21305		gb:Human alpha satellite and satellite 3	38.15	1114.00
406967	M24349		gb:Human parathyroid hormone-like protei	1.00	1.00
406974	M57293		gb:Human parathyroid hormone-related pep	1.00	1.00
407103	AA424881	Hs.256301	hypothetical protein MGC13170	1.77	1.10
407128	R83312	Hs.237260	EST	1.00	1.00
407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	142.70	135.00
407168	R45175	Hs.117183	ESTs	2.16	18.00
407239	AA076350	Hs.67846	leukocyte immunoglobulin-like receptor,	1.10	1.57
407242	M18728		gb:Human nonspecific crossreacting antig	1.12	2.85
407244	M10014	Hs.75431	fibrinogen, gamma polypeptide	3.24	15.38
407289	AA135159	Hs.203349	Homo sapiens cDNA FLJ12149 fis, clone MA	3.53	3.68
407300	AA102616	Hs.120769	gb:zn43e07.s1 Stratagene HeLa cell s3 93	19.74	73.00
407366	AF026942	Hs.271530	gb:Homo sapiens cig33 mRNA, partial sequ	0.06	8.25
407378	AA29264	Hs.57776	ESTs, Moderately similar to I38022 hypot	1.00	26.00
407430	AF169351		gb:Homo sapiens protein tyrosine phospho	1.00	25.00
407453	AJ132087		gb:Homo sapiens mRNA for axonemal dynein	1.00	75.00
407577	AW131324	Hs.246759	hypothetical protein MGC12538	1.00	1.00
407634	AW016569	Hs.136414	UDP-GlcNAc:betaGal beta-1,3-N-acetylgluc	111.20	228.00
407710	AW022727	Hs.23616	ESTs	1.00	28.00
407720	AB037776	Hs.38002	KIAA1355 protein	1.89	1.31
407746	AK001962		hypothetical protein FLJ11100	1.00	1.00
407756	AA116021	Hs.38260	ubiquitin specific protease 18	4.51	5.00
407758	D50915	Hs.38365	KIAA0125 gene product	1.00	28.00
407782	AA608956	Hs.112619	ESTs, Moderately similar to PURKINJE CEL	0.97	1.14
407788	BE514982	Hs.38991	S100 calcium-binding protein A2	7.88	3.83
407790	AJ027274	Hs.288941	Homo sapiens cDNA FLJ14866 fis, clone PL	3.63	42.00
407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	89.96	109.00
407839	AA045144	Hs.161566	ESTs	173.91	108.00
407944	R34008	Hs.239727	desmocollin 2	111.30	70.00
408000	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	151.17	8.00
408031	AA081395	Hs.42173	Homo sapiens cDNA FLJ10366 fis, clone NT	9.91	93.00
408063	BE086548	Hs.42346	calcineurin-binding protein calcarsin-1	195.78	231.00
408070	AW148852		gb:xf05d05.x1 NCI_CGAP_Bm35 Homo sapien	1.00	1.00
408101	AW968504	Hs.123073	CDC2-related protein kinase 7	37.84	61.00
408122	AI432652	Hs.42824	hypothetical protein FLJ10718	0.85	1.71
408212	AA297567	Hs.43728	hypothetical protein	5.88	7.91
408243	Y00787	Hs.624	interleukin 8	4.27	9.98
408349	BE546947	Hs.44276	homeo box C10	3.79	3.46
408353	BE439838	Hs.44298	mitochondrial ribosomal protein S17	1.88	1.65
408354	AI382803	Hs.159235	ESTs	1.00	73.00
408369	R38438	Hs.182575	solute carrier family 15 (H7??) transport	1.41	16.50
408380	AF123050	Hs.44532	diubiquitin	15.19	37.22
408482	NM_000676	Hs.45743	adenosine A2b receptor	1.65	1.19
408522	AI541214	Hs.46320	Small proline-rich protein SPRK (human,	1.98	1.24
408536	AW381532	Hs.135188	ESTs	1.55	1.50
408545	AW235405	Hs.253690	ESTs	1.00	1.00
408572	AA055611	Hs.226568	ESTs, Moderately similar to ALU4_HUMAN A	1.00	44.00
408633	AW963372	Hs.46677	PRO2000 protein	107.16	56.00
408660	AA525775		ESTs, Moderately similar to PC4259 ferri	1.00	1.00
408761	AA057264	Hs.238936	ESTs, Weakly similar to (define not ava	52.24	141.00
408771	AW732573	Hs.47584	potassium voltage-gated channel, delayed	3.05	109.00

	408783	AF192522	Hs.47701	NPC1 (Niemann-Pick disease, type C1, gen	1.02	1.07
	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	41.19	61.00
	408805	H69912	Hs.48269	vaccinia related kinase 1	24.67	45.00
5	408841	AW438865	Hs.256862	ESTs	1.00	58.00
	408873	AL046017	Hs.182278	calmodulin 2 (phosphorylase kinase, del	1.00	89.00
	408908	BE296227	Hs.250822	serine/threonine kinase 15	7.76	1.00
	408992	AA059325	Hs.71642	guanine nucleotide binding protein (G pr	1.00	1.00
	408996	AI979168	Hs.344096	glycoprotein (transmembrane) nmb	3.71	5.50
10	409015	BE389387	Hs.49767	NM_004553:Homo sapiens NADH dehydrogenas	1.44	1.24
	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	4.28	5.32
	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	112.42	195.00
	409077	AA401369	Hs.190721	ESTs	1.00	17.00
	409093	BE243834	Hs.50441	CGI-04 protein	2.02	1.93
	409103	AF251237	Hs.112208	XAGE-1 protein	80.44	40.00
15	409142	AL136877	Hs.50758	SMC4 (structural maintenance of chromoso	14.87	6.00
	409187	AF154830	Hs.50966	carbamoyl-phosphate synthetase 1, mitoch	1.00	1.00
	409228	AI654298	Hs.271695	ESTs, Weakly similar to 2109260A B cell	1.22	1.00
	409234	AI879419	Hs.27206	ESTs	1.00	1.00
20	409268	AA625304	Hs.187579	ESTs	11.90	23.00
	409269	AA576953	Hs.22972	hypothetical protein FLJ13352	1.00	1.00
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	168.91	35.00
	409404	BE220053	Hs.129056	ESTs	1.00	1.00
	409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini	79.74	96.00
25	409430	R21945	Hs.346735	splicing factor, arginine/serine-rich 5	1.45	2.10
	409446	AI561173	Hs.67688	ESTs	1.00	4.00
	409506	NM_006153	Hs.54589	NCK adaptor protein 1	3.97	28.00
	409522	AA075382		gb:zm87b03.s1 Stratagene ovarian cancer	15.98	141.00
	409582	AA401369	Hs.190721	ESTs	1.00	17.00
30	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	292.12	79.00
	409705	M37762	Hs.56023	brain-derived neurotrophic factor	1.00	82.00
	409719	AI769160	Hs.108681	Homo sapiens brain tumor associated prot	1.00	1.00
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	0.12	18.12
	409744	AW675258	Hs.56265	Homo sapiens mRNA; cDNA DKFZp586P2321 (f	20.75	51.00
35	409757	NM_001898	Hs.123114	cystatin SN	22.46	15.80
	409866	AW502152		gb:UI-HF-BR0p-ajr-f-11-0-UI.r1 NIH_MGC_5	1.00	1.00
	409893	AW247090	Hs.57101	minichromosome maintenance deficient (S.	1.50	1.09
	409902	AI337658	Hs.156351	ESTs	25.92	50.00
	409935	AW511413	Hs.278025	ESTs	2.63	2.11
40	409956	AW103364	Hs.727	inhibin, beta A (activin A, activin AB a	2.17	4.01
	409958	NM_001523	Hs.57697	hyaluronan synthase 1	0.91	2.07
	410001	AB041036	Hs.57771	kallikrein 11	1.04	2.28
	410032	BE065985		gb:RC3-BT0319-120200-014-a09 BT0319 Homo	1.00	58.00
	410037	AB020725	Hs.58009	KIAA0918 protein	1.00	34.00
45	410044	BE566742	Hs.58169	highly expressed in cancer, rich in leuc	1.00	1.00
	410048	W76467	Hs.58218	proline oxidase homolog	1.03	1.44
	410076	T05387	Hs.7991	ESTs	1.12	1.50
	410102	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	9.89	1.00
	410153	BE311926	Hs.15830	hypothetical protein FLJ12691	1.00	1.00
50	410166	AK001376	Hs.59346	hypothetical protein FLJ10514	1.00	1.00
	410193	AJ132592	Hs.59757	zinc finger protein 281	42.01	51.00
	410274	AA381807	Hs.61762	hypoxia-inducible protein 2	1.72	1.32
	410309	BE043077	Hs.278153	ESTs	1.00	2.00
	410340	AW182833	Hs.112188	hypothetical protein FLJ13149	32.08	75.00
55	410348	AW182663	Hs.95469	ESTs	1.00	1.00
	410407	X66839	Hs.63287	carbonic anhydrase IX	1.40	1.11
	410418	D31382	Hs.63325	transmembrane protease, serine 4	4.30	2.03
	410438	AB037756	Hs.45207	hypothetical protein KIAA1335	1.00	18.00
	410553	AW016824	Hs.255527	hypothetical protein MGC14128	1.34	1.04
60	410555	W27235	Hs.64311	a disintegrin and metalloproteinase doma	23.99	1.41
	410561	BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	10.04	1.00
	410681	AW246890	Hs.65425	calbindin 1, (28kD)	10.88	18.92
	410781	AI375672	Hs.165028	ESTs	1.00	57.00
	411027	AF072099	Hs.67846	leukocyte immunoglobulin-like receptor,	1.62	3.78
65	411074	X60435	Hs.68137	adenylate cyclase activating polypeptide	1.00	1.15
	411089	AA456454		cell division cycle 2-like 1 (PITSLRE pr	1.56	1.58
	411152	BE069199		gb:QV3-BT0379-010300-105-g03 BT0379 Homo	1.00	84.00
	411248	AA551538	Hs.334605	Homo sapiens cDNA FLJ14408 fis, clone HE	1.82	1.45
	411252	AB018549	Hs.69328	MD-2 protein	7.32	12.74
70	411263	BE297802	Hs.69360	kinesin-like 6 (mitotic centromere-assoc	3.44	2.55
	411365	M76477	Hs.289082	GM2 ganglioside activator protein	1.35	2.02
	411402	BE297855	Hs.69855	NRAS-related gene	1.00	46.00
	411573	AB029000	Hs.70823	KIAA1077 protein	11.40	11.35
	411579	AC005258	Hs.70830	U6 snRNA-associated Sm-like protein LSm7	1.08	1.90
75	411617	AA247994	Hs.90063	neurocalcin delta	1.74	2.57
	411732	AA059325	Hs.71642	guanine nucleotide binding protein (G pr	1.02	1.00
	411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	1.34	2.19
	411789	AF245505	Hs.72157	Adilcan	2.19	2.79
	411800	N39342	Hs.103042	microtubule-associated protein 1B	23.34	34.00
80	411945	AL033527	Hs.92137	v-myc avian myelocytomatosis viral oncog	1.00	8.00
	412115	AK001763	Hs.73239	hypothetical protein FLJ10901	2.07	1.64
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkinas	118.48	92.00
	412276	BE262621	Hs.73798	macrophage migration inhibitory factor (1.98	1.98
	412464	T78141	Hs.22826	ESTs, Weakly similar to I55214 salivary	1.16	1.34
	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	41.52	84.00
85	412537	AL031778		nuclear transcription factor Y, alpha	17.90	55.00

	412659	AW753865	Hs.74376	olfactomedin related ER localized protei	14.65	47.00
	412719	AW016610	Hs.816	ESTs	382.46	128.00
	412723	AA648459	Hs.335951	hypothetical protein AF301222	54.90	1.00
5	412811	H06382		ESTs	1.00	11.00
	412817	AL037159	Hs.74619	proteasome (prosome, macropain) 26S subu	1.63	1.42
	412863	AA121673	Hs.59757	zinc finger protein 281	17.63	56.00
	412924	BE018422	Hs.75258	H2A histone family, member Y	1.00	22.00
	413004	T35901	Hs.75117	interleukin enhancer binding factor 2, 4	2.19	2.05
10	413011	AW068115	Hs.821	biglycan	1.22	1.88
	413048	M93221	Hs.75182	mannose receptor, C type 1	0.30	6.23
	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	3.43	8.71
	413129	AF292100	Hs.104613	RP42 homolog	4.67	4.77
	413142	M81740	Hs.75212	ornithine decarboxylase 1	1.92	2.59
15	413223	AI732182	Hs.191866	ESTs	5.73	27.00
	413248	T64858	Hs.21433	hypothetical protein DKFZp547J036	0.99	1.06
	413273	U75679	Hs.75257	stem-loop (histone) binding protein	1.00	18.00
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	1.10	1.09
	413281	AA861271	Hs.222024	transcription factor BMAL2	95.94	69.00
20	413364	BE536218	Hs.137516	fidgetin-like 1	1.00	1.00
	413385	M34455	Hs.840	indoleamine-pyrrole 2,3 dioxygenase	0.95	2.09
	413409	AI638418	Hs.1440	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	1.00	1.00
	413453	AA129640	Hs.128065	ESTs	1.00	31.00
	413527	BE250788	Hs.179882	hypothetical protein FLJ12443	1.08	1.45
25	413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	79.15	114.00
	413573	AI733859	Hs.149089	ESTs	1.00	1.00
	413582	AW295647	Hs.71331	hypothetical protein MGC5350	8.80	10.00
	413597	AW302885	Hs.117183	ESTs	1.00	1.00
	413690	BE157489		gb:RC1-HT0375-120200-011-e06 HT0375 Homo	1.00	1.00
30	413691	AB023173	Hs.75478	ATPase, Class VI, type 11B	3.16	2.32
	413719	BE439580	Hs.75498	small inducible cytokine subfamily A (Cy	2.88	9.52
	413753	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin	144.10	108.00
	413801	M62246	Hs.35406	ESTs, Highly similar to unnamed protein	1.00	17.00
	413833	Z15005	Hs.75573	centromere protein E (312kD)	1.00	1.00
35	413882	AA132973	Hs.184492	ESTs	64.24	148.00
	413926	AA133338	Hs.54310	ESTs	1.00	67.00
	413943	AW294416	Hs.144687	Homo sapiens cDNA FLJ12981 fis, clone NT	43.42	42.00
	413995	BE048146	Hs.75671	syntaxin 1A (brain)	1.23	1.11
	414035	Y00630	Hs.75716	serine (or cysteine) proteinase inhibito	2.02	2.51
40	414142	AW368397	Hs.334485	Homo sapiens cDNA FLJ14438 fis, clone HE	1.00	102.00
	414180	AI863304	Hs.120905	Homo sapiens cDNA FLJ11448 fis, clone HE	6.92	77.00
	414245	BE148072	Hs.75850	WAS protein family, member 1	1.00	1.00
	414275	AW970254	Hs.889	Charot-Leyden crystal protein	1.00	59.00
	414317	BE263280	Hs.75888	phosphogluconate dehydrogenase	1.52	1.73
45	414334	AA824298	Hs.21331	hypothetical protein FLJ10036	1.78	1.72
	414341	D80004	Hs.75909	KIAA0182 protein	33.90	151.00
	414368	W70171	Hs.75939	uridine monophosphate kinase	171.60	97.00
	414416	AW409985	Hs.76084	hypothetical protein MGC2721	2.32	1.85
	414430	AI346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1	226.15	66.00
50	414570	Y00285	Hs.76473	insulin-like growth factor 2 receptor	1.64	1.98
	414618	AI204600	Hs.96978	hypothetical protein MGC10764	1.87	72.00
	414675	R79015	Hs.296281	interleukin enhancer binding factor 1	1.51	1.39
	414683	S78296	Hs.76888	hypothetical protein MGC12702	43.61	64.00
	414696	AF002020	Hs.76918	Niemann-Pick disease, type C1	28.63	71.00
55	414711	AI310440	Hs.288735	Homo sapiens cDNA FLJ13522 fis, clone PL	14.86	42.00
	414718	H95348	Hs.107987	ESTs	1.00	5.00
	414732	AW410976	Hs.77152	minichromosome maintenance deficient (S.	1.64	1.44
	414747	U30872	Hs.77204	centromere protein F (350/400kD, mitosis	65.01	74.00
	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	130.35	121.00
60	414774	X02419	Hs.77274	plasminogen activator, urokinase	2.24	2.19
	414806	D14694	Hs.77329	phosphatidylserine synthase 1	1.63	1.53
	414809	AI434699	Hs.77356	transferrin receptor (p90, CD71)	1.97	2.60
	414812	X72755	Hs.77367	monokine induced by gamma interferon	3.48	10.60
	414825	X06370	Hs.77432	epidermal growth factor receptor (avian	103.22	143.00
65	414839	X63692	Hs.77462	DNA (cytosine-5)-methyltransferase 1	1.80	1.69
	414883	AA926960		CDC28 protein kinase 1	14.29	10.06
	414907	X90725	Hs.77597	polo (Drosophila)-like kinase	1.95	2.20
	414914	U49844	Hs.77613	ataxia telangiectasia and Rad3 related	3.00	2.90
	414945	BE076358	Hs.77667	lymphocyte antigen 6 complex, locus E	1.02	1.21
70	414972	BE263782	Hs.77695	KIAA0008 gene product	1.00	1.00
	415014	AW954064	Hs.24951	ESTs	1.42	2.84
	415091	AL044872	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	1.00	30.00
	415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	34.72	107.00
75	415227	AW821113	Hs.72402	ESTs	1.87	49.00
	415238	R37780	Hs.21422	ESTs	1.00	1.00
	415263	AA948033	Hs.130853	ESTs	1.00	1.00
	415295	R41450	Hs.6546	ESTs	1.00	1.00
	415339	NM_015156	Hs.78398	KIAA0071 protein	51.18	166.00
	415669	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibito	30.84	63.00
80	415674	BE394784	Hs.78596	proteasome (prosome, macropain) subunit,	1.48	1.39
	415709	AA649850	Hs.278558	ESTs	1.00	1.00
	415735	AA704162	Hs.120811	ESTs, Weakly similar to I38022 hypothesi	1.00	72.00
	415799	AA653718	Hs.225841	DKFZP434D193 protein	6.23	31.00
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	24.30	1.00
85	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	32.51	35.00
	415989	AI267700		ESTs	78.89	1.00

	416018	AW138239	Hs.78977	proprotein convertase subtilisin/kexin 1	1.00	1.00
	416065	BE267931	Hs.78996	proliferating cell nuclear antigen	3.35	2.32
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (39.03	3.00
5	416177	AA174069	Hs.187607	ESTs	1.00	9.00
	416178	AI808527	Hs.192822	serologically defined breast cancer anti	3.83	3.76
	416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	3.67	1.00
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	9.70	1.00
	416239	AL038450	Hs.48948	ESTs	83.87	129.00
10	416250	AA581386	Hs.73452	hypothetical protein MGC10791	1.96	2.12
	416322	BE019494	Hs.79217	pyrroline-5-carboxylate reductase 1	2.08	1.73
	416423	H54375	Hs.268921	ESTs	1.00	89.00
	416448	L13210	Hs.79339	lectin, galactoside-binding, soluble, 3	1.28	1.54
	416498	U33632	Hs.79351	potassium channel, subfamily K, member 1	27.29	67.00
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	53.29	51.00
15	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	9.96	5.00
	416722	AA354604	Hs.122546	hypothetical protein FLJ23017	3.68	33.00
	416819	U77735	Hs.80205	pim-2 oncogene	1.59	1.84
	416936	N21352	Hs.42987	ESTs, Weakly similar to S21348 probable	1.00	1.00
	417034	NM_006183	Hs.80962	neurotensin	1.00	1.00
20	417061	AI675944	Hs.188691	Homo sapiens cDNA FLJ12033 fis, clone HE	32.95	156.00
	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	3.91	4.93
	417218	AA129547	Hs.285754	mel proto-oncogene (hepatocyte growth fa	1.00	51.00
	417233	W25005	Hs.24395	small inducible cytokine subfamily B (Cy	3.38	2.05
	417308	H60720	Hs.81892	KIAA0101 gene product	82.94	25.36
25	417315	AI080042	Hs.180450	ribosomal protein S24	106.61	121.00
	417324	AW265494		ESTs	1.20	1.28
	417366	BE185289	Hs.1076	small proline-rich protein 18 (cornifin)	8.97	3.27
	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor	2.59	1.82
30	417428	N87579	Hs.278871	gb:LL2030F Human fetal heart, Lambda ZAP	1.00	52.00
	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	304.75	173.00
	417466	AI681547	Hs.59457	hypothetical protein FLJ22127	1.24	1.34
	417512	AI979168	Hs.344096	glycoprotein (transmembrane) nmb	2.14	5.50
	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	2.66	1.68
35	417542	J04129	Hs.82269	progestagen-associated endometrial prote	1.28	1.35
	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	42.76	51.00
	417715	AW969587	Hs.86366	ESTs	6.35	2.75
	417720	AA205625	Hs.208067	ESTs	113.31	56.00
	417791	AW965339	Hs.111471	ESTs	39.98	16.00
40	417830	AW504786	Hs.122579	hypothetical protein FLJ10461	2.61	31.00
	417866	AW067903	Hs.82772	collagen, type XI, alpha 1	2.35	2.44
	417900	BE250127	Hs.82906	CDC20 (cell division cycle 20, S. cerevi	1.52	1.11
	417933	X02308	Hs.82962	thymidylate synthetase	4.74	2.55
	417944	AU077196	Hs.82985	collagen, type V, alpha 2	3.61	5.21
	417975	AA641836	Hs.30085	hypothetical protein FLJ23186	12.49	38.00
45	417991	AA731452	Hs.190008	ESTs	1.00	26.00
	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	3.02	2.12
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	187.59	1.00
	418054	NM_002318	Hs.83354	lysyl oxidase-like 2	2.85	2.63
50	418057	NM_012151	Hs.83363	coagulation factor VIII-associated (intr	1.54	1.69
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	6.82	5.22
	418140	BE613836	Hs.83551	microfibrillar-associated protein 2	1.26	1.46
	418203	X54942	Hs.83758	CDC28 protein kinase 2	134.19	144.00
	418207	C14685	Hs.34772	ESTs	1.00	1.00
55	418216	AA662240	Hs.283099	AF15q14 protein	64.66	61.00
	418236	AW994005	Hs.337534	ESTs	18.53	147.00
	418249	H89226	Hs.34892	KIAA1323 protein	30.53	106.00
	418281	U09550	Hs.1154	oviductal glycoprotein 1, 120kD (mucin 9	1.00	3.00
	418283	S79895	Hs.83942	calhepsin K (pseudodysostosis)	3.96	5.16
60	418300	AI433074	Hs.86682	Homo sapiens cDNA: FLJ21578 fis, clone C	3.18	2.91
	418322	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	11.96	6.68
	418327	U70370	Hs.84136	paired-like homeodomain transcription fa	9.23	2.22
	418345	AJ001696	Hs.241407	serine (or cysteine) proteinase inhibito	1.00	1.00
	418379	AA218940	Hs.137516	fidgulin-like 1	21.68	44.00
65	418397	NM_001269	Hs.84746	chromosome condensation 1	1.00	8.00
	418403	D86978	Hs.84790	KIAA0225 protein	16.91	18.98
	418462	BE001596	Hs.85266	integrin, beta 4	1.56	1.16
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	3.22	2.38
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	2.66	2.22
70	418526	BE019020	Hs.85838	solute carrier family 16 (monocarboxylic	2.04	2.21
	418538	BE244323	Hs.85951	exportin, tRNA (nuclear export receptor	1.33	37.00
	418543	NM_005329	Hs.85962	hyaluronan synthase 3	1.04	1.23
	418574	N28754		M-phase phosphoprotein 9	48.60	85.00
	418592	X99226	Hs.284153	Fanconi anemia, complementation group A	18.24	26.00
75	418641	BE243136	Hs.86947	a disintegrin and metalloproteinase doma	1.19	1.41
	418661	NM_001949	Hs.1189	E2F transcription factor 3	29.05	43.00
	418663	AK001100	Hs.41690	desmocollin 3	112.17	19.00
	418678	NM_001327	Hs.87225	cancer/testis antigen	1.18	1.10
	418686	Z36830	Hs.87268	annexin A8	1.54	1.98
80	418689	AI360883	Hs.274448	hypothetical protein FLJ11029	1.19	1.04
	418712	Z42183		gb:HSC0BF041 normalized infant brain cDN	1.00	12.00
	418727	AA227609	Hs.94834	ESTs	1.00	49.00
	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	49.85	1.00
	418819	AA228776	Hs.191721	ESTs	1.00	140.00
	418830	BE513731	Hs.88959	hypothetical protein MGC4816	20.97	23.00
85	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	57.09	35.00

	418971	AA360392	Hs.87113	ESTs	1.00	12.00
	418973	AA233056	Hs.191518	ESTs	4.89	28.00
	419078	M93119	Hs.89584	insulinoma-associated 1	1.00	10.00
5	419079	AW014836	Hs.18844	ESTs	1.09	1.98
	419080	AW150835	Hs.18878	hypothetical protein FLJ21620	2.06	1.68
	419088	AI538323	Hs.52620	integrin, beta 8	15.60	51.00
	419092	J05581	Hs.89603	mucin 1, transmembrane	1.11	1.83
	419121	AA374372	Hs.89626	parathyroid hormone-like hormone	1.00	1.00
10	419171	NM_002846	Hs.89655	protein tyrosine phosphatase, receptor I	1.10	1.14
	419183	U60689	Hs.89663	cytochrome P450, subfamily XXIV (vitamin	1.00	1.00
	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	3.18	2.43
	419288	AA256105	Hs.87507	ESTs	1.00	34.00
	419335	AW960146	Hs.284137	hypothetical protein FLJ12888	1.00	8.00
15	419354	M62839	Hs.1252	apolipoprotein H (beta-2-glycoprotein I)	22.63	54.00
	419359	AL043202	Hs.90073	chromosome segregation 1 (yeast homolog)	2.50	1.98
	419423	D26488	Hs.90315	KIAA0007 protein	1.00	7.00
	419443	D62703		gb:HUM316G10B Clontech human aorta polyA	1.00	12.00
	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	1.64	1.84
20	419474	AW968619	Hs.155849	ESTs	13.63	62.00
	419485	AA489023	Hs.99807	ESTs, Weakly similar to unnamed protein	4.27	2.26
	419488	AA316241	Hs.90691	nucleophosmin/nucleoplasmin 3	3.66	3.63
	419502	AU076704		fibrinogen, A alpha polypeptide	13.05	115.00
	419539	AF070590	Hs.90869	Homo sapiens clones 24622 and 24623 mRNA	74.60	117.00
25	419556	U29615	Hs.91093	chitinase 1 (chitotriosidase)	1.47	4.98
	419569	AI971651	Hs.91143	jagged 1 (Alagille syndrome)	1.00	4.00
	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	94.30	94.00
	419703	AI793257	Hs.128151	ESTs	15.26	50.00
	419721	NM_001650	Hs.288650	aquaporin 4	1.00	191.00
30	419729	AA588442	Hs.21411	gb:nc53a03.s1 NCI_CGAP_SS1 Homo sapiens	1.00	59.00
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	2.02	1.08
	419745	AF042001	Hs.93005	slug (chicken homolog), zinc finger prot	1.00	1.00
	419752	AA249573	Hs.152618	ESTs, Moderately similar to ZN91_HUMAN Z	29.87	77.00
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	50.99	214.00
35	419936	AI792788		gb:cl91d05.y5 NCI_CGAP_Kid5 Homo sapiens	1.00	1.00
	419937	AB040959	Hs.93836	DKFZP434N014 protein	1.64	2.47
	419983	W55956	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (f	15.72	94.00
	420005	AW271106	Hs.133294	ESTs	3.15	1.43
	420047	AI478658	Hs.94631	brefeldin A-inhibited guanine nucleotide	12.45	39.00
40	420058	AK001423	Hs.94694	Homo sapiens cDNA FLJ10561 fis, clone NT	1.00	117.00
	420162	BE378432	Hs.95577	cyclin-dependent kinase 4	1.43	1.21
	420251	AW374968	Hs.348112	Human DNA sequence from clone RP5-1103G7	2.35	3.23
	420259	AF004884	Hs.96253	calcium channel, voltage-dependent, P/Q	0.77	1.15
	420281	AI623693	Hs.323494	ESTs	45.04	54.00
45	420309	AW043637	Hs.21766	ESTs, Weakly similar to ALU5_HUMAN ALU S	49.22	31.00
	420332	NM_001756	Hs.1305	serine (or cysteine) proteinase inhibito	0.05	2.82
	420380	AA640891	Hs.102406	ESTs	0.99	2.74
	420462	AF050147	Hs.97932	chondromodulin I precursor	1.00	1.00
	420520	AK001978	Hs.98510	similar to rab11-binding protein	49.74	133.00
50	420552	AK000492	Hs.98806	hypothetical protein	94.65	88.00
	420560	AW207748	Hs.59115	ESTs	1.00	17.00
	420610	AI683183	Hs.99348	distal-less homeo box 5	1.00	13.00
	420689	H79979	Hs.88678	ESTs	50.09	95.00
55	420721	AA927802	Hs.159471	ZAP3 protein	1.00	31.00
	420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	1.00	48.00
	420783	AI659838	Hs.99923	lectin, galactoside-binding, soluble, 7	3.04	1.25
	420900	AL045633	Hs.44269	ESTs	2.24	7.00
	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	1.00	8.00
	421002	AF116030	Hs.100932	transcription factor 17	1.00	27.00
60	421027	AA761198	Hs.55254	ESTs	2.87	38.00
	421037	AI684808	Hs.197653	ESTs	1.00	46.00
	421041	N36914	Hs.14691	ESTs, Moderately similar to I38022 hypot	1.00	98.00
	421073	NM_004689	Hs.101448	metastasis associated 1	1.34	1.46
	421110	AJ250717	Hs.1355	cathepsin E	119.47	427.00
65	421133	AA401369	Hs.190721	ESTs	1.10	17.00
	421150	AI913562	Hs.189902	ESTs	1.45	1.63
	421155	H87879	Hs.102267	lysyl oxidase	1.00	15.00
	421307	BE539976	Hs.103305	Homo sapiens mRNA; cDNA DKFZp434B0425 (f	1.37	1.10
	421316	AA287203	Hs.324728	SMA5	1.00	21.00
70	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	1.92	3.94
	421451	AA291377	Hs.50831	ESTs	5.89	14.00
	421474	U76362	Hs.104637	solute carrier family 1 (glutamate trans	1.46	1.76
	421506	BE302796	Hs.105097	thymidine kinase 1, soluble	1.56	1.08
	421508	NM_004833	Hs.105115	absent in melanoma 2	5.11	5.23
75	421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase I, I	1.00	3.00
	421524	AA312082	Hs.105445	GDNF family receptor alpha 1	2.63	10.58
	421526	AL080121	Hs.105460	DKFZP564O0823 protein	1.46	1.88
	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	30.21	50.32
	421574	AJ000152	Hs.105924	defensin, beta 2	1.67	1.74
80	421582	AI910275		trefoil factor 1 (breast cancer, estroge	1.23	1.00
	421633	AF121860	Hs.106260	sorting nexin 10	1.00	116.00
	421659	NM_014459	Hs.106511	protocadherin 17	0.05	6.33
	421677	H64092	Hs.38282	ESTs	1.31	1.42
	421753	BE314828	Hs.107911	ATP-binding cassette, sub-family B (MDR/	1.41	1.20
85	421773	W69233	Hs.112457	ESTs	1.12	1.14
	421777	BE562088	Hs.108196	HSPC037 protein	1.97	1.29

	421800	AA298151	Hs.222969	ESTs	1.03	1.30
	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	1.88	1.59
	421896	N62293	Hs.45107	ESTs	11.84	22.80
5	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	45.89	90.00
	421931	NM_000814	Hs.1440	gamma-aminobutyric acid (GABA) A recepto	1.13	1.49
	421948	L42583	Hs.334309	keratin 6A	51.83	20.25
	421975	AW961017	Hs.6459	hypothetical protein FLJ11856	1.17	1.15
	422026	U80736	Hs.110826	trinucleotide repeat containing 9	1.00	52.00
10	422094	AF129535	Hs.272027	F-box only protein 5	67.61	62.00
	422095	AI868872	Hs.282804	hypothetical protein FLJ22704	4.37	2.34
	422109	S73265	Hs.1473	gastrin-releasing peptide	4.18	95.50
	422128	AW881145		gb:QV0-OT0033-010400-182-a07 OT0033 Homo	40.89	71.00
	422129	AU076635	Hs.1478	serine (or cysteine) proteinase inhibito	1.13	1.38
	422134	AW179019	Hs.112110	mitochondrial ribosomal protein L42	41.59	96.00
15	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	2.37	1.10
	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias	3.29	1.68
	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	4.93	5.73
	422282	AF019225	Hs.114309	apolipoprotein L	1.49	1.71
20	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	25.99	10.91
	422310	AA316622	Hs.98370	cytochrome P450, subfamily IIS, polypept	1.54	1.41
	422311	AF073515	Hs.114948	cytokine receptor-like factor 1	1.15	1.78
	422330	D30783	Hs.115263	epiregulin	1.00	112.00
	422364	AF067800	Hs.115515	C-type (calcium dependent, carbohydrate-	9.39	60.00
25	422406	AF025441	Hs.116206	Opa-interacting protein 5	18.33	53.00
	422424	AJ186431	Hs.296638	prostate differentiation factor	1.71	3.21
	422440	NM_004812	Hs.116724	aldo-keto reductase family 1, member B10	47.53	32.00
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	73.68	35.54
	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	173.97	26.00
	422515	AW500470	Hs.117950	multifunctional polypeptide similar to S	4.68	2.92
30	422656	AJ870435	Hs.1569	LIM homeobox protein 2	1.00	1.00
	422737	M26939	Hs.119571	collagen, type III, alpha 1 (Ehlers-Danl	3.89	4.55
	422756	AA441787	Hs.119689	glycoprotein hormones, alpha polypeptide	1.05	1.46
	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	3.88	1.53
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	99.56	53.00
35	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	1.69	3.17
	422938	NM_001809	Hs.1594	centromere protein A (17kD)	70.46	61.00
	422956	BE545072	Hs.122579	ECT2 protein (Epithelial cell transformi	77.74	3.00
	422960	AW890487	Hs.63984	cadherin 13, H-cadherin (heart)	5.88	8.55
	422963	AA401369	Hs.190721	ESTs	171.41	17.00
40	422976	AU076657	Hs.1600	chaperonin containing TCP1, subunit 5 (e	2.12	1.62
	422981	AF026445	Hs.122752	TATA box binding protein (TBP)-associate	10.49	35.00
	422986	AA319777	Hs.221974	ESTs	12.40	32.47
	423034	AL119930		gb:DKFZp761A092_r1 761 (synonym: hamy2)	16.41	60.00
	423049	X59373	Hs.188023	ESTs, Moderately similar to HXDA_HUMAN H	1.00	1.00
45	423081	AF262992	Hs.123159	sperm associated antigen 4	1.82	2.96
	423184	NM_004428	Hs.1624	ephrin-A1	1.14	1.53
	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	2.14	1.69
	423248	AA380177	Hs.125845	ribulose-5-phosphate-3-epimerase	7.18	14.00
	423309	BE006775	Hs.126782	sushi-repeat protein	21.90	64.00
50	423361	AW170055	Hs.47628	ESTs	1.00	1.00
	423453	AW450737	Hs.128791	CGI-09 protein	55.52	66.00
	423511	AF036329	Hs.129715	gonadotropin-releasing hormone 2	0.88	1.17
	423516	AB007933	Hs.129729	ligand of neuronal nitric oxide synthase	1.76	5.40
	423551	AA327598	Hs.233785	ESTs	3.54	4.33
55	423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	1.00	50.00
	423575	C18863	Hs.163443	Homo sapiens cDNA FLJ11576 fis, clone HE	38.88	70.00
	423624	AI807408	Hs.166368	ESTs	1.00	67.00
	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	76.02	1.00
60	423642	AW452650	Hs.157148	hypothetical protein MGC13204	19.14	58.00
	423662	AA642452	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro	3.61	13.57
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	240.73	40.00
	423698	AA329796	Hs.1098	DKFZp434J1813 protein	1.00	59.00
	423725	AJ403108	Hs.132127	hypothetical protein LOC57822	4.20	1.00
	423761	NM_006194	Hs.132576	paired box gene 9	1.00	1.00
65	423787	AJ295745	Hs.236204	nuclear pore complex protein	7.18	6.64
	423816	AF151064		hypothetical protein	1.00	44.00
	423826	U20325	Hs.1707	cocaine- and amphetamine-regulated trans	1.00	1.00
	423849	AL157425	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (f	1.00	1.00
70	423887	AL080207	Hs.134585	DKFZP434G232 protein	1.00	1.00
	423934	U89995	Hs.159234	forkhead box E1 (thyroid transcription f	31.33	31.00
	423954	AW753164	Hs.288604	KIAA1632 protein	5.81	10.87
	423961	D13666	Hs.136348	osteoblast specific factor 2 (fasciclin	3.55	3.30
	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	233.42	68.00
75	424016	AW163729	Hs.6140	hypothetical protein MGC15730	0.93	1.01
	424028	AF055084	Hs.153692	Homo sapiens cDNA FLJ14354 fis, clone Y7	21.30	52.00
	424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibito	1.00	1.00
	424086	AI351010	Hs.102267	lysyl oxidase	21.91	70.00
	424098	AF077374	Hs.139322	small proline-rich protein 3	137.82	54.00
	424120	T80579	Hs.290270	ESTs	1.00	1.00
80	424165	AW582904	Hs.142255	islet amyloid polypeptide	1.00	34.00
	424200	AA337221		gb:EST41944 Endometrial tumor Homo sapie	13.06	48.00
	424279	L29306	Hs.171814	tryptophan hydroxylase (tryptophan 5-mon	1.00	1.00
	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	164.58	87.00
	424326	NM_014479	Hs.145296	disintegrin protease	53.72	302.00
85	424340	AA339036	Hs.7033	ESTs	0.88	1.15

	424351	BE622117	Hs.145567	hypothetical protein	0.93	1.03
	424364	AW383226	Hs.201189	ESTs, Weakly similar to G01763 atrophin-	7.02	3.24
	424381	AA285249	Hs.146329	protein kinase Chk2	95.55	92.00
5	424411	NM_005209	Hs.146549	crystallin, beta A2	1.63	3.25
	424420	BE614743	Hs.146588	prostaglandin E synthase	1.63	1.33
	424441	X14850	Hs.147097	H2A histone family, member X	1.82	1.29
	424502	AF242388	Hs.149585	lengsin	1.00	1.00
	424503	X06256	Hs.149609	Integrin, alpha 5 (fibronectin receptor,	1.02	2.24
10	424513	BE385864	Hs.149894	mitochondrial translational initiation f	1.00	17.00
	424539	L02911	Hs.150402	Activin A receptor, type I (ACVR1) (ALK	32.46	108.00
	424558	AF005418	Hs.150595	cytochrome P450, subfamily XXVI, polype	3.40	2.58
	424602	AK002055	Hs.151046	hypothetical protein FLJ11193	31.87	25.00
	424629	M90656	Hs.151393	glutamate-cysteine ligase, catalytic sub	3.58	2.37
	424645	NM_014682	Hs.151449	KIAA0535 gene product	1.00	1.00
15	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	2.12	2.23
	424717	AW992292	Hs.152213	wingless-type MMTV integration site fami	1.00	1.00
	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	56.19	12.00
	424840	D79987	Hs.153479	extra spindle poles, S. cerevisiae, homo	2.65	1.30
	424867	AJ024860	Hs.153591	Nol56 (D. melanogaster)-like protein	1.23	1.05
20	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	21.35	1.00
	424979	D87989	Hs.154073	UDP-galactose transporter related	1.36	1.35
	424999	AW953120		gb:EST365190 MAGE resequences, MAGB Homo	1.24	1.41
	425048	H05468	Hs.164502	ESTs	1.00	11.00
25	425057	AA826434	Hs.1619	achaete-scute complex (Drosophila) homol	7.46	87.00
	425081	X74794	Hs.154443	minichromosome maintenance deficient (S.	2.52	3.82
	425118	AU076611	Hs.154672	methylene tetrahydrofolate dehydrogenase	4.84	4.03
	425159	NM_004341	Hs.154868	carbamoyl-phosphate synthetase 2, aspart	3.62	2.73
	425202	AW962282	Hs.152049	ESTs, Weakly similar to I38022 hypotheti	1.00	53.00
30	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheti	100.77	44.00
	425236	AW067800	Hs.155223	stanniocalcin 2	3.30	2.90
	425245	AI751768	Hs.155314	KIAA0095 gene product	1.91	2.32
	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	1.41	1.49
	425266	J00077	Hs.155421	alpha-fetoprotein	1.00	68.00
35	425274	BE281191	Hs.155462	minichromosome maintenance deficient (mi	1.97	1.63
	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	141.49	123.00
	425349	AA425234	Hs.79886	ribose 5-phosphate isomerase A (ribose 5	1.00	84.00
	425371	D49441	Hs.155981	mesothelin	0.87	1.59
	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	14.90	5.76
40	425420	BE536911	Hs.234545	hypothetical protein NUF2R	1.00	1.00
	425424	NM_004954	Hs.157199	ELK1 motif kinase	10.58	9.74
	425483	AF231022	Hs.158159	FAT tumor suppressor (Drosophila) homolo	1.74	1.40
	425566	AW162943	Hs.250618	UL16 binding protein 2	1.49	1.14
	425580	L11144	Hs.1907	galanin	53.29	233.00
45	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	33.45	1.00
	425692	D90041	Hs.155956	N-acetyltransferase 1 (arylamine N-acety	1.00	55.00
	425695	NM_005401	Hs.159238	protein tyrosine phosphatase, non-recept	1.00	10.00
	425734	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxyg	1.00	41.00
	425776	U25128	Hs.159499	parathyroid hormone receptor 2	1.00	48.00
50	425810	AI923627	Hs.31903	ESTs	27.39	98.00
	425811	AL039104	Hs.159557	karyopherin alpha 2 (RAG cohort 1, impor	1.99	1.58
	425849	AI077288	Hs.296323	serum/glucocorticoid regulated kinase	71.16	3.42
	425852	AK001504	Hs.159651	death receptor 6, TNF superfamily member	1.35	1.34
	426067	AA401369	Hs.190721	ESTs	1.01	17.00
55	426088	AF038007	Hs.166196	ATPase, Class I, type 8B, member 1	26.26	47.00
	426215	AW067800	Hs.155223	stanniocalcin 2	1.91	2.90
	426227	U67058	Hs.154299	Human proteinase activated receptor-2 mR	22.40	25.00
	426269	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f	1.00	1.00
	426283	NM_003937	Hs.169139	kynureninase (L-kynurenine hydrolase)	91.39	229.00
60	426329	AL389951	Hs.271623	nucleoporin 50kD	4.34	4.08
	426427	M86699	Hs.169840	TTK protein kinase	7.02	1.00
	426432	AF001601	Hs.169857	paraoxonase 2	1.16	1.68
	426440	BE382756	Hs.169902	solute carrier family 2 (facilitated glu	2.59	1.71
	426459	AF151812	Hs.169992	hypothetical 43.2 Kd protein	1.56	1.66
65	426471	M22440	Hs.170009	transforming growth factor, alpha	20.60	26.00
	426496	D31765	Hs.170114	KIAA0061 protein	9.81	22.00
	426501	AA401369	Hs.190721	ESTs	19.23	17.00
	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	103.74	41.00
	426536	AI949749	Hs.44441	ESTs	4.65	23.00
70	426572	AB037783	Hs.170623	hypothetical protein FLJ11183	1.00	43.00
	426682	AV660038	Hs.2056	UDP glycosyltransferase 1 family, polype	160.06	8.00
	426691	NM_006201	Hs.171834	PCTAIRE protein kinase 1	1.51	1.35
	426746	J03626	Hs.2057	uridine monophosphate synthetase (orolat	2.13	1.68
	426752	X69490	Hs.172004	titin	0.02	5.14
75	426784	U03749	Hs.172216	chromogranin A (parathyroid secretory pr	1.72	1.71
	426807	AA385315	Hs.156682	ESTs	1.30	1.64
	426812	AF105365	Hs.172613	solute carrier family 12 (potassium/chlo	1.47	1.53
	426814	AF036943	Hs.172619	myelin transcription factor 1-like	1.00	1.00
	426831	BE296216	Hs.172673	S-adenosylhomocysteine hydrolase	1.51	1.25
80	426897	AA401369	Hs.190721	ESTs	141.56	17.00
	426925	NM_001196	Hs.315689	Homo sapiens cDNA: FLJ22373 fis, clone H	32.61	38.00
	426935	NM_000088	Hs.172928	collagen, type I, alpha 1	2.65	3.16
	426964	AA393739	Hs.287416	Homo sapiens cDNA FLJ11439 fis, clone HE	1.97	3.49
	426966	AI493134		sclerostin	1.00	1.00
	426991	AK001536		Homo sapiens cDNA FLJ10674 fis, clone NT	3.39	2.28
85	427099	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	4.24	17.00

	427239	BE270447	Hs.174070	ubiquitin carrier protein	1.58	1.05
	427260	AA663848		gb:ae70b06.s1 Stralagene schizo brain S1	1.34	1.60
	427281	AA906147	Hs.102869	ESTs	1.00	66.00
5	427335	AA448542	Hs.251677	G antigen 7B	51.83	4.00
	427354	T57896	Hs.191095	ESTs	1.17	1.95
	427356	AW023482	Hs.97849	ESTs	7.31	41.00
	427376	AA401533	Hs.19440	ESTs	1.00	57.00
	427383	NM_005411	Hs.177582	surfactant, pulmonary-associated protein	0.42	1.32
10	427427	AF077345	Hs.177936	lectin, superfamily member 1 (cartilage-	1.00	20.00
	427441	AA412605	Hs.343879	SPANX family, member C	1.00	1.00
	427445	X80818	Hs.178078	glutamate receptor, metabotropic 4	0.97	1.03
	427505	AA361552	Hs.178761	26S proteasome-associated pad1 homolog	4.60	4.04
	427510	Z47542	Hs.179312	small nuclear RNA activating complex, po	22.00	45.00
	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	97.45	92.00
15	427546	AA188763	Hs.36793	hypothetical protein FLJ23188	1.50	3.24
	427562	R56424	Hs.26534	ESTs	6.81	40.00
	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	69.91	62.00
	427660	AJ741320	Hs.114121	Homo sapiens cDNA: FLJ23228 fis, clone C	2.70	49.00
20	427666	AJ791495	Hs.180142	calmodulin-like skin protein	1.37	1.88
	427668	AA298760	Hs.180191	hypothetical protein FLJ14904	29.55	67.00
	427677	NM_007045	Hs.180296	FGFR1 oncogene partner	3.52	2.63
	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	7.41	34.00
	427711	M31659	Hs.180408	solute carrier family 25 (mitochondrial	15.84	70.00
	427719	AJ393122	Hs.134726	ESTs	7.03	4.52
25	427722	AK000123	Hs.180479	hypothetical protein FLJ20116	2.92	1.74
	427747	AW411425	Hs.180655	serine/threonine kinase 12	1.76	1.26
	427912	AL022310	Hs.181097	tumor necrosis factor (ligand) superfami	9.63	59.00
	427961	AW293165	Hs.143134	ESTs	41.97	118.00
30	428004	AA449563	Hs.151393	glutamate-cysteine ligase, catalytic sub	23.82	1.00
	428023	AL038843		Homo sapiens cDNA: FLJ23602 fis, clone L	1.40	1.33
	428046	AW812795	Hs.337534	ESTs, Moderately similar to I38022 hypot	96.28	167.00
	428093	AW594506	Hs.104830	ESTs	1.25	1.29
	428098	AU077258	Hs.182429	protein disulfide isomerase-related prot	1.86	1.60
35	428129	AJ244311	Hs.26912	ESTs	1.00	42.00
	428169	AJ928984	Hs.182793	golgi phosphoprotein 2	2.76	2.11
	428182	BE386042	Hs.293317	ESTs, Weakly similar to GGC1_HUMAN G ANT	1.00	1.00
	428227	AA321649	Hs.22448	small inducible cytokine subfamily B (Cy	85.59	181.00
	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	8.57	21.64
40	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	7.77	15.90
	428434	AJ909935	Hs.65551	Homo sapiens, Similar to DNA segment, Ch	0.58	1.43
	428450	NM_014791	Hs.184339	KIAA0175 gene product	237.53	204.00
	428471	X57348	Hs.184510	stratiferin	6.00	4.60
	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to	56.54	16.00
45	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	3.53	2.15
	428505	AL035461	Hs.2281	chromogranin B (secretogranin 1)	1.00	1.00
	428532	AF157326	Hs.184786	TBP-interacting protein	1.00	58.00
	428645	AA431400	Hs.98729	ESTs, Weakly similar to 2017205A dihydro	1.00	16.00
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	1.00	1.00
50	428698	AA852773	Hs.334838	KIAA1866 protein	187.37	255.00
	428728	NM_016625	Hs.191381	hypothetical protein	47.24	80.00
	428748	AW593206	Hs.98785	Ksp37 protein	1.00	87.00
	428758	AA433988	Hs.98502	hypothetical protein FLJ14303	1.06	1.13
	428771	AB028992	Hs.193143	KIAA1069 protein	1.98	92.00
55	428801	AW277121	Hs.254881	ESTs	1.67	6.15
	428810	AF068236	Hs.193788	nitric oxide synthase 2A (inducible, hep	1.03	1.27
	428839	AJ767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	124.17	43.00
	428845	AL157579	Hs.153610	KIAA0751 gene product	1.00	1.00
	428959	AF100779	Hs.194680	WNT1 inducible signaling pathway protein	15.16	27.00
60	428969	AF120274	Hs.194689	artemin	1.36	1.24
	429038	AL023513	Hs.194766	seizure related gene 6 (mouse)-like	0.97	3.31
	429065	AJ753247	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT	6.82	16.47
	429164	AI688663	Hs.116586	ESTs	19.08	67.00
	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	16.18	105.00
65	429183	AB014604	Hs.197955	KIAA0704 protein	79.72	104.00
	429201	X03178	Hs.198246	group-specific component (vitamin D bind	1.00	1.00
	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	1.33	1.09
	429220	AW207206		ESTs	1.00	7.00
	429228	AI553633	Hs.326447	ESTs	39.47	29.25
70	429259	AA420450	Hs.292911	ESTs, Highly similar to S60712 band-6-pr	2.01	1.18
	429263	AA019004	Hs.198396	ATP-binding cassette, sub-family A (ABC1	1.07	1.00
	429276	AF056085	Hs.198612	G protein-coupled receptor 51	3.70	142.00
	429359	W00482	Hs.2399	matrix metalloproteinase 14 (membrane-in	1.30	1.94
	429412	NM_006235	Hs.2407	POU domain, class 2, associating factor	94.09	86.00
75	429413	NM_014058	Hs.201877	DESC1 protein	41.91	10.00
	429486	AF155827	Hs.203963	hypothetical protein FLJ10339	12.19	1.00
	429504	X99133	Hs.204238	lipocalin 2 (oncogene 24p3)	1.61	1.08
	429538	BE182592	Hs.11261	small proline-rich protein 2A	4.43	2.90
	429547	AA401369	Hs.190721	ESTs	1.06	17.00
80	429551	AW450624	Hs.220931	ESTs	2.89	65.00
	429563	BE619413	Hs.2437	eukaryotic translation initiation factor	1.49	1.37
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	61.86	100.00
	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas	1.59	1.69
	429612	AF062649	Hs.252587	pituitary tumor-transforming 1	2.78	1.74
85	429616	AI982722	Hs.120845	ESTs	1.00	1.00
	429656	X05608	Hs.211584	neurofilament, light polypeptide (68kD)	1.00	4.00

	429663	M58874	Hs.211587	phospholipase A2, group IVA (cytosolic,	69.95	104.00
	429736	AF125304	Hs.212680	tumor necrosis factor receptor superfam	1.25	1.21
	429782	NM_005754	Hs.220689	Ras-GTPase-activating protein SH3-domain	1.00	7.00
	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	11.80	1.00
5	429918	AW873986	Hs.119383	ESTs	1.00	78.00
	429978	AA249027		ribosomal protein S6	1.98	3.09
	429986	AF092047	Hs.227277	sine oculis homeobox (Drosophila) homolo	1.00	48.00
	430044	AA464510	Hs.152812	ESTs	69.27	59.00
10	430114	AA847744	Hs.99640	ESTs	1.00	1.00
	430134	BE380149	Hs.105223	ESTs, Weakly similar to T33188 hypotheti	1.00	51.00
	430147	R60704	Hs.234434	hairly/enhancer-of-split related with YRP	1.10	2.22
	430287	AW182459	Hs.125759	ESTs, Weakly similar to LEU5_HUMAN LEUKE	1.00	127.00
	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	3.80	1.47
	430300	U60805	Hs.238648	oncosterin M receptor	1.00	35.00
15	430315	NM_004293	Hs.239147	guanine deaminase	92.31	28.00
	430337	M36707	Hs.239600	calmodulin-like 3	1.18	1.08
	430378	Z29572	Hs.2556	tumor necrosis factor receptor superfam	5.28	66.00
	430388	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	16.76	38.00
	430393	BE185030	Hs.241305	estrogen-responsive B box protein	1.63	1.50
20	430439	AL133561		DKFZP434B061 protein	1.00	1.00
	430451	AA836472	Hs.297939	cathepsin B	1.64	2.12
	430454	AW469011	Hs.105635	ESTs	63.35	44.00
	430466	AF052573	Hs.241517	polymerase (DNA directed), theta	2.47	1.91
	430481	AA479678	Hs.203269	ESTs, Moderately similar to ALU8_HUMAN A	1.00	31.00
25	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	12.28	41.00
	430508	AI015435	Hs.104637	ESTs	4.75	7.27
	430533	AA480895	Hs.57749	ESTs, Weakly similar to T17288 hypotheti	1.00	1.00
	430563	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	1.00	1.59
	430677	Z26317	Hs.94560	desmoglein 2	1.72	1.30
30	430678	AA401369	Hs.190721	ESTs	0.90	17.00
	430686	NM_001942	Hs.2633	desmoglein 1	1.00	1.00
	430788	AI742925	Hs.7179	ESTs, Weakly similar to 2004399A chromos	1.62	1.84
	430890	X54232	Hs.2699	glypican 1	1.58	1.40
35	430935	AW072916		zinc finger protein 131 (clone pHZ-10)	90.28	132.00
	430985	AA490232	Hs.27323	ESTs, Weakly similar to I7885 serine/th	0.94	1.28
	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3	60.25	28.00
	431089	BE041395		ESTs, Weakly similar to unknown protein	23.32	941.00
	431092	AI332764	Hs.125757	ESTs	13.46	63.00
40	431124	AF284221	Hs.59506	doublesex and mab-3 related transcriptio	49.43	62.00
	431164	AA493650	Hs.94367	Homo sapiens cDNA: FLJ23494 fis, clone L	0.44	2.20
	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	182.26	101.00
	431221	AW207837	Hs.286145	SRB7 (suppressor of RNA polymerase B, ye	4.15	13.97
	431277	AA501806	Hs.345824	ESTs	1.00	86.00
45	431322	AW970822		gb:EST382704 MAGE resequences, MAGK Homo	40.55	200.00
	431342	AW971018	Hs.21659	ESTs	1.00	53.00
	431384	BE158000	Hs.285026	gb:MR2-HT0377-150200-202-e03 HT0377 Homo	0.94	1.14
	431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu	1.30	1.25
	431494	AA991355	Hs.298312	hypothetical protein DKFZp434A1315	3.90	26.00
50	431515	NM_012152	Hs.258583	endothelial differentiation, lysophospha	1.41	1.87
	431548	AI834273	Hs.9711	novel protein	5.66	15.00
	431630	NM_002204	Hs.265829	integrin, alpha 3 (antigen CD49C, alpha	0.99	1.44
	431745	AW972448	Hs.163425	ESTs	0.99	3.51
	431770	BE221880	Hs.268555	5'-3' exonuclease 2	67.12	91.00
55	431830	Y16645	Hs.271387	small inducible cytokine subfamily A (Cy	3.36	4.71
	431846	BE019924	Hs.271580	uroplakin 1B	4.49	2.51
	431890	X17033	Hs.271986	integrin, alpha 2 (CD49B, alpha 2 subuni	2.20	3.32
	431934	AB031481	Hs.272214	STG protein	1.01	1.04
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	51.17	46.35
60	432006	AL137382	Hs.272320	Homo sapiens mRNA; cDNA DKFZp434L1226 (f	0.94	1.65
	432023	R43020	Hs.236223	EST	0.94	47.00
	432201	AI538613	Hs.298241	Transmembrane protease, serine 3	1.10	2.24
	432210	AI567421	Hs.273330	Homo sapiens, clone IMAGE:3544662, mRNA,	1.42	1.45
	432226	AW182766	Hs.273558	phosphate cytidylyltransferase 1, cholin	1.00	1.00
65	432239	X81334	Hs.2936	matrix metalloproteinase 13 (collagenase	18.67	1.00
	432265	BE382679	Hs.285753	SCG10-like-protein	1.09	1.21
	432281	AK001239	Hs.274263	hypothetical protein FLJ10377	40.98	58.00
	432365	AK001106	Hs.274419	hypothetical protein FLJ10244	1.00	214.00
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	157.34	37.00
70	432375	BE536069	Hs.2962	S100 calcium-binding protein P	1.65	1.06
	432407	AA221036		gb:zr03f12.r1 Stralagene NT2 neuronal pr	73.71	75.00
	432441	AW292425	Hs.163484	ESTs	56.35	72.00
	432489	AI804855	Hs.207530	ESTs	1.00	24.00
	432543	AA552690	Hs.152423	Homo sapiens cDNA: FLJ21274 fis, clone C	137.72	98.00
75	432552	AI537170	Hs.173725	ESTs, Weakly similar to ALU8_HUMAN ALU S	1.00	31.00
	432583	AW023624	Hs.162282	potassium channel TASK-4; potassium chan	0.27	35.18
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	2.87	6.22
	432625	AI243596	Hs.94830	ESTs, Moderately similar to T03094 A-kin	26.63	56.00
	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci	1.92	5.29
80	432677	NM_004482	Hs.278611	UDP-N-acetyl-alpha-D-galactosamine:polyp	1.00	48.00
	432715	AA247152	Hs.200483	ESTs, Weakly similar to KIAA1074 protein	45.13	31.00
	432753	NM_014075	Hs.336938	Homo sapiens PRO0593 mRNA, complete cds	1.00	68.00
	432788	AA521091	Hs.178499	Homo sapiens cDNA: FLJ23117 fis, clone L	2.69	3.67
	432842	AW674093	Hs.334822	hypothetical protein MGC4485	1.22	1.34
	432867	AW016936	Hs.233364	ESTs	1.00	1.00
85	432917	NM_014125	Hs.241517	PRO0327 protein	10.25	6.62

	432920	U37689	Hs.3128	polymerase (RNA) II (DNA directed) polyp	1.44	1.30
	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	154.79	85.64
	433023	AW864793	Hs.87409	thrombospondin 1	20.96	100.00
5	433042	AW193534	Hs.281895	Homo sapiens cDNA FLJ11660 fis, clone HE	1.00	10.00
	433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	1.20	1.09
	433159	AB035898	Hs.150587	kinesin-like protein 2	13.82	39.00
	433183	AF231338	Hs.222024	transcription factor BMAL2	1.00	69.00
	433258	AA622788	Hs.203613	ESTs, Weakly similar to ALUB_HUMAN IIII	1.00	1.25
10	433409	AI278802	Hs.25661	ESTs	44.81	117.00
	433437	U20536	Hs.3280	caspase 6, apoptosis-related cysteine pr	70.39	105.00
	433485	AI493076	Hs.201967	aldo-keto reductase family 1, member C2	11.55	2.00
	433537	AI733692	Hs.112488	ESTs	8.66	55.00
	433547	W04978	Hs.303023	beta tubulin 1, class VI	25.16	83.00
	433556	W56321	Hs.111460	calcium/calmodulin-dependent protein kin	1.00	19.00
15	433647	AA603367	Hs.222294	ESTs	20.30	49.00
	433658	L03678	Hs.156110	immunoglobulin kappa constant	5.92	10.03
	433800	AI094221	Hs.135150	lung type-I cell membrane-associated gly	2.29	2.22
	433819	AW511097	Hs.112765	ESTs	3.71	8.00
	433862	D86960	Hs.3610	KIAA0205 gene product	62.08	104.00
20	433980	AA137152	Hs.286049	phosphoserine aminotransferase	108.91	47.00
	434088	AF116677	Hs.249270	hypothetical protein PRO1966	1.00	1.00
	434094	AA305599	Hs.238205	hypothetical protein PRO2013	121.27	87.00
	434105	AW952124	Hs.13094	presenilins associated rhomboid-like pro	1.22	1.23
	434217	AW014795	Hs.23349	ESTs	14.11	57.00
25	434340	AI193043	Hs.128685	ESTs, Weakly similar to T17226 hypotheti	2.10	2.56
	434360	AA401369	Hs.190721	ESTs	40.98	17.00
	434414	AI798376		gb:tr34b07.x1 NCI_CGAP_Ov23 Homo sapiens	1.48	1.56
	434424	AI811202	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	1.00	64.00
	434467	BE552368	Hs.231853	Homo sapiens cDNA FLJ13445 fis, clone PL	54.91	85.00
30	434551	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	2.46	2.00
	434627	AI221894	Hs.39311	ESTs	1.00	1.00
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	1.00	23.00
	434769	AA648884	Hs.134278	Homo sapiens cDNA FLJ12676 fis, clone NT	7.08	56.00
	434792	AA649253	Hs.132458	ESTs	8.52	44.00
35	434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	11.33	1.00
	434828	D90070	Hs.96	phorbol-12-myristate-13-acetate-induced	1.00	1.00
	434876	AF160477	Hs.61460	Ig superfamily receptor LNIR	1.25	1.29
	434891	AA814309	Hs.123583	ESTs	1.00	6.00
	434928	AW015595	Hs.4267	Homo sapiens clones 24714 and 24715 mRNA	1.00	1.00
40	435013	H91923	Hs.110024	Target CAT	1.26	1.10
	435066	BE261750	Hs.4747	dyskeratosis congenita 1, dyskerin	1.69	1.37
	435087	AW975241	Hs.23567	ESTs	1.00	1.00
	435099	AC004770	Hs.4756	flap structure-specific endonuclease 1	2.90	1.93
	435159	AA668879	Hs.116649	ESTs	1.00	1.00
45	435205	X54136	Hs.181125	immunoglobulin lambda locus	1.02	1.46
	435232	NM_001262	Hs.4854	cyclin-dependent kinase inhibitor 2C (p1	2.04	2.70
	435304	H10709	Hs.269524	ESTs	27.58	139.00
	435313	AI769400	Hs.189729	ESTs	1.00	14.00
	435505	AF200492	Hs.211238	interleukin-1 homolog 1	1.00	38.00
50	435509	AI458679	Hs.181915	ESTs	1.00	1.00
	435525	AI831297	Hs.123310	ESTs	1.00	56.00
	435532	AW291488	Hs.117305	Homo sapiens, clone IMAGE:3682908, mRNA	1.00	2.00
	435550	AI224456	Hs.324507	H.sapiens polyA site DNA	3.42	3.92
	435602	AF217515	Hs.283532	uncharacterized bone marrow protein BM03	3.95	1.80
55	435766	R11673	Hs.186498	ESTs	1.00	28.00
	435793	AB037734	Hs.4993	KIAA1313 protein	23.68	42.00
	436069	AI056879	Hs.263209	ESTs	1.00	58.00
	436170	AW450381	Hs.14529	ESTs	1.00	18.00
	436211	AK001581	Hs.334828	hypothetical protein FLJ10719; KIAA1794	5.84	22.00
60	436213	AA325512	Hs.71472	hypothetical protein FLJ10774; KIAA1709	1.42	1.27
	436217	T53925	Hs.107	fibrinogen-like 1	57.97	31.00
	436238	AK002163	Hs.301724	hypothetical protein FLJ11301	2.51	1.71
	436251	BE515065	Hs.296585	nucleolar protein (KKE/D repeat)	2.33	1.64
	436291	BE568452	Hs.344037	protein regulator of cytokinesis 1	108.99	52.00
65	436302	AL355841	Hs.99330	hypothetical protein FLJ23588	0.75	2.81
	436396	AW992292	Hs.152213	wingless-type MMTV integration site fami	60.01	1.00
	436414	BE264633	Hs.143638	WD repeat domain 4	2.50	2.19
	436419	AI948626	Hs.171356	ESTs	0.95	1.33
	436443	AW138211	Hs.128746	ESTs	1.12	9.26
70	436474	AJ270693	Hs.199887	ESTs	1.00	1.00
	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	3.28	1.56
	436486	AA742221	Hs.120633	ESTs	1.00	19.00
	436511	AA721252	Hs.291502	ESTs	16.76	14.00
	436553	X57809	Hs.181125	immunoglobulin lambda locus	1.08	1.74
75	436557	W15573	Hs.5027	ESTs, Weakly similar to A47582 B-cell gr	19.20	9.75
	436608	AA628980		down syndrome critical region protein DS	33.92	25.00
	436667	AW025183	Hs.127680	ESTs	0.89	1.19
	436771	AW975687	Hs.292979	ESTs	1.00	10.00
	436839	AA401369	Hs.190721	ESTs	1.00	17.00
80	436887	AW953157	Hs.193235	hypothetical protein DKFZp547D155	1.05	1.15
	436944	AW268614	Hs.5840	ESTs	1.00	1.00
	436961	AW375974	Hs.156704	ESTs	25.13	25.00
	436972	AA284679	Hs.25640	claudin 3	1.59	1.46
	437016	AU076916	Hs.5398	guanine monophosphate synthetase	2.35	1.78
85	437044	AL035864	Hs.69517	cDNA for differentially expressed CO16 g	1.34	1.13

	437181	AI306615	Hs.125343	ESTs, Weakly similar to KIAA0758 protein	1.00	17.00
	437204	AL110216	Hs.22826	ESTs, Weakly similar to I55214 salivary	40.55	82.00
	437205	AL110232	Hs.279243	Homo sapiens mRNA; cDNA DKFZp564D2071 (f	1.00	112.00
5	437259	AI377755	Hs.120695	ESTs	1.00	205.00
	437270	R18087	Hs.323769	cisplatin resistance related protein CRR	1.56	1.54
	437271	AL137445	Hs.28846	Homo sapiens mRNA; cDNA DKFZp566O134 (fr	113.25	125.00
	437370	AL359567	Hs.161962	Homo sapiens mRNA; cDNA DKFZp547D023 (fr	1.82	4.57
	437390	AI125859	Hs.112607	ESTs	1.35	1.75
10	437412	BE069288	Hs.34744	Homo sapiens mRNA; cDNA DKFZp547C136 (fr	3.58	3.20
	437435	AI306152	Hs.27027	hypothetical protein DKFZp762H1311	3.03	1.08
	437444	H46008	Hs.31518	ESTs	1.00	39.00
	437568	AI954795	Hs.156135	ESTs	1.00	19.00
	437623	D63880	Hs.5719	chromosome condensation-related SMC-asso	1.95	1.57
	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti	1.00	3.00
15	437814	AI088192	Hs.135474	ESTs, Weakly similar to DDX9_HUMAN ATP-D	1.00	45.00
	437840	AA884836	Hs.292014	ESTs	1.07	1.78
	437852	BE001836	Hs.256897	ESTs, Weakly similar to dJ365O12.1 [H.s	1.68	3.26
	437879	BE262082	Hs.5894	hypothetical protein FLJ10305	1.87	2.52
20	437915	AI637993	Hs.202312	Homo sapiens clone N11 Ntera2D1 teratoca	74.05	35.00
	437916	BE566249	Hs.20999	hypothetical protein FLJ23142	23.15	89.00
	437937	AI917222	Hs.121655	ESTs	1.00	1.00
	437942	AI888256	Hs.307526	ESTs	12.28	31.00
	438091	AW373062		nuclear receptor subfamily 1, group I, m	1.53	10.85
25	438113	AI467908	Hs.8882	ESTs	1.80	2.39
	438119	AW963217	Hs.203961	ESTs, Moderately similar to AF116721 89	22.67	36.90
	438274	AI918906	Hs.55080	ESTs	1.00	1.00
	438378	AW970529	Hs.86434	hypothetical protein FLJ21816	38.92	38.00
	438403	AA806607	Hs.292206	ESTs	1.00	1.00
30	438494	AA908678	Hs.130183	ESTs	2.05	80.00
	438546	AW297204	Hs.125811	ESTs	1.00	131.00
	438552	AJ245820	Hs.6314	type I transmembrane receptor (seizure-r	1.43	1.45
	438702	AI879064	Hs.54618	ESTs	1.00	34.00
	438724	AW612553	Hs.114670	Human DNA sequence from clone RP11-16L21	1.33	1.10
	438746	AI885815	Hs.184727	Human melanoma-associated antigen p97 (m	2.42	1.59
35	438779	NM_003787	Hs.6414	nucleolar protein 4	1.00	18.00
	438821	AA826425	Hs.192375	ESTs	2.03	2.57
	438885	AI886558	Hs.184987	ESTs	6.42	88.00
	438898	AA401369	Hs.190721	ESTs	22.41	17.00
40	438915	AA280174	Hs.285881	Williams-Beuren syndrome chromosome regi	1.00	1.00
	438956	W00847	Hs.135056	Human DNA sequence from clone RP5-850E9	2.20	1.88
	439000	AW979121		gb:EST391231 MAGE resequences, MAGP Homo	2.78	4.81
	439023	AA745978	Hs.28273	ESTs	1.17	1.31
	439024	R96696	Hs.35598	ESTs	1.00	28.00
45	439128	AI949371	Hs.153089	ESTs	1.00	67.00
	439146	AW138909	Hs.156110	immunoglobulin kappa constant	1.38	1.41
	439223	AW238299	Hs.250618	UL16 binding protein 2	1.93	1.64
	439285	AL133916		hypothetical protein FLJ20093	46.23	139.00
	439318	AW837046	Hs.6527	G protein-coupled receptor 56	2.00	2.20
50	439343	AF086161	Hs.114611	hypothetical protein FLJ11808	6.10	7.37
	439394	AA401369	Hs.190721	ESTs	3.39	17.00
	439410	AA632012	Hs.188746	ESTs	1.83	3.07
	439451	AF086270	Hs.278554	heterochromatin-like protein 1	23.28	52.00
	439452	AA918317	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	18.76	122.00
55	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13	2.78	1.58
	439477	W69813	Hs.58042	ESTs, Moderately similar to GFR3_HUMAN G	1.22	1.44
	439492	AF086310	Hs.103159	ESTs	7.46	39.00
	439523	W72348	Hs.185029	ESTs	1.00	1.19
	439592	AF086413	Hs.58399	ESTs	1.00	1.00
60	439606	W79123	Hs.58561	G protein-coupled receptor 87	33.61	1.00
	439670	AF088076	Hs.59507	ESTs, Weakly similar to AC004858 3 U1 sm	1.00	1.00
	439702	AW085525	Hs.134182	ESTs	4.30	10.00
	439705	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	86.55	11.00
	439738	BE246502	Hs.9598	sema domain, immunoglobulin domain (Ig)	2.36	1.88
65	439750	AL359053	Hs.57664	Homo sapiens mRNA full length insert cDN	2.02	6.08
	439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN	1.00	21.00
	439780	AL109688		gb:Homo sapiens mRNA full length insert	7.27	25.00
	439840	AW449211	Hs.105445	GDNF family receptor alpha 1	1.00	1.00
	439926	AW014875	Hs.137007	ESTs	32.58	71.00
70	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola	21.28	9.55
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	68.83	61.00
	440006	AK000517	Hs.6844	hypothetical protein FLJ20510	1.83	4.02
	440028	AW473675	Hs.125843	ESTs, Weakly similar to T17227 hypotheti	1.42	2.54
	440106	AA864968	Hs.127699	KIAA1603 protein	1.00	54.00
75	440138	AB033023	Hs.318127	hypothetical protein FLJ10201	24.18	52.00
	440273	AI805392	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	3.21	4.72
	440289	AW450991	Hs.192071	ESTs	38.63	113.00
	440325	NM_003812	Hs.7164	a disintegrin and metalloproteinase doma	62.88	147.00
	440492	R39127	Hs.21433	hypothetical protein DKFZp547J036	2.35	3.62
80	440527	AV657117	Hs.184164	ESTs, Moderately similar to S65657 alpha	10.84	57.00
	440659	AF134160	Hs.7327	claudin 1	3.18	2.37
	440704	M69241	Hs.162	insulin-like growth factor binding prote	2.89	2.09
	440943	AW082298	Hs.146161	hypothetical protein MGC2408	2.02	1.41
	440994	AI160011	Hs.272068	ESTs	1.29	1.14
85	441020	AA401369	Hs.190721	ESTs	142.99	17.00
	441031	AI110684	Hs.7645	fibrinogen, B beta polypeptide	1.41	99.00

	441128	AA570256	ESTs, Weakly similar to T23273 hypotheti	4.13	3.50
	441290	W27501	Hs.89605 cholinergic receptor, nicotinic, alpha p	1.00	1.00
	441362	BE614410	Hs.23044 RAD51 (S. cerevisiae) homolog (E coli Re	130.23	43.00
5	441377	BE218239	Hs.202656 ESTs	22.03	1.00
	441390	AI692560	Hs.131175 ESTs	3.65	7.70
	441497	R51064	Hs.23172 ESTs	1.00	1.00
	441525	AW241867	Hs.127728 ESTs	1.53	1.42
	441553	AA281219	Hs.121296 ESTs	1.89	1.57
10	441607	NM_005010	Hs.7912 neuronal cell adhesion molecule	1.47	2.11
	441633	AW958544	Hs.112242 normal mucosa of esophagus specific 1	216.22	363.00
	441636	AA081846	Hs.7921 Homo sapiens mRNA; cDNA DKFZp566E183 (fr	2.31	2.05
	441737	X79449	Hs.7957 adenosine deaminase, RNA-specific	1.30	1.49
	441790	AA401369	Hs.190721 ESTs	44.15	17.00
15	441801	AW242799	Hs.86366 ESTs	1.00	1.00
	441919	AI553802	Hs.128121 ESTs	1.00	122.00
	441937	R41782	Hs.22279 ESTs	0.86	1.37
	441954	AI744935	Hs.8047 Fanconi anemia, complementation group G	1.48	1.39
	442025	AW887434	Hs.11810 CDA11 protein	1.00	46.00
20	442029	AW956698	Hs.14456 neural precursor cell expressed, develop	9.92	45.00
	442072	AI740832	Hs.12311 Homo sapiens clone 23570 mRNA sequence	25.05	77.00
	442108	AW452649	Hs.166314 ESTs	3.61	3.14
	442117	AW664964	Hs.128899 ESTs	3.00	5.49
	442137	AA977235	Hs.128830 ESTs, Weakly similar to Z192_HUMAN ZINC	1.00	1.00
25	442159	AW163390	Hs.278554 heterochromatin-like protein 1	1.92	1.66
	442179	AA983842	Hs.333555 chromosome 2 open reading frame 2	27.22	50.00
	442328	AI952430	Hs.150614 ESTs, Weakly similar to ALU4_HUMAN ALU S	5.00	3.42
	442432	BE093589	Hs.38178 hypothetical protein FLJ23468	181.59	76.00
	442530	AI580830	Hs.176508 Homo sapiens cDNA FLJ14712 fis, clone NT	10.59	144.00
30	442547	AA306997	Hs.217484 ESTs, Weakly similar to ALU1_HUMAN ALU S	109.23	98.00
	442556	AL137761	Hs.8379 Homo sapiens mRNA; cDNA DKFZp586L2424 (f	1.00	53.00
	442619	AA447492	Hs.20183 ESTs, Weakly similar to AF164793 1 prote	29.02	50.00
	442710	AI015631	Hs.23210 ESTs	1.00	19.00
	442717	R88362	Hs.180591 ESTs, Weakly similar to T23976 hypotheti	1.00	5.00
35	442875	BE623003	Hs.23625 Homo sapiens clone TCCCTA00142 mRNA sequ	22.85	50.00
	442914	AW188551	Hs.99519 hypothetical protein FLJ14007	25.33	82.00
	442932	AA457211	Hs.8858 bromodomain adjacent to zinc finger doma	3.18	4.41
	442942	AW167087	Hs.131562 ESTs	8.45	64.00
	443068	AI188710	ESTs	1.00	27.00
40	443204	AW205878	Hs.29643 Homo sapiens cDNA FLJ13103 fis, clone NT	1.00	24.00
	443211	AI128388	Hs.143655 ESTs	12.42	2.00
	443247	BE614387	Hs.333893 c-Myc target JPO1	128.84	96.00
	443324	R44013	Hs.164225 ESTs	0.02	4.59
	443383	AI792453	Hs.166507 ESTs	1.00	47.00
45	443400	R28424	Hs.250648 ESTs	18.52	61.00
	443426	AF098158	Hs.9329 chromosome 20 open reading frame 1	4.02	1.75
	443572	AA025610	Hs.9605 cleavage and polyadenylation specific fa	2.98	2.57
	443575	AI078022	Hs.269636 ESTs, Weakly similar to ALU1_HUMAN ALU S	1.00	29.00
	443614	AV655386	Hs.7645 fibrinogen, B beta polypeptide	1.00	16.00
50	443633	AL031290	Hs.9654 similar to pregnancy-associated plasma p	1.00	39.00
	443648	AI085377	Hs.143610 ESTs	39.81	70.00
	443715	AI583187	Hs.9700 cyclin E1	48.74	7.00
	443723	AI144442	Hs.157144 syntaxin 6	1.29	1.30
	443802	AW504924	Hs.9805 KIAA1291 protein	1.75	1.61
55	443859	NM_013409	Hs.9914 follistatin	1.35	1.13
	443892	AA401369	Hs.190721 ESTs	1.00	17.00
	443947	W24187	gb:zb47f09.r1 Soares_fetal_lung_NbHL19W	1.33	1.64
	443991	NM_002250	Hs.10082 potassium intermediate/small conductance	5.71	6.87
	444006	BE395085	Hs.10086 type I transmembrane protein Fn14	1.47	1.92
60	444009	AI380792	Hs.135104 ESTs	1.00	77.00
	444017	U04840	Hs.214 neuro-oncological ventral antigen 1	1.00	1.00
	444127	N63620	Hs.13281 ESTs	1.00	29.00
	444129	AW294292	Hs.256212 ESTs	1.00	1.00
	444279	U62432	Hs.89605 cholinergic receptor, nicotinic, alpha p	0.60	7.80
65	444371	BE540274	Hs.239 forkhead box M1	2.91	1.14
	444378	R41339	Hs.12569 ESTs	1.00	1.00
	444381	BE387335	Hs.283713 ESTs, Weakly similar to S64054 hypotheti	469.00	556.00
	444461	R53734	Hs.25978 ESTs, Weakly similar to 2109260A B cell	12.88	105.00
	444471	AB020684	Hs.11217 KIAA0877 protein	24.91	90.00
70	444489	AI151010	Hs.157774 ESTs	1.00	111.00
	444619	BE538082	Hs.8172 ESTs, Moderately similar to A46010 X-fin	1.00	70.00
	444665	BE613126	Hs.47783 B aggressive lymphoma gene	30.56	139.00
	444707	AI188613	Hs.41690 desmocollin 3	1.00	1.00
	444735	BE019923	Hs.243122 hypothetical protein FLJ13057 similar to	77.02	90.00
75	444781	NM_014400	Hs.11950 GPI-anchored metastasis-associated prote	1.57	1.31
	444783	AK001468	Hs.62180 anillin (Drosophila Scraps homolog), act	77.55	2.00
	445236	AK001676	Hs.12457 hypothetical protein FLJ10814	1.00	27.00
	445258	AI635931	Hs.147613 ESTs	1.00	73.00
	445413	AA151342	Hs.12677 CGI-147 protein	28.14	50.00
80	445417	AK001058	Hs.12680 Homo sapiens cDNA FLJ10196 fis, clone HE	1.81	2.62
	445443	AV653838	Hs.322971 ESTs	1.00	1.00
	445462	AA378776	Hs.288649 hypothetical protein MGC3077	2.09	1.70
	445517	AF208855	Hs.12830 hypothetical protein	1.87	70.00
	445537	AJ245671	Hs.12844 EGF-like-domain, multiple 6	1.71	2.72
85	445580	AF167572	Hs.12912 skbl (S. pombe) homolog	1.52	1.34
	445654	X91247	Hs.13046 thioredoxin reductase 1	1.51	1.52

	445669	AJ570830	Hs.174870	ESTs	10.95	11.45
	445818	BE045321	Hs.136017	ESTs	1.00	1.00
	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-	49.42	54.00
5	445885	AJ734009	Hs.127699	KIAA1603 protein	1.00	132.00
	445898	AF070623	Hs.13423	Homo sapiens clone 24468 mRNA sequence	1.00	1.00
	445903	AJ347487	Hs.132781	class I cytokine receptor	1.00	36.00
	445932	BE046441	Hs.333555	Homo sapiens clone 24859 mRNA sequence	2.41	2.88
	445982	BE410233	Hs.13501	pescadillo (zebrafish) homolog 1, contai	1.60	1.35
10	446078	AJ339982	Hs.156061	ESTs	1.00	42.00
	446102	AW168067	Hs.317694	ESTs	1.00	1.00
	446157	BE270828	Hs.131740	Homo sapiens cDNA: FLJ22562 fis, clone H	1.70	1.53
	446269	AW263155	Hs.14559	hypothetical protein FLJ10540	73.01	48.00
	446292	AF081497	Hs.279682	Rh type C glycoprotein	1.55	1.26
15	446293	AJ420213	Hs.149722	ESTs	1.00	2.00
	446423	AW139655	Hs.150120	ESTs	1.10	4.19
	446428	AW082270	Hs.12496	ESTs, Weakly similar to ALU4_HUMAN ALU S	0.53	3.26
	446432	AJ377320	Hs.150058	ESTs	1.00	5.00
	446528	AU076640	Hs.15243	nucleolar protein 1 (120kD)	1.36	1.31
	446574	AJ310135	Hs.335933	ESTs	3.89	72.00
20	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	32.03	20.23
	446636	AC002563	Hs.15767	citron (rho-interacting, serine/threonin	4.19	5.07
	446783	AW138343	Hs.141867	ESTs	2.82	9.47
	446839	BE091926	Hs.16244	mitotic spindle coiled-coil related prot	110.28	28.00
	446849	AU076617	Hs.16251	cleavage and polyadenylation specific fa	3.26	2.94
25	446856	AE14373	Hs.164175	ESTs	6.38	11.30
	446872	X97058	Hs.16362	pyrimidinergic receptor P2Y, G-protein c	1.98	2.03
	446880	AI811807	Hs.108646	Homo sapiens cDNA FLJ14934 fis, clone PL	94.90	113.00
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	1.67	3.90
	446989	AK001898	Hs.16740	hypothetical protein FLJ11035	2.82	3.12
30	447022	AW291223	Hs.157573	ESTs	1.00	170.00
	447033	AJ357412	Hs.157601	ESTs	7.15	107.00
	447078	AW885727	Hs.9914	ESTs	47.24	24.00
	447081	Y13896	Hs.17287	potassium inwardly-rectifying channel, s	0.12	17.88
35	447131	NM_004585	Hs.17466	retinoic acid receptor responder (tazaro	0.97	1.48
	447149	BE299857	Hs.326	TAR (HIV) RNA-binding protein 2	1.24	1.26
	447153	AA805202	Hs.315562	ESTs	1.00	54.00
	447164	AF026941	Hs.17518	Homo sapiens cig5 mRNA, partial sequence	1.00	67.00
	447178	AW594641	Hs.192417	ESTs	3.42	50.00
40	447250	AJ878909	Hs.17883	protein phosphatase 1G (formerly 2C), ma	1.60	1.52
	447289	AW247017	Hs.36978	melanoma antigen, family A, 3	1.00	1.00
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	28.63	1.00
	447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m	146.62	51.00
	447350	AJ375572	Hs.172634	ESTs	1.00	12.00
45	447377	N27687	Hs.334334	transcription factor AP-2 alpha (activat	2.55	63.00
	447415	AW937335	Hs.28149	ESTs, Weakly similar to KF3B_HUMAN KINES	0.91	1.13
	447425	AJ963747	Hs.18573	acylphosphatase 1, erythrocyte (common)	1.00	35.00
	447519	U46258	Hs.339665	ESTs	59.89	49.00
	447532	AK000614	Hs.18791	hypothetical protein FLJ20607	1.23	1.63
50	447534	AA401369	Hs.190721	ESTs	1.00	17.00
	447636	Y10043		high-mobility group (nonhistone chromoso	1.41	1.11
	447688	N87079	Hs.19236	Target CAT	1.00	39.00
	447733	AF157482	Hs.19400	MAD2 (mitotic arrest deficient, yeast, h	1.17	1.12
	447769	AW873704	Hs.320831	Homo sapiens cDNA FLJ14597 fis, clone NT	6.47	5.95
55	447802	AW593432	Hs.161455	ESTs	0.73	2.34
	447850	AB018298	Hs.19822	SEC24 (S. cerevisiae) related gene famil	86.45	116.00
	447924	AB172226	Hs.313413	ESTs, Weakly similar to T23110 hypotheti	1.00	1.00
	447973	AB011169	Hs.20141	similar to S. cerevisiae SSM4	3.50	4.27
	448030	N30714	Hs.325960	membrane-spanning 4-domains, subfamily A	4.13	142.00
60	448105	AJ538613	Hs.298241	Transmembrane protease, serine 3	1.15	2.24
	448243	AW369771	Hs.52620	integrin, beta 8	15.84	1.00
	448278	W07369	Hs.11782	ESTs	0.97	1.90
	448290	AK002107	Hs.20843	Homo sapiens cDNA FLJ11245 fis, clone PL	1.00	1.00
	448296	BE622756	Hs.10949	Homo sapiens cDNA FLJ14162 fis, clone NT	2.42	2.17
65	448357	BE274396	Hs.108923	RAB38, member RAS oncogene family	1.44	1.08
	448390	AL035414	Hs.21068	hypothetical protein	1.00	43.00
	448469	AW504732	Hs.21275	hypothetical protein FLJ11011	2.63	2.49
	448569	BE382657	Hs.21486	signal transducer and activator of trans	1.84	2.53
	448663	BE614599	Hs.106823	hypothetical protein MGC14797	3.29	46.00
70	448672	AI955511	Hs.225106	ESTs	1.00	21.00
	448733	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitte	1.82	1.08
	448741	BE614567	Hs.19574	hypothetical protein MGC5469	2.48	1.92
	448757	AJ366784	Hs.48820	TATA box binding protein (TBP)-associate	23.53	20.00
	448775	AB025237	Hs.388	nudix (nucleoside diphosphate linked moi	2.34	1.97
75	448826	AI580252	Hs.293246	ESTs, Weakly similar to putative p150 [H	74.07	62.67
	448830	AL031658	Hs.22181	hypothetical protein dJ310013.3	1.37	1.31
	448844	AI581519	Hs.177164	ESTs	1.00	31.00
	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	1.84	1.95
	448993	AJ471630		KIAA0144 gene product	1.63	1.49
80	449003	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o	1.00	1.00
	449029	N28989	Hs.22891	solute carrier family 7 (cationic amino	1.97	2.26
	449040	AF040704	Hs.149443	putative tumor suppressor	0.97	1.56
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	27.13	90.00
	449053	AI625777	Hs.344766	ESTs	8.33	44.00
85	449054	AF148848	Hs.22934	myoneurin	73.85	104.00
	449101	AA205847	Hs.23016	G protein-coupled receptor	2.58	27.00

	449167	T05095	Hs.19597	KIAA1694 protein	1.61	2.36
	449207	AL044222	Hs.23255	nucleoporin 155kD	2.36	1.56
	449228	AJ403107	Hs.148590	protein related with psoriasis	1.15	1.15
5	449230	BE613348	Hs.211579	melanoma cell adhesion molecule	206.65	151.00
	449305	AI638293		gb:tt09b07.x1 NCI_CGAP_GC6 Homo sapiens	17.28	45.00
	449318	AW236021	Hs.78531	Homo sapiens, Similar to RUKEN cDNA 5730	26.39	35.00
	449448	D60730	Hs.57471	ESTs	1.00	1.00
	449467	AW205006	Hs.197042	ESTs	1.00	1.00
10	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	56.80	216.86
	449722	BE280074	Hs.23960	cyclin B1	150.03	1.00
	449976	H06350	Hs.135056	Human DNA sequence from clone RP5-850E9	2.16	2.85
	450001	NM_001044	Hs.406	solute carrier family 6 (neurotransmitter)	1.17	1.45
	450098	W27249	Hs.8109	hypothetical protein FLJ21080	1.79	2.38
15	450101	AV649989	Hs.24385	Human hbc647 mRNA sequence	1.00	69.00
	450149	AW969781	Hs.132863	Zic family member 2 (odd-paired Drosophila)	1.00	1.00
	450193	AI916071	Hs.15607	Homo sapiens Fanconi anemia complementation	29.85	34.00
	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	1.00	1.00
	450372	BE218107	Hs.202436	ESTs	1.00	1.00
20	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase domain	51.26	93.00
	450447	AF212223	Hs.25010	hypothetical protein P15-2	123.20	181.00
	450568	AL050078	Hs.25159	Homo sapiens cDNA FLJ10784 fis, clone NT	1.00	19.00
	450589	AI701505	Hs.202526	ESTs	1.00	23.00
	450684	AA872605	Hs.25333	interleukin 1 receptor, type II	1.00	100.00
25	450701	H39960	Hs.288467	Homo sapiens cDNA FLJ12280 fis, clone MA	1.89	1.55
	450705	U90304	Hs.25351	iroquois homeobox protein 2A (IRX-2A) (1.00	45.00
	450832	AA401369	Hs.190721	ESTs	25.17	17.00
	450937	R49131	Hs.26267	ATP-dependant interferon response protein	90.92	90.00
	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	3.33	1.70
30	451105	AI761324		gb:wi60b11.x1 NCI_CGAP_Co16 Homo sapiens	15.02	124.00
	451110	AI955040	Hs.265398	ESTs, Weakly similar to transformation-related	1.00	143.00
	451253	H48299	Hs.26126	claudin 10	3.02	2.29
	451291	R39288	Hs.6702	ESTs	1.00	1.00
	451320	AW498974		diacylglycerol kinase, zeta (104kD)	2.92	18.00
35	451380	H09280	Hs.13234	ESTs	6.90	6.67
	451386	AB029006	Hs.26334	spastic paraplegia 4 (autosomal dominant)	35.75	72.00
	451437	H24143	Hs.31945	hypothetical protein FLJ11071	1.00	69.00
	451462	AK000367	Hs.26434	hypothetical protein FLJ20360	1.83	2.10
	451524	AK001466	Hs.26516	hypothetical protein FLJ10604	1.13	1.07
40	451541	BE279383	Hs.26557	plakophilin 3	1.88	1.33
	451592	AI805416	Hs.213897	ESTs	1.00	1.00
	451635	AA018899	Hs.127179	cryptic gene	1.52	1.92
	451743	AA401369	Hs.190721	ESTs	4.95	17.00
	451806	NM_003729	Hs.27076	RNA 3'-terminal phosphate cyclase	13.55	31.00
45	451807	W52854		hypothetical protein FLJ23293 similar to	1.55	35.00
	451871	AI821005	Hs.118599	ESTs	1.81	2.53
	451952	AL120173	Hs.301663	ESTs	1.00	22.00
	452012	AA307703	Hs.279766	kinesin family member 4A	3.43	2.26
	452046	AB018345	Hs.27657	KIAA0802 protein	56.59	19.00
50	452194	AI694413	Hs.332649	olfactory receptor, family 2, subfamily	1.67	4.09
	452206	AW340281	Hs.33074	Homo sapiens, clone IMAGE:3606519, mRNA,	9.31	53.00
	452240	AA401369	Hs.190721	ESTs	13.42	17.00
	452256	AK000933	Hs.28661	Homo sapiens cDNA FLJ10071 fis, clone HE	39.03	94.00
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	153.01	340.00
55	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisiae)	1.95	23.00
	452295	BE379936	Hs.28866	programmed cell death 10	42.33	61.00
	452304	AA025386	Hs.61311	ESTs, Weakly similar to S10590 cysteine	1.17	2.14
	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodomain	1.00	13.00
	452349	AB028944	Hs.29189	ATPase, Class VI, type 11A	1.09	1.42
60	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	54.49	53.00
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced protein	1.00	32.00
	452410	AL133619		Homo sapiens mRNA; cDNA DKFp434E2321 (f	1.26	1.99
	452461	N78223	Hs.108106	transcription factor	24.47	35.00
	452571	W31518	Hs.34665	ESTs	54.61	102.00
65	452613	AA461599	Hs.23459	ESTs	1.39	1.32
	452699	AW295390	Hs.213062	ESTs	1.00	26.00
	452705	H49805	Hs.246005	ESTs	1.00	1.00
	452747	AF160477	Hs.61460	Ig superfamily receptor LNIR	112.87	1.29
	452787	AW294022	Hs.222707	KIAA1718 protein	1.00	1.00
70	452795	AW392555	Hs.18878	hypothetical protein FLJ21620	1.00	1.00
	452823	AB012124	Hs.30696	transcription factor-like 5 (basic helix	7.91	75.00
	452833	BE558681	Hs.30736	KIAA0124 protein	3.16	1.92
	452838	U65011	Hs.30743	preferentially expressed antigen in melanoma	174.35	1.00
	452862	AA401369	Hs.190721	ESTs	98.26	17.00
75	452865	AW173720	Hs.345805	ESTs, Weakly similar to A47582 B-cell granule	1.55	1.00
	452934	AA581322	Hs.4213	hypothetical protein MGC16207	1.73	1.19
	452946	X95425	Hs.31092	EphA5	1.00	1.00
	452976	R44214	Hs.101189	ESTs	1.58	1.98
	453028	AB006532	Hs.31442	RecQ protein-like 4	1.80	1.60
80	453095	AW295660	Hs.252766	ESTs	0.77	1.50
	453102	NM_007197	Hs.31664	frizzled (Drosophila) homolog 10	1.00	1.00
	453103	AI301052	Hs.153444	ESTs	1.00	1.00
	453120	AA292891	Hs.31773	pregnancy-induced growth inhibitor	1.23	1.20
	453153	N53893	Hs.24360	ESTs	1.00	83.00
	453160	AI263307	Hs.239884	H2B histone family, member L	1.00	30.00
85	453197	AI916269	Hs.109057	ESTs, Weakly similar to ALU5_HUMAN ALU S	1.00	134.00

5	453210	AL133161	Hs.32360	hypothetical protein FLJ10867	1.69	1.93		
	453240	AI969564	Hs.166254	hypothetical protein DKFZp5661133	1.00	1.00		
	453317	NM_002277	Hs.41696	keratin, hair, acidic, 1	1.19	1.27		
	453323	AF034102	Hs.32951	solute carrier family 29 (nucleoside tra	4.90	4.11		
	453331	AI240665	Hs.8850	ESTs	199.42	340.00		
	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	1.00	16.00		
	453431	AF094754	Hs.32973	glycine receptor, beta	1.00	1.00		
	453439	AI572438	Hs.32976	guanine nucleotide binding protein 4	3.44	5.17		
	453459	BE047032	Hs.257789	ESTs	2.84	5.58		
10	453563	AW608906.comp		Hs.181163	hypothetical protein MGC5629	4.58	90.00	
	453633	AA357001	Hs.34045	hypothetical protein FLJ20764	1.74	1.60		
	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	19.49	1.00		
	453830	AA534296	Hs.20953	ESTs	24.92	25.00		
15	453857	AL080235	Hs.35861	DKFZP586E1621 protein	167.59	66.00		
	453867	AI929383	Hs.33032	hypothetical protein DKFZp434N185	1.00	39.00		
	453883	AI638516	Hs.347524	cofactor required for Sp1 transcriptiona	1.97	1.58		
	453884	AA355925	Hs.36232	KIAA0186 gene product	63.89	20.00		
	453900	AW003582	Hs.226414	ESTs, Weakly similar to ALU8_HUMAN ALU S	20.41	16.00		
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	7.09	22.00		
20	453941	U39817	Hs.36820	Bloom syndrome	29.75	19.00		
	453964	AI961486	Hs.12744	ESTs	1.00	1.00		
	453968	AA847843	Hs.62711	Homo sapiens, clone IMAGE:3351295, mRNA	2.06	1.81		
	453976	BE463830	Hs.163714	ESTs	3.02	131.00		
	454024	AA993527	Hs.293907	hypothetical protein FLJ23403	1.00	131.00		
25	454034	NM_000691	Hs.575	aldehyde dehydrogenase 3 family, member	1.23	1.02		
	454042	T19228	Hs.172572	hypothetical protein FLJ20093	30.63	171.00		
	454059	NM_003154	Hs.37048	statherin	1.00	1.00		
	454066	X00356	Hs.37058	calcitonin/calcitonin-related polypeptid	1.01	1.45		
30	454098	W27953	Hs.292911	ESTs, Highly similar to S60712 band-6-pr	1.26	1.11		
	454241	BE144666		gb:CM2-HT0176-041099-017-c02 HT0176 Homo	6.33	5.04		
	454417	AI244459	Hs.110826	trinucleotide repeat containing 9	4.30	7.82		
	454439	AW819152	Hs.154320	DKFZP566O1646 protein	1.00	1.00		
	455175	AW993247		gb:RC2-BN0033-180200-014-h09 BN0033 Homo	13.75	103.00		
35	455601	AI368680	Hs.816	SRY (sex determining region Y)-box 2	206.11	1.00		
	456237	AA203682		gb:zx52e07.r1 Soares_fetal_liver_spleen_	1.00	1.00		
	456321	NM_001327	Hs.87225	cancer/testis antigen	1.14	1.10		
	456475	NM_000144	Hs.95998	Friedreich ataxia	1.00	48.00		
	456508	AA502764	Hs.123469	ESTs, Weakly similar to AF208855 1 BM-01	162.25	189.00		
40	456534	X91195	Hs.100623	phospholipase C, beta 3, neighbor pseudo	2.12	1.80		
	456736	AW248217	Hs.1619	achaete-scute complex (Drosophila) homol	1.15	1.94		
	456759	BE259150	Hs.127792	delta (Drosophila)-like 3	1.00	1.00		
	456990	NM_004504	Hs.171545	HIV-1 Rev binding protein	16.42	84.00		
	457200	U33749	Hs.197764	thyroid transcription factor 1	0.57	1.76		
45	457234	AW968360	Hs.14355	Homo sapiens cDNA FLJ13207 fis, clone NT	2.71	4.15		
	457465	AW301344	Hs.122908	DNA replication factor	46.37	47.00		
	457489	AI693815	Hs.127179	cryptic gene	1.12	1.35		
	457646	AA725650	Hs.112948	ESTs	1.55	2.51		
	457733	AW974812	Hs.291971	ESTs	1.00	55.00		
50	457819	AA057484	Hs.35406	ESTs, Highly similar to unnamed protein	4.36	3.18		
	458092	BE545684	Hs.343566	KIAA0251 protein	1.00	1.32		
	458098	BE550224		metallothionein 1E (functional)	1.00	22.00		
	458207	T28472	Hs.7655	U2 small nuclear ribonucleoprotein auxil	2.06	1.88		
	458242	BE299588	Hs.28465	Homo sapiens cDNA: FLJ21869 fis, clone H	1.00	1.00		
55	458247	R14439	Hs.209194	ESTs	7.00	9.85		
	458679	AW975460	Hs.142913	ESTs	1.00	3.00		
	458778	AW451034	Hs.326525	arylsulfatase D	1.31	2.01		
	458933	AI638429	Hs.24763	RAN binding protein 1	1.98	1.71		
	459352	AW810383	Hs.206828	ESTs	12.60	63.00		
60	459670	F01020	Hs.172004	titin	1.00	1.00		
	459702	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	1.00	237.00		

TABLE 98

65	Pkey:	Unique Eos probeset identifier number
	CAT number:	Gene cluster number
	Accession:	Genbank accession numbers
70	Pkey	CAT Number
	407746	10125_1
		AK001962 R69415 BE464605 AA418699 AA053293 AA149075 AA058396 AW338226 AW272659 AA454607 AI139535 AW469852 AI275461
		AW271982 AA730033 AA576507 AA991217 AA782067 AI985851 AA805864 AA505598 AW469857 R69546 AA988279 AW001647 N63320
		D82661 T27343 AA306950 AA360989 R58778
	408070	1036688_1
	408660	107294_1
75	409522	113735_1
	409866	1156522_1
	410032	1170435_1
	411089	123172_1
		AA525775 AA056342 AI538978 AW975281 AA664986
		AA075382 AA075431
		AW502152 H41202 H29772
		BE065985 BE065944 BE066008 BE066083 BE066093
		AA456454 AA713730 AA091294 AA584921 N86077 AW836781 AA601031 AA579876 AA551106 AA633188 AW905577 AI955808 AI679386
		AI679895 AA514764 AA454562 AI082382 AA595822 AA551351 AA586369 AA666384 AA188934 AA666398 AA551297 AA565188
80	411152	1234028_1
		BE069199 AW936012 AW877466 AW819782 AW935798 AW835546 AW936042 BE069121 AW835625 AW877536 AW935885 BE069202
		AW820019 AW935937 BE160180 AW935946 BE069101 BE069125 AW877527 BE160316 BE160398 AW935794 AW835701 AW935784
	412537	1304_1
		AL031778 X59711 NM_002505 M59079 AI870439 AI494259 AW664010 AA405063 AA436132 BE174516 AA412691 AI400314 AA436024
		T29403 BE079412 BE079428 N90322 AI631202 AI141758 AI016793 AI167566 AI862075 AI375230 AI208445 AW235763 AL044113 AA382556
		AW953918 AA927051 AA889823 BE003094 AW390155 AW360805 AW360823 AW360810 AA425472 AI694282 AL044114 AI684577 AI809865

			AI478773 AI160445 AI674630 N69088 AW665529 N49278 AI129239 AI457890 AI621264 AW297152 AI268215 AA907787 AI286170 AI017982 AI963541 AI469807 AI969353 BE552356 N66509 AA736741 AA382555 AW075811 AW292026 H06382 AW957730 AA352014 R13591 AA121201 D60420 BE263253 BE047862 Z41952 AI424991 AI693507 AI863108 AA599060 AI091148 AA598889 R39887 AA813482 AW016452 H06383 R41807 AI364268 AA620528 AI241940 AW089149 AW090733 AW088875 Z38240 AA121202 R17734 BE157489 BE157560 AA926960 AA926959 W76521 W24270 W21526 AA037172 BE267636 H83186 AA469909 N86396 AA001348 BE535736 AA081745 BE566245 AA082436 H72525 H77575 N49786 W80565 H78746 BE569085 W04339 R98127 T55938 BE279271 AW960304 T29812 AA476873 BE297387 AA292753 AA177048 NM_001826 X54941 BE314366 AA908783 AI719075 BE270172 BE269819 AA889955 AI204630 W25243 AI935150 AA872039 W72395 T99530 AI422691 H98460 N31428 BE255916 H03265 AI857576 AA776920 AA910644 AA459522 AA293140 AW514667 R75953 AW662396 AA662522 AI865147 AI423153 AW262230 AA584410 AA583187 AW024595 AW069734 AI828995 AA282997 AA876046 AW613002 AA527373 AW972459 AI831360 AA621337 AA100926 AA772418 AA594628 AI033892 W95096 AI034317 AA398727 AI085031 N95210 AI459432 AI041437 AA932124 AA627684 AA935829 AI004827 AI423513 AI094597 H42079 R54703 AI630359 AA617681 AA978045 AA643280 W44561 AI991988 AI537692 AI090262 AA740817 AI312104 AI911822 AA416871 AI185409 AA129784 AA701623 AI075239 AI139549 AA633648 AI339996 AI336880 AA399239 AI078708 AI085351 AI362835 AI346618 AI146955 AI989380 AI348243 N92892 AA765850 AI494230 AI278887 AA962596 AI492600 W80435 AA001979 R97424 AI129015 N24127 AA157451 AA235549 AA459292 AA037114 AA129785 AI94211 AW059601 AW886710 R92790 N59755 AI361128 AW589407 H47725 H97534 H48076 H48450 T99631 AW300758 H03431 R76789 AA954344 H77576 R96823 AI457100 N92845 N49682 H42038 BE220698 BE220715 H99552 AA701624 N74173 R54704 H79520 H72923 H03266 BE261919 AA769633 AA480310 AA507454 AA910586 AI203723 AW104725 W25611 W25071 T88980 H03513 T77589 R99156 W95095 R97470 AA702275 T77551 AA911952 H82956 N83673 AA283672 AI267700 AI720344 AA191424 AI023543 AI469633 AA172056 AW958465 AA172236 AW953397 AA355086 AW265494 AA455904 AA195677 AW265432 AW991605 AA456370 N28754 N28747 AI568146 AI979339 AA322671 AA322672 AW955043 AI990326 AA776406 AI016250 AA843678 AW451882 N23137 N23129 W70051 AI038748 AA831327 AI925845 AW945895 Z42183 T31621 T97478 D62703 AA242966 D79798 AU076704 T74854 T74860 T72098 T73265 T73873 T69180 T74658 T58786 T60385 T73410 T68781 T67845 T67593 T73952 T67864 T60630 T68367 T68401 T53959 T72360 T72099 T60377 T58961 T71712 T72821 T64738 T74645 T72037 T68688 T72063 T73258 T72826 T64242 T68220 T74673 T71800 T68355 T61227 T62738 T69317 T53850 T64692 T73768 T73962 T73382 T68914 T70975 T73400 T60631 T73277 T73203 T70498 T61409 T58925 NM_000508 M64982 T68301 T73729 T69445 T60424 T67922 T67736 T68716 T67755 T74765 T73819 T58719 T74756 T60477 T74863 T61109 T68329 T58850 T71857 T73425 T53736 T68607 T58898 T64309 T72031 T72079 T64305 T71908 T68107 T71916 T73787 T56035 T64425 T71870 T60476 T61376 T67820 T71895 T41006 T69441 T68170 T74617 T71958 T69440 T61875 R06796 H483370 T71914 T53939 T64121 AA693996 T72525 T67779 T68078 AA011465 AA345378 AV654847 AV654272 AV656001 AI064740 T82897 N33594 AA344542 AW805054 AI207457 T61743 AA026737 H94389 AA382695 AA918409 T68044 S82092 T39959 AI017721 AA312395 AA312919 T40156 H66239 AV652989 H38728 R98521 AV655200 R95790 W03250 W00913 AA344136 AV660126 R97923 AA343596 AW407774 AV651256 N54417 AA812862 AW182929 AI111192 H61463 H72060 AA344503 H38639 AI277511 AV661108 AI207625 T47810 AA235252 T27853 T47778 R95746 H70620 AA701463 AW827166 R98475 C20925 AV657287 T71959 T71313 T73920 T73333 T61618 T69293 T69283 T73931 T72178 T72456 AV645639 AV653476 T72957 T72300 T58906 T71457 T70494 T72956 T70495 T68267 T74407 T85778 AA344726 T27854 T74485 T74101 T73868 T71518 T72304 AA343853 T73909 T68070 T72065 H72149 T73493 T73495 AV645993 R02293 T70475 T64751 AA344441 AA343657 AA345732 AA344328 AI110539 AA344603 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AI910083 M12075 BE074052 AW004668 AA578674 AA582084 BE074053 BE074126 BE074140 AA514776 AA588034 BE074051 BE074068 AW009769 AW050690 AA858276 R55389 AI001051 AW050700 AW750216 AA614539 BE074045 AI307407 AW602303 BE073575 AI202532 AA524242 AI970839 AI909751 BE076078 AI909749 R55292 AW881145 AA490718 M85637 AA304575 T06067 AA331991 AL119930 AA320696 AW752565 AI031985 AL137241 AI792386 AI733664 AI857654 AI049911 AA337221 AA336756 AW966196 AW953120 R56325 AA349562 AI493134 AI498691 AW771508 AI498457 AI768408 AI783524 AI383985 AI580267 D79813 AA393768 AK001536 AA191092 AW510354 AI554256 AL353968 AA134266 AA663848 AA400100 AA401424 AI038843 AA161338 BE268213 AA425597 N87306 AA092969 BE566038 AA247451 N47392 AI928802 AW182584 AW027872 AI819831 AI936994 W56258 AI653448 AI278611 AI283557 AI824306 AW338658 AW150899 AA687514 N47393 N29885 AA973469 AI038904 AI292064 AI034339 AW674593 N72156 AI079733 AI038683 AI291616 AA491599 AA93675 AA837380 BE006554 BE006473 AI087090 T33044 AA652043 AI203503 AA583959 W35283 AI129926 Z41844 AW020925 AW575848 AI684603 AA493297 AI140589 AI277175 AA425444 AI932767 W02632 BE396786 R37261 AW207206 AW341473 AA448195 AI951341 AA249027 AL038984 AK001993 AL080066 AV652725 BE566226 AA345557 AA315222 AA090585 AA375688 AA301092 AA298454 W05762 AW607939 H51658 D83880 N84323 BE296821 AW947007 D61461 AW079261 AA329482 AW901780 AI354442 AA772275 R31663 AI354441 AI767525 H92431 AI916735 H93575 AI394255 AW014741 AI573090 C06195 AW612857 AW265195 AI339558 AI377532 AI308821 AI919424 AI589705 AW055215 AI336532 AI338051 AA806547 C75509 C0618 AW071172 AW769904 AA630381 AI678018 AI863985 D79662 BE221049 AW265018 AI589700 AW196655 N76573 AI370908 BE042393 N75017 AI698870 AW960115 AL133551 AL041090 AL117481 AL122069 AW439292 AI968826 AW072916 AI184913 AA489195 AW466994 AW469044 N59350 AI819642 AI280239 AI220572 AA789302 AI473611 AW841126 D60937 BE041395 AA491826 AA621946 AA715980 AA666102 AW970622 AA503009 AA502998 AA502989 AA502805 T92188 AA221036 R87170 BE537068 BE544757 C18935 AW812058 T92565 AA227415 AA233942 AA223237 AA668403 AA601627 AW869639 BE061833 BE000620 AW961170 AW847519 AA308542 AW821833 AW945688 C04699 AA205504 AA377241 AW821687 AA055720 AW817981 AW856468 AA155719 AA179928 T03007 AW754298 AA227407 AA113928 AA307904 C16859 AW89376 S46400 AW811617 AW811616 W00557 BE142245 AW858232 AW861851 AW858362 AA232351 AA218567 AA055556 AW858231 AW857541 AW814172 H66214 AW814398 AF134164 AA243093 AA173345 AA199942 AA223384 AA227092 AA227080 T12379 AA092174 T61139 AA149776 AA699829 AW879188 AW813567 AW813538 AI267168 AA157718 AA157719 AA100472 AA100774 AA130756 AA157705 AA157730 AA157715 AA053524 AW849581 AW854566 C05254 AW882836 T92637 AW812621 AA206583 AA209204 BE156909 AA226824 AI829309 AW991957 N66951 AA527374 H66215 AA045564 AI694265 H60808 AA149726 AW195620 BE081333 BE073424 AW817662 AW817705 AW817703 AW817659 BE081531 H59570 AA628980 AI126603 BE504035
5	412811	132943_1	
	413690	1383256_1	
	414883	15024_1	
10			
15			
20	415989	156454_1	
	417324	166714_1	
	418574	17690_1	
25	418712	1784125_1	
	419443	184788_1	
	419502	18535_1	
30			
35			
40			
45			
50	419936	189181_1	
	421582	2041_1	
	422128	211994_1	
	423034	224122_1	
55	423816	23234_1	
	424200	236595_1	
	424999	245835_1	
	426966	273896_1	
	426991	27415_1	
60	427260	276598_1	
	428023	28589_2	
65	429220	301384_1	
	429978	31150_1	
70			
	430439	31808_1	
	430935	325772_1	
	431089	327825_1	
	431322	331543_1	
	432407	34624_1	
75			
80	434414	38585_1	
85	436608	42361_3	

438091 44964_1 AW373062 T55562 AI299190 BE174210 AW579001 H01811 W40186 R67100 AI923886 AW952164 AA628440 AW898607 AW898616
AA709126 AW898628 AW898644 AA947932 AW898625 AW898622 AI276125 AI185720 AW510698 AA987230 T52522 BE467708 AW243400
AW043642 AI288245 AI186932 D52654 D55017 D52715 D52477 D53933 D54679 AI298739 AI146984 AI922204 N98343 BE174213 AA845571
AI813854 AI214518 AI635262 AI139455 AI707807 AI698085 AW884528 AI024768 AI004723 AW087420 AI565133 N94964 AI268939
AW513280 AI061126 AI435818 AI859106 AI360506 AI024767 AA513019 AA757598 X56196 AA902959 AI334784 AI860794 AA010207
AW890091 AW513771 AI951391 AI337671 T52499 AA890205 AI640908 H75966 AA463487 AA358688 AI961767 AI866295 AA780994
AI985913 BE174196 AA029094 AW592159 T55581 N79072 AI611201 AA910812 AI220713 AW149306 AI758412 AA045713 R79750 N76096
AW979121 AA847986 AA829098
439000 467716_1 AL133916 N79113 AF086101 N76721 AW950828 AA364013 AW955684 AI346341 AI867454 N54784 AI655270 AI421279 AW014882
439285 47065_1 AA775552 N62351 N59253 AA626243 AI341407 BE175639 AA456968 AI358918 AA457077
439780 47673_1 AL109688 R23665 R26578
441128 51021_2 AA570256 AW014761 AA573721 AI473237 AI022165 AA554071 AA127551 N90525 AW973623 AA447991 AA243852 BE328850 AI148171
AI359627 AI005068 AI356567 AA232991 AW016855 AA908902 AA233101 AA127550 BE512923
443068 558874_1 AI188710 AI032142 AW078833 N30308 AW675632 AI219028 AI341201 N22181 H95390
443947 586160_1 W24187 W24194 R17789
447636 7301_1 Y10043 NM_005342 L05085 AL034450 BE614226 AW749053 AA379173 AA248230 BE514634 AA334622 R70656 AA367593 AA214649
AA369318 AW957081 R05760 AA039903 AI886597 AW630122 AA906264 AA041527 R01145 AI088688 BE463637 AA398795 AI354883
AI768938 AI569996 AI452952 AI168582 AI189869 AI086670 AW262560 AW613854 AA862839 AA435840 AA670197 AI024032 AI990659
AI990089 N81095 AA847919 AW960150 AA211075 AA044704 AA367594 AW582587 AW858854 AW818630 AW818281 AW818433 AW582595
AA096002 N83992
448993 79225_1 AI471630 BE540637 BE265481 AW407710 BE513882 BE546739 AA053597 BE140503 BE218514 AW956702 AI656234 AI636283 AI567265
AW340858 BE207794 AA053085 R69173 AA292343 AA454908 AA293504 AI659741 AI927478 AA399460 AI760441 AA346416 BE047245
AA730380 AA394063 AA454833 AI982791 AI567270 AI813332 AI767858 AA427705 D20284 AI221458 BE048537 AI263048 AA346417
AA911497 BE537702
449305 804424_1 AI638293 AW813561
451105 859083_1 AI761324 AW880941 AW880937
451320 86576_1 AW118072 AI631982 T15734 AA224195 AI701458 W20198 F26326 AA890570 N90552 AW071907 AI671352 AI375892 T03517 R88265
AI124088 AA224388 AI084316 AI354686 T33652 AI140719 AI720211 T03490 AI372637 T15415 AW205836 AA630384 T03515 T33230
AA017131 AA443303 T33623 AI222556 T33511 T33785 AI419606 D55612
451807 8865_1 W52854 AL117600 BE208116 BE208432 BE206239 BE082291 AW953423 AA351619 BE180648 BE140560 W60080 AA865478 N90291
AW450652 AW449519 AA93634 AI806539 AA351618 AW449522 AI827626 AA904788 AA380381 AA886045 AA774409 BE003229 Z41756
452410 9163_1 AL133619 AA468118 AA383064 AI476447 T09430 AI673758 AA524895 AI581345 AI300820 AW498812 AA256162 AI559724 AI685732
AA602400 AA905453 AI204595 AW166541 AA157456 AA156269 AA383652 AA431072 AW592707 AI435410 AW272464 AI215594 AA622747
R74039 N35031 AI804128 AW513521 AA868351 AI026826 AI493388 AA614641 W81604 AI567080 AI214351 AA730140 AI125754 AI200813
AI269603 AI565082 AI807095 AI476629 AA505909 AI368449 AI686077 AI582930 AW085038 AA757863 AA730154 AI767072 AA468316
AI734130 AI734138 AA426284 AA433997 AI741241 AW043563 AI732741 AI732734 AA437369 AA425820 AA664048 R74130
454241 1067807_1 BE144666 BE184942 AW238414 BE184946
455175 1257335_1 AW993247 AW861464
456237 168730_1 AA203682 R11958
458098 47395_1 BE550224 AA632519 N45402 AW885857 N29245 BE465409 W07677 AW970089 AI299731 AA482971 BE503548 H18151 W79223 AF086393
AA461301 W74510 R34182 AI090689 N46003 BE071550 R28075 AW134982 AI240204 AI138906 AW026179 AI572316 BE466182 AI206395
AI276154 AI273269 AI422817 AI371014 AI421274 AI188525 AA939164 BE549810 AW137865 AI694996 BE503841 AA459718 BE327407
BE467534 BE218421 BE467767 AA989054 BE467063 AI797130 BE327781

TABLE 9C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA
sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
400512	9796593	Minus	1439-1615
400517	9796686	Minus	49996-50346
400560	9843598	Plus	94182-94323, 97056-97243, 101095-101236, 102824-103005
400664	8118496	Plus	13558-13721, 13942-14090, 14554-14679
400665	8118496	Plus	16879-17023
400666	8118496	Plus	17982-18115, 20297-20456
400749	7331445	Minus	9162-9293
400763	8131616	Minus	35537-35784
401027	7230983	Minus	70407-70554, 71060-71160
401093	8516137	Minus	22335-23166
401203	9743387	Minus	172961-173056, 173868-173928
401212	9858408	Plus	87839-88028
401411	7799787	Minus	144144-144329
401435	8217934	Minus	54508-55233
401464	6682291	Minus	170688-170834
401714	6715702	Plus	96484-96681
401747	9789672	Minus	118596-118816, 119119-119244, 119609-119761, 120422-120990, 130161-130381, 130468-130593, 131097-131258, 131866-131932, 132451-132575, 133580-134011
401760	9929699	Plus	83126-83250, 85320-85540, 94719-95287
401780	7249190	Minus	28397-28617, 28920-29045, 29135-29296, 29411-29567, 29705-29787, 30224-30573
401781	7249190	Minus	83215-83435, 83531-83656, 83740-83901, 84237-84393, 84955-85037, 86290-86814
401785	7249190	Minus	165776-165996, 166189-166314, 166408-166569, 167112-167268, 167387-167469, 168634-168942
401797	6730720	Plus	6973-7118
401961	4581193	Minus	124054-124209
401985	2580474	Plus	61542-61750
401994	4153858	Minus	42904-43124, 43211-43336, 44607-44763, 45199-45281, 46337-46732
402075	8117407	Plus	121907-122035, 122804-122921, 124019-124161, 124455-124610, 125672-126076
402260	3399665	Minus	113765-113910, 115653-115765, 116808-116940
402265	3287673	Plus	21059-21168
402297	6598824	Plus	35279-35405, 35573-35659
402408	9796239	Minus	110326-110491

	402420	9796339	Plus	129750-129919
	402674	8077108	Minus	39290-39502
	402802	3287156	Minus	53242-53432
5	402994	2996643	Minus	4727-4969
	403137	9211494	Minus	92349-92572,92958-93084,93579-93712,93949-94072,94591-94748,95214-95337
	403306	8099945	Plus	127100-127251
	403329	8516120	Plus	96450-96598
	403381	9438267	Minus	26009-26178
10	403478	9958258	Plus	116458-116564
	403485	9966528	Plus	2888-3001,3198-3532,3655-4117
	403627	8569879	Minus	23868-24342
	403715	7239669	Plus	85128-85292
	404044	9558573	Minus	225757-225939
	404076	9931752	Minus	3848-3967
15	404101	8076925	Minus	125742-125997
	404140	9843520	Plus	37761-38147
	404165	9926489	Minus	69025-69128
	404185	4572584	Minus	129171-129327
	404210	5006246	Plus	169926-170121
20	404253	9367202	Minus	55675-56055
	404287	2326514	Plus	53134-53281
	404298	9944263	Minus	73591-73723
	404347	9838195	Plus	74493-74829
	404440	7528051	Plus	80430-81581
25	404721	9856648	Minus	173763-174294
	404794	4826439	Plus	101619-101898
	404854	7143420	Plus	14260-14537
	404877	1519284	Plus	1095-2107
	404927	7342002	Plus	68690-69563
30	404996	6007890	Plus	37999-38145,38652-38998,39727-39872,40557-40674,42351-42450
	405449	7622497	Plus	42236-42570
	405568	6006906	Plus	35912-36065
	405572	3800891	Plus	85230-85938
35	405646	4914350	Plus	741-969
	405676	4557087	Plus	73195-73917
	405770	2735037	Plus	61057-62075
	405932	7767812	Minus	123525-123713
	406137	9166422	Minus	30487-31058
40	406360	9256107	Minus	7513-7673
	406399	9256288	Minus	63448-63554
	406467	9795551	Plus	182212-182958

TABLE 10A: Potential Therapeutic, Diagnostic and Prognostic targets for Therapy of Lung Cancer and Non-malignant Lung Disease

Table 2A shows about 307 genes up-regulated in non-malignant lung disease relative to lung tumors and normal body tissues and/or down-regulated in lung tumors relative to normal lung and non-malignant lung disease. These genes were selected from about 59680 probesets on the Eos/Affymetrix Hu03 Genechip array.

Table 10B show the accession numbers for those Pkey's lacking UnigenelD's for table 10A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Table 10C show the genomic positioning for those Pkey's lacking Unigene ID's and accession numbers in table 10A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Average of lung tumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatous and carcinoid tumors) divided by the average of normal lung samples
 R2: Average of non-malignant lung disease samples (including bronchitis, emphysema, fibrosis, atelectasis, asthma) divided by the average of normal lung samples

	Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2
65	404394			ENSP00000241075:TRRAP PROTEIN.	0.79	3.10
	404916			Target Exon	1.00	159.00
	405257			Target Exon	1.00	422.00
70	407228	M25079	Hs.155376	hemoglobin, beta	0.47	2.33
	407568	AA740964	Hs.62699	ESTs	1.00	123.00
	408562	AI436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,	1.00	230.00
	409031	AA376836	Hs.76728	ESTs	1.00	128.00
	410434	AF051152	Hs.63668	tol-like receptor 2	39.65	149.00
75	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	1.00	109.00
	410808	T40326	Hs.167793	ESTs	1.14	13.14
	412351	AL135960	Hs.73828	T-cell acute lymphocytic leukemia 1	0.37	2.27
	412372	R65998	Hs.285243	hypothetical protein FLJ22029	1.00	173.00
	413795	AL040178	Hs.142003	ESTs	0.10	11.90
80	414154	AW205314	Hs.323060	ESTs	0.62	2.09
	414214	D49958	Hs.75819	glycoprotein M6A	0.03	4.55
	414998	NM_002543	Hs.77729	oxidised low density lipoprotein (lectin	0.64	2.97
	415122	D60708	Hs.22245	ESTs	0.07	8.97
	415765	NM_005424	Hs.78824	tyrosine kinase with immunoglobulin and	0.67	1.65
85	415775	H00747	Hs.29792	ESTs, Weakly similar to I38022 hypotheri	0.29	2.64
	415910	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	1.00	145.00

	416319	AI815601	Hs.79197	CD83 antigen (activated B lymphocytes, i	15.32	237.00
	416402	NM_000715	Hs.1012	complement component 4-binding protein,	0.64	4.00
	417355	D13168	Hs.82002	endothelin receptor type B	0.01	3.90
5	417421	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, m	36.30	357.00
	417511	AL049176	Hs.82223	chordin-like	1.00	179.00
	418489	U76421	Hs.85302	adenosine deaminase, RNA-specific, B1 (h	0.02	6.00
	418726	BE241812	Hs.87860	protein tyrosine phosphatase, non-recept	1.00	113.00
	418741	H83265	Hs.8881	ESTs, Weakly similar to S41044 chromosom	0.44	1.90
10	418883	BE387036	Hs.1211	acid phosphatase 5, tartrate resistant	0.96	2.04
	419086	NM_000216	Hs.89591	Kallmann syndrome 1 sequence	0.62	2.74
	419150	T29618	Hs.89640	TEK tyrosine kinase, endothelial (venous	0.03	6.90
	419235	AW470411	Hs.288433	neurotrophin	1.48	5.13
	419407	AW410377	Hs.41502	hypothetical protein FLJ21276	37.55	336.00
15	420556	AA278300	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	0.80	3.65
	420656	AA279098	Hs.187636	ESTs	1.65	8.07
	420729	AW964897	Hs.290825	ESTs	2.99	25.82
	421177	AW070211	Hs.102415	Homo sapiens mRNA; cDNA DKFZp586N0121 (f	0.46	1.95
	422060	R20893	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	1.00	156.00
20	422426	W79117	Hs.58559	ESTs	0.03	7.44
	422652	AW967969	Hs.118958	syntaxin 11	0.14	3.62
	423099	NM_002837	Hs.123641	protein tyrosine phosphatase, receptor t	0.01	3.16
	424433	H04607	Hs.9218	ESTs	0.75	141.75
	424585	AA464840	Hs.131987	ESTs	1.00	167.00
25	424711	NM_005795	Hs.152175	calcitonin receptor-like	0.43	3.01
	424973	X92521	Hs.154057	matrix metalloproteinase 19	0.37	19.45
	425023	AW956889	Hs.154210	endothelial differentiation, sphingolipi	0.14	3.35
	425664	AJ006276	Hs.159003	transient receptor potential channel 6	1.00	94.00
	425998	AU076629	Hs.165950	fibroblast growth factor receptor 4	0.68	1.42
30	426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	0.03	3.74
	426753	T89832	Hs.170278	ESTs	1.00	141.00
	427558	D49493	Hs.2171	growth differentiation factor 10	1.00	117.00
	427983	M17706	Hs.2233	colony stimulating factor 3 (granulocyte	0.75	2.20
	428467	AK002121	Hs.184465	hypothetical protein FLJ11259	0.76	2.25
35	428927	AA441837	Hs.90250	ESTs	0.01	3.62
	429496	AA453800	Hs.192793	ESTs	1.00	138.00
	430468	NM_004673	Hs.241519	angiopoietin-like 1	1.00	132.00
	431385	BE178536	Hs.11090	membrane-spanning 4-domains, subfamily A	1.00	157.00
	431728	NM_007351	Hs.268107	multimerin	1.00	157.00
40	431848	AI378857	Hs.126758	ESTs, Highly similar to AF175283 1 zinc	0.34	2.24
	432128	AA127221	Hs.117037	ESTs	0.00	1.15
	432519	AI221311	Hs.130704	ESTs, Weakly similar to BCHUIA S-100 pro	0.01	2.06
	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	1.00	267.00
	433803	AI823593	Hs.27688	ESTs	1.00	105.00
45	434730	AA644669	Hs.193042	ESTs	1.05	3.15
	435472	AW972330	Hs.283022	triggering receptor expressed on myeloid	0.83	1.94
	436532	AA721522		gb:nv54h12.r1 NCI_CGAP_Ew1 Homo sapiens	1.00	218.00
	437119	AI379921	Hs.177043	ESTs	1.00	133.00
	437140	AA312799	Hs.283689	activator of CREM in testis	0.67	122.67
50	437211	AA382207	Hs.5509	ecotropic viral integration site 2B	1.00	142.00
	437960	AI669586	Hs.222194	ESTs	1.00	147.00
	438202	AW169287	Hs.22588	ESTs	1.00	141.00
	438873	AI302471	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	0.71	3.66
	438875	AA827640	Hs.189059	ESTs	23.32	370.00
55	441048	AA913488	Hs.192102	ESTs	0.77	8.50
	441188	AW292830	Hs.255609	ESTs	3.43	16.36
	441499	AW298235	Hs.101689	ESTs	1.00	167.00
	444513	AL120214	Hs.7117	glutamate receptor, ionotropic, AMPA 1	1.00	151.00
	444527	NM_005408	Hs.11383	small inducible cytokine subfamily A (Cy	46.47	153.00
60	444561	NM_004469	Hs.11392	c-fos induced growth factor (vascular en	0.01	3.08
	445279	R41900	Hs.22245	ESTs	0.60	141.00
	446017	N98238	Hs.55185	ESTs	0.18	2.39
	446984	AB020722	Hs.16714	Rho guanine exchange factor (GEF) 15	0.10	2.16
	446998	N99013	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	0.01	2.53
65	447357	AI375922	Hs.159367	ESTs	0.46	2.64
	448106	AI800470	Hs.171941	ESTs	18.05	296.00
	448253	H25899	Hs.201591	ESTs	1.00	141.00
	449275	AW450848	Hs.205457	periastin	0.56	1.38
	450400	AI694722	Hs.279744	ESTs	0.88	4.33
70	450696	AI654223	Hs.16026	hypothetical protein FLJ23191	0.52	2.08
	450726	AW204600	Hs.250505	retinoic acid receptor, alpha	0.79	2.01
	451497	H83294	Hs.284122	Wnt inhibitory factor-1	0.35	2.03
	451533	NM_004657	Hs.26530	serum deprivation response (phosphatidyl	0.13	2.25
	453636	R67837	Hs.169872	ESTs	1.00	116.00
	458332	AI000341	Hs.220491	ESTs	1.00	192.00
75	459580	AA022888	Hs.176065	ESTs	0.20	2.98
	400269			Eos Control	0.40	2.40
	403421			NM_016369*:Homo sapiens claudin 18 (CLDN	0.53	1.77
	407570	Z19002	Hs.37096	zinc finger protein 145 (Kruppel-like, e	0.01	3.18
80	412295	AW088826	Hs.117176	poly(A)-binding protein, nuclear 1	0.56	1.74
	414517	M24461	Hs.76305	surfactant, pulmonary-associated protein	0.64	1.50
	417204	N81037	Hs.1074	surfactant, pulmonary-associated protein	0.33	1.16
	418307	U70867	Hs.83974	solute carrier family 21 (prostaglandin	0.53	1.55
	418935	T28499	Hs.89485	carbonic anhydrase IV	0.20	1.28
85	421502	AF111856	Hs.105039	solute carrier family 34 (sodium phospho	0.78	1.90
	421798	N74880	Hs.29877	N-acylsphingosine amidohydrolase (acid c	0.59	1.54

	423354	AB011130	Hs.127436	calcium channel, voltage-dependent, alph	0.59	1.55
	423738	AB002134	Hs.132195	airway trypsin-like protease	10.14	51.00
	425211	M18667	Hs.1867	progastricsin (pepsinogen C)	0.35	1.62
5	425438	T62216	Hs.270840	ESTs	0.23	9.45
	426828	NM_000020	Hs.172670	activin A receptor type II-like 1	0.03	1.71
	427019	AA001732	Hs.173233	hypothetical protein FLJ10970	0.01	1.49
	428043	T92248	Hs.2240	uteroglobin	0.42	1.26
	430280	AA361258	Hs.237868	interleukin 7 receptor	0.46	2.43
10	431433	X65018	Hs.253495	surfactant, pulmonary-associated protein	0.57	1.59
	431723	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	0.29	1.80
	432985	T92363	Hs.178703	ESTs	0.32	2.27
	441835	AB036432	Hs.184	advanced glycosylation end product-speci	0.31	1.51
	442275	AW449467	Hs.54795	ESTs	0.55	1.78
15	443709	AI082692	Hs.134562	ESTs	0.00	3.02
	444325	AW152618	Hs.16757	ESTs	0.32	2.49
	450954	AI904740	Hs.25691	receptor (calcitonin) activity modifying	0.46	1.74
	451558	NM_001089	Hs.26630	ATP-binding cassette, sub-family A (ABC1	0.52	1.87
	453310	X70697	Hs.553	solute carrier family 6 (neurotransmitte	0.00	3.30
20	456855	AF035528	Hs.153863	MAD (mothers against decapentaplegic, Dr	0.01	2.31
	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	0.66	2.20
	400754			Target Exon	1.00	297.00
	401045			C11001883*:gij[6753278]ref[NP_033938.1] c	1.00	109.00
	401083			NM_016582*:Homo sapiens peptide transpor	0.89	1.39
25	402474			NM_004079:Homo sapiens cathepsin S (CTSS	1.45	4.47
	402808			ENSP00000235229:SEMB.	1.00	1.87
	403021			C21000030:gij[9955960]ref[NP_063957.1] AT	1.00	149.00
	403438			NM_031419*:Homo sapiens molecule possess	1.06	2.96
	403687			NM_007037*:Homo sapiens a disintegrin-li	0.04	4.89
30	403764			NM_005463:Homo sapiens heterogeneous nuc	1.00	225.00
	404277			NM_019111*:Homo sapiens major histocompa	0.97	1.93
	404288			NM_002944*:Homo sapiens v-ros avian UR2	1.00	68.00
	404518	AI815601		CD83 antigen (activated B lymphocytes, i	0.02	1.83
	405106			C11001637*:gij[5032241]ref[NP_005732.1] z	1.00	235.00
35	405381			Target Exon	1.00	93.00
	406387			Target Exon	1.37	6.02
	406646	M33600		major histocompatibility complex, class	0.86	2.46
	406714	AI219304	Hs.266959	hemoglobin, gamma G	0.01	3.19
	406753	AA505665	Hs.217493	annexin A2	1.00	147.00
40	406973	M34996	Hs.198253	major histocompatibility complex, class	1.03	2.04
	407248	U82275	Hs.94498	leukocyte immunoglobulin-like receptor,	1.00	64.00
	407510	U96191		gb:Human trophoblast hypoxia-regulated f	1.00	90.00
	407731	NM_000066	Hs.38069	complement component 8, beta polypeptide	1.00	67.00
	407830	NM_001086	Hs.587	arylacetamide deacetylase (esterase)	1.00	102.00
45	408045	AW138959	Hs.245123	ESTs	1.00	70.00
	408074	R20723		ESTs	1.00	112.00
	408374	AW025430	Hs.155591	forkhead box F1	0.07	10.17
	409064	AA062954	Hs.141883	ESTs	0.39	2.31
	409083	AF050083	Hs.673	interleukin 12A (natural killer cell sti	1.00	95.00
50	409153	W03754	Hs.50813	hypothetical protein FLJ20022	0.01	4.55
	409203	AA780473	Hs.687	cytochrome P450, subfamily IVB, polypept	0.01	3.72
	409238	AI049990	Hs.51515	Homo sapiens mRNA; cDNA DKFZp564G112 (fr	1.00	79.00
	409389	AB007979	Hs.301281	Homo sapiens mRNA, chromosome 1 specific	0.14	27.35
	409718	D86640	Hs.56045	src homology three (SH3) and cysteine ri	1.00	113.00
55	410798	BE178622	Hs.16291	gb:PM3-HT0605-270200-001-a02 HT0605 Homo	0.64	2.47
	411020	NM_006770	Hs.67726	macrophage receptor with collagenous str	0.55	2.40
	411667	BE160198		gb:QV1-HT0413-010200-059-h03 HT0413 Homo	1.00	111.00
	412000	AW576555	Hs.15780	ATP-binding cassette, sub-family A (ABC1	1.00	95.00
	412358	BE047490	Hs.24172	ESTs	1.00	87.00
60	412420	AL035668	Hs.73853	bone morphogenetic protein 2	1.43	8.07
	412564	X83703	Hs.31432	cardiac ankyrin repeat protein	0.02	3.07
	412869	AA290712	Hs.82407	CXC chemokine ligand 16	0.93	1.72
	412870	N22788	Hs.82407	CXC chemokine ligand 16	0.97	1.51
	413529	U11874	Hs.846	interleukin 8 receptor, beta	0.02	2.42
65	413533	BE146973		gb:QV4-HT0222-011199-019-e05 HT0222 Homo	0.65	1.50
	413689	BE157286	Hs.20631	zinc finger protein, subfamily 1A, 5 (Pe	20.87	232.00
	413724	AA131466	Hs.23767	hypothetical protein FLJ12666	1.00	80.00
	413800	AI129238	Hs.192235	ESTs	1.00	85.00
	413802	AW964490	Hs.32241	ESTs, Weakly similar to S65657 alpha-1C-	1.00	213.00
70	413829	NM_001872	Hs.75572	carboxypeptidase B2 (plasma)	0.02	3.93
	414376	BE393856	Hs.66915	ESTs, Weakly similar to 16.7Kd protein [1.00	115.00
	414577	AI056548	Hs.72116	hypothetical protein FLJ20992 similar to	0.49	1.94
	414700	H63202	Hs.38163	ESTs	0.03	3.75
	415078	AA311223	Hs.283091	found in inflammatory zone 3	0.86	1.95
75	415120	N64464	Hs.34950	ESTs	1.00	120.00
	415323	BE269352	Hs.949	neutrophil cytosolic factor 2 (65kD, chr	0.60	2.48
	415335	AA847758	Hs.111030	ESTs	1.00	95.00
	415582	W92445	Hs.165195	Homo sapiens cDNA FLJ14237 fis, clone NT	1.00	136.00
	416030	H15261	Hs.21948	ESTs	0.02	8.07
80	416427	BE244050	Hs.79307	Rac/Cdc42 guanine exchange factor (GEF)	1.00	73.00
	416464	NM_000132	Hs.79345	coagulation factor VIII, procoagulant co	0.70	3.36
	416585	X54162	Hs.79386	leiomodulin 1 (smooth muscle)	0.06	6.56
	416847	L43821	Hs.80261	enhancer of filamentation 1 (cas-like do	0.70	3.66
	417148	AA359896	Hs.293885	hypothetical protein FLJ14902	1.00	114.00
85	417370	T28651	Hs.82030	tryptophanyl-tRNA synthetase	0.85	1.30
	417673	T87281	Hs.16355	ESTs	0.15	15.54

	418067	AI127958	Hs.83393	cystatin E/M	0.81	1.74
	418296	C01566	Hs.86671	ESTs	1.00	99.00
	418643	J03798	Hs.86948	small nuclear ribonucleoprotein D1 polyp	1.00	60.00
5	418832	X04011	Hs.88974	cytochrome b-245, beta polypeptide (chro	2.40	14.74
	418945	BE246762	Hs.89499	arachidonate 5-lipoxygenase	0.67	3.16
	419261	X07876	Hs.89791	wingless-type MMTV integration site fami	1.00	73.00
	419564	U08989	Hs.91139	solute carrier family 1 (neuronal/epith	1.00	192.00
	419574	AK001989	Hs.91165	hypothetical protein	1.00	94.00
10	419968	X04430	Hs.93913	interleukin 6 (interferon, beta 2)	61.16	500.00
	420256	U84722	Hs.76205	cadherin 5, type 2, VE-cadherin (vascula	0.52	1.70
	420285	AA258124	Hs.293878	ESTs, Moderately similar to ZN91_HUMAN Z	1.00	172.00
	420577	AA278436	Hs.186649	ESTs	1.00	97.00
	421262	AA286746	Hs.9343	Homo sapiens cDNA FLJ14265 fis, clone PL	1.00	64.00
15	421445	AA913059	Hs.104433	Homo sapiens, clone IMAGE:4054868, mRNA	0.88	1.51
	421470	R27496	Hs.1378	annexin A3	0.05	11.26
	421478	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribos	1.00	73.00
	421563	NM_006433	Hs.105806	granulysin	0.82	2.42
	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	5.50	31.57
20	421855	F06504	Hs.27384	ESTs, Moderately similar to ALU4_HUMAN A	1.00	129.00
	421913	AI934365	Hs.109439	osteoglycin (osteoinductive factor, mime	1.00	101.00
	421952	AA300900	Hs.98849	ESTs, Moderately similar to AF161511 1 H	0.60	63.60
	422232	D43945	Hs.113274	transcription factor EC	1.00	148.00
	422386	AF105374	Hs.115830	heparan sulfate (glucosamine) 3-O-sulfot	1.40	3.98
25	423168	R34385	Hs.124940	GTP-binding protein	0.34	3.59
	423196	AK001866	Hs.125139	hypothetical protein FLJ11004	0.55	2.00
	423387	AJ012074		vasoactive intestinal peptide receptor 1	0.09	2.13
	423424	AF150241	Hs.128433	prostaglandin D2 synthase, hematopoietic	1.00	141.00
	423456	AL110151	Hs.128797	DKFZP586D0824 protein	1.00	66.00
30	423696	Z92546		Sushi domain (SCR repeat) containing	0.73	1.27
	424027	AW337575	Hs.201591	ESTs	0.54	2.58
	424212	NM_005814	Hs.143131	glycoprotein A33 (transmembrane)	0.77	2.47
	425087	R62424	Hs.126059	ESTs	1.00	74.00
	425175	AF020202	Hs.155001	UNC13 (C. elegans)-like	0.85	1.96
35	425771	BE561776	Hs.159494	Bruton agammaglobulinemia tyrosine kinas	1.18	2.56
	426486	BE178285	Hs.170056	Homo sapiens mRNA; cDNA DKFZp586B0220 (f	1.00	76.00
	427507	AF240467	Hs.179152	tol1-like receptor 7	1.00	63.00
	427618	NM_000760	Hs.2175	colony stimulating factor 3 receptor (gr	0.60	2.19
	427732	NM_002980	Hs.2199	secretin receptor	0.97	1.42
40	427952	AA765368	Hs.293941	ESTs, Moderately similar to A53959 throm	1.00	105.00
	428709	BE268717	Hs.104916	hypothetical protein FLJ21940	1.00	80.00
	428769	AW207175	Hs.106771	ESTs	0.09	2.55
	428780	AJ478578	Hs.50636	ESTs	1.00	98.00
	428833	AI928355	Hs.185805	ESTs	1.00	113.00
45	429657	D13626	Hs.2465	KIAA0001 gene product; putative G-protei	1.00	52.00
	430212	AA469153		gb:nc67f04.s1 NCI_CGAP_Pr1 Homo sapiens	1.00	132.00
	430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	0.11	15.60
	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	1.00	103.00
	430414	AW365665	Hs.120388	ESTs	0.50	6.96
50	430656	AA482900	Hs.162080	ESTs	1.00	70.00
	430843	AI734149	Hs.119514	ESTs	1.00	90.00
	430998	AF128847	Hs.204038	indolethylamine N-methyltransferase	0.29	1.84
	431217	NM_013427	Hs.250830	Rho GTPase activating protein 6	1.00	79.00
	431921	N46466	Hs.58879	ESTs	0.91	1.67
55	432176	AW090386	Hs.112278	arrestin, beta 1	0.66	2.63
	432203	AA305746	Hs.49	macrophage scavenger receptor 1	1.00	76.00
	432231	AA339977	Hs.274127	CLST 11240 protein	0.46	1.46
	432485	N90866	Hs.276770	CDW52 antigen (CAMPATH-1 antigen)	0.79	2.25
	432522	D11466	Hs.51	phosphatidylinositol glycan, class A (pa	1.93	4.83
60	432596	AJ224741	Hs.278461	matrilin 3	0.04	5.79
	432850	X87723	Hs.3110	angiotensin receptor 2	1.00	167.00
	433138	AB029496	Hs.59729	semaphorin sem2	0.04	9.16
	433563	AI732637	Hs.277901	ESTs	1.00	91.00
	433588	AI056872	Hs.133386	ESTs	120.16	315.00
65	434445	AI349306	Hs.11782	ESTs	0.60	1.84
	435496	AW840171	Hs.265398	ESTs, Weakly similar to transformation-r	1.00	128.00
	435974	U29690	Hs.37744	Homo sapiens beta-1 adrenergic receptor	1.00	108.00
	436061	AI248584	Hs.190745	Homo sapiens cDNA: FLJ21326 fis, clone C	1.00	91.00
	437157	BE048860	Hs.120655	ESTs	1.00	87.00
70	437207	T27503	Hs.15929	hypothetical protein FLJ12910	1.00	105.00
	437311	AA370041	Hs.9456	SWI/SNF related, matrix associated, acti	1.00	71.00
	437439	H29796	Hs.269622	ESTs	1.00	115.00
	438199	AW016531	Hs.122147	ESTs	1.00	80.00
	439551	W72062	Hs.11112	ESTs	0.30	3.10
75	440515	AJ131245	Hs.7239	SEC24 (S. cerevisiae) related gene fami	1.00	77.00
	440887	AI799488	Hs.135905	ESTs	1.00	85.00
	441025	AA913880	Hs.176379	ESTs	1.00	82.00
	441384	AA447849	Hs.288660	Homo sapiens cDNA: FLJ22182 fis, clone H	0.79	1.89
	441735	AI738675	Hs.127346	ESTs	1.00	75.00
80	442200	AW590572	Hs.235768	ESTs	0.78	5.83
	442832	AW206560	Hs.253569	ESTs	0.03	10.88
	442957	AI949952	Hs.49397	ESTs	1.00	70.00
	443282	T47764	Hs.132917	ESTs	1.00	197.00
	443547	AW271273	Hs.23767	hypothetical protein FLJ12666	1.00	253.00
85	443951	F13272	Hs.111334	ferritin, light polypeptide	0.55	2.09
	444330	AI597655	Hs.49265	ESTs	1.00	90.00

	444515	AW204908	Hs.169979	ESTs	1.00	84.00
	445769	AI741471	Hs.23666	ESTs	0.02	4.38
	445908	R13580	Hs.13436	Homo sapiens clone 24425 mRNA sequence	1.00	97.00
5	446291	BE397753	Hs.14623	interferon, gamma-inducible protein 30	0.93	1.69
	446917	AI347863	Hs.156672	ESTs	1.00	106.00
	447261	NM_006691	Hs.17917	extracellular link domain-containing 1	0.40	47.20
	447432	AW958473	Hs.301957	nudix (nucleoside diphosphate linked moi	1.00	100.00
	447482	AB033059	Hs.18705	KIAA1233 protein	0.05	8.21
10	447997	H00656	Hs.29792	ESTs, Weakly similar to I38022 hypotheli	0.02	5.42
	448299	AA497044	Hs.20887	hypothetical protein FLJ10392	1.00	79.00
	448782	AL050295	Hs.22039	KIAA0758 protein	0.42	1.56
	450575	NM_005859	Hs.29117	purine-rich element binding protein A	0.17	11.33
	450584	AA040403	Hs.60371	ESTs	1.00	94.00
15	450693	AW450461	Hs.203965	ESTs	1.00	91.00
	450715	AI266484	Hs.31570	ESTs, Weakly similar to KIAA1324 protein	1.00	152.00
	451103	R52804	Hs.25956	DKFZP564D206 protein	1.00	86.00
	451220	AF124251	Hs.26054	novel SH2-containing protein 3	0.60	1.30
	451668	Z43948	Hs.326444	cartilage acidic protein 1	0.54	1.91
20	452197	AW023595	Hs.232048	ESTs	1.00	67.00
	452331	AA598509	Hs.29117	purine-rich element binding protein A	4.53	11.07
	452353	C18825	Hs.29191	epithelial membrane protein 2	0.72	2.24
	453049	BE537217	Hs.30343	ESTs	1.00	68.00
	453107	NM_016113	Hs.279746	vanilloid receptor-like protein 1	0.83	1.70
	453355	AW295374	Hs.31412	Homo sapiens cDNA FLJ11422 fis, clone HE	1.00	132.00
25	453390	AA862496	Hs.28482	ESTs	1.00	72.00
	453531	AA417940		ESTs, Weakly similar to JC5795 CDEP prot	1.00	68.00
	454741	BE154396		gb:CM2-HT0342-091299-050-b05 HT0342 Homo	0.57	2.89
	455579	AA287827	Hs.284205	up-regulated by BCG-CWS	1.00	82.00
30	456672	AK002016	Hs.114727	Homo sapiens, clone MGC:16327, mRNA, com	0.79	1.96
	457400	AF032906	Hs.252549	cathepsin Z	1.03	3.25
	457718	F18572	Hs.22978	ESTs, Weakly similar to ALU4_HUMAN ALU S	1.00	113.00
	459696	F03027		gb:HSC1KA072 normalized infant brain cDN	1.00	544.00

TABLE 10B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
408074	103684_1	R20723 AA263003 AA333976 AA334725 AA334151 AW965490 AA310513 AI810530 D31302 AW134897 AA830127 AA046953 AI668930 C06094 AW104534
411667	1253334_1	BE160198 AW935898 T11520 AW935930 AW856073 AW861034
413533	1375344_1	BE146973 BE146972 BE147042 BE147018 BE146783 BE147020 BE146781 BE147019 BE146766 BE147021 BE146952 BE146767 BE147044 BE146797 BE146776 BE146985 BE146793 BE146768 BE146771 BE146954 BE146760 BE147048 BE147025 BE147030
423387	22779_1	AJ012074 U11087 L13288 X75299 L20295 AW630780 H14880 T28037 AI872991 R72136 AW449839 T81622 T79697 T29519 R94105 T83923 R73300 AI797007 R73390 AA961010 H74168 AI689932 BE045543 AI808418 AI608912 AI806573 AW884084 AW872978 AW872985 AA565655 AI022915 R50647 R73210 H45098 R46451 AW166269 T71132 AI264547 R52146 AI304920 R73391 AW884059 AW884085 H73241 T60038 T79612 R73145 R50549 AI094557 AI668793 R72302 AI564366 W01956 AA418962 W32571 R72840 H45409 R72085 R46356 R46758 AA508805 AA418798 T83751 R94072 T16182 AA928785 AA903896
423696	23112_1	Z92546 AA330586 AI570568 AW341487 AI827050 AW298668 AI792189 AI015693 AI733599 AI572251 AI672488 AW193262 AI244716 AI864375 AI206100 AA912444 AI269365 AI640254 AW772466 AI867336 AA627604 H16914 AA358477 AA338009
430212	314437_1	AA469153 AI718503 AA469225
436532	421802_1	AA721522 AW975443 T93070
453531	97026_1	AA417940 AA036735 T07025
454741	1232559_1	BE154396 AW817959 BE154393

TABLE 10C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
400754	7331445	Plus	144559-144684
401045	8117619	Plus	90044-90184,91111-91345
401083	3242744	Plus	33192-33360
402474	7547175	Minus	53526-53628,55755-55920,57530-57757
402808	6456148	Minus	114964-115136,115461-115585,115931-116047,117666-117771,118004-118102
403021	7547270	Plus	120799-120966
403421	9665041	Minus	126609-126773,139986-140205
403438	9719679	Plus	90792-90938
403687	7387384	Plus	9009-9534
403764	7717105	Minus	118692-118853
404277	1834458	Minus	91665-91946
404288	2769644	Plus	3512-3691
404394	3135305	Minus	37121-37205,37491-37762,41053-41140,41322-41593,41773-41919
404518	8151988	Plus	84494-84603
404916	7341826	Plus	91057-91188
405106	8079395	Minus	80877-81418
405257	7329310	Plus	73121-73273
405381	6006920	Minus	7636-8054

TABLE 11A: Genes Distinguishing Adenocarcinoma from Other Lung Diseases and Normal Lung

Table 11A shows about 84 genes upregulated in lung adenocarcinomas relative to other lung tumors, non-malignant lung disease, and normal lung. These genes were selected from about 59680 probesets on the Eos/Affymetrix Hu03 Genechip array.

Table 11B shows the accession numbers for those Pkey's lacking UnigenelD's for table 11A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Table 11C show the genomic positioning for those Pkey's lacking UnigenelD's and accession numbers in table 11A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique Eos probeset Identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigenel number
 Unigenel Title: Unigenel gene title
 R1: Average of lung tumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatous and carcinoid tumors) divided by the average of normal lung samples
 R2: Average of non-malignant lung disease samples (including bronchitis, emphysema, fibrosis, atelectasis, asthma) divided by the average of normal lung samples

Pkey	ExAccn	UnigenelD	Unigenel Title	R1	R2
403329			Target Exon	1.00	61.00
406399			NM_003122: Homo sapiens serine protease	1.00	39.00
406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	226.37	350.00
407869	AI827976	Hs.24391	hypothetical protein FLJ13612	0.77	1.18
407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfot	1.00	10.00
408908	BE296227	Hs.250822	serine/threonine kinase 15	7.76	1.00
409103	AF251237	Hs.112208	XAGE-1 protein	80.44	40.00
409187	AF154830	Hs.50966	carbamoyl-phosphate synthetase 1, mitoch	1.00	1.00
409269	AA576953	Hs.22972	hypothetical protein FLJ13352	1.00	1.00
410076	T05387	Hs.7991	ESTs	1.12	1.50
410102	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	9.89	1.00
410399	BE068889		synuclein, gamma (breast cancer-specific	0.92	1.06
411908	L27943	Hs.72924	cytidine deaminase	1.00	1.00
412612	NM_000047	Hs.74131	arylsulfatase E (chondrodysplasia puncta	1.02	1.03
414075	U11862	Hs.75741	amiloride binding protein 1 (amine oxida	0.84	1.07
416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	3.67	1.00
417542	J04129	Hs.82269	progesterone-associated endometrial prote	1.28	1.35
419183	U60669	Hs.89663	cytochrome P450, subfamily XXIV (vitamin	1.00	1.00
419502	AU076704		fibrinogen, A alpha polypeptide	13.05	115.00
419631	AW188117	Hs.303154	popeye protein 3	1.00	13.00
420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	1.00	8.00
421155	H87879	Hs.102267	lysyl oxidase	1.00	15.00
421190	U95031	Hs.102482	mucin 5, subtype B, tracheobronchial	1.17	1.55
421474	U76362	Hs.104637	solute carrier family 1 (glutamate trans	1.46	1.76
421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase 1, l	1.00	3.00
421582	AI910275		trefoil factor 1 (breast cancer, estroge	1.23	1.00
422026	U80736	Hs.110826	trinucleotide repeat containing 9	1.00	52.00
422095	AI868872	Hs.282804	hypothetical protein FLJ22704	4.37	2.34
422311	AF073515	Hs.114948	cytokine receptor-like factor 1	1.15	1.78
422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	1.69	3.17
423472	AF041260	Hs.129057	breast carcinoma amplified sequence 1	48.13	72.00
423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	1.00	50.00
424502	AF242388	Hs.149585	lengsin	1.00	1.00
424544	M88700	Hs.150403	dopa decarboxylase (aromatic L-amino aci	1.00	59.00
424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	21.35	1.00
424960	BE245380	Hs.153952	5' nucleotidase (CD73)	1.00	1.00
425523	AB007948	Hs.158244	KIAA0479 protein	1.00	35.00
426230	AA367019	Hs.241395	protease, serine, 1 (trypsin 1)	1.00	83.00
427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	7.41	34.00
428585	AB007863	Hs.185140	KIAA0403 protein	1.00	6.00
428758	AA433988	Hs.98502	hypothetical protein FLJ14303	1.06	1.13
429170	NM_001394	Hs.2359	dual specificity phosphatase 4	16.18	105.00
429263	AA019004	Hs.198396	ATP-binding cassette, sub-family A (ABC1	1.07	1.00
429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas	1.59	1.69
430508	AI015435	Hs.104637	ESTs	4.75	7.27
430985	AA490232	Hs.27323	ESTs, Weakly similar to I78885 serine/th	0.94	1.28
431548	AI834273	Hs.9711	novel protein	5.66	15.00
431566	AF176012	Hs.260720	J domain containing protein 1	49.76	37.00
431986	AA536130	Hs.149018	Novel human gene mapping to chromosome 20	1.19	1.47
432375	BE536069	Hs.2962	S100 calcium-binding protein P	1.65	1.06
432677	NM_004482	Hs.278611	UDP-N-acetyl-alpha-D-galactosamine:polyp	1.00	48.00
433556	W56321	Hs.111460	calcium/calmodulin-dependent protein kin	1.00	19.00
433819	AW511097	Hs.112765	ESTs	3.71	8.00
434001	AW950905	Hs.3697	serine (or cysteine) proteinase inhibito	29.31	72.00
434424	AI811202	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	1.00	64.00
434792	AA649253	Hs.132458	ESTs	8.52	44.00
436217	T53925	Hs.107	fibrinogen-like 1	57.97	31.00
436749	AA584890	Hs.5302	lectin, galactoside-binding, soluble, 4	1.10	1.41
436972	AA284679	Hs.25640	claudin 3	1.59	1.46
437866	AA156781		metallothionein 1E (functional)	3.62	101.00
437935	AW939591	Hs.5940	mucin 13, epithelial transmembrane	1.60	1.39
438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	1.00	1.00
439451	AF086270	Hs.278554	heterochromatin-like protein 1	23.28	52.00

439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN	1.00	21.00
441031	AI110684	Hs.7645	fibrinogen, B beta polypeptide	1.41	99.00
441377	BE218239	Hs.202656	ESTs	22.03	1.00
443614	AV655386	Hs.7645	fibrinogen, B beta polypeptide	1.00	16.00
443813	AA876372	Hs.93961	Homo sapiens mRNA; cDNA DKFZp667D095 (fr	1.20	1.99
443991	NM_002250	Hs.10082	potassium intermediate/small conductance	5.71	6.87
444670	H58373	Hs.332938	hypothetical protein MGC5370	1.98	38.00
444931	AV652066	Hs.75113	general transcription factor IIA	1.00	54.00
446102	AW168067	Hs.317694	ESTs	1.00	1.00
446163	AA026880	Hs.25252	Homo sapiens cDNA FLJ13603 fis, clone PL	1.00	36.00
446469	BE094848	Hs.15113	homogentisate 1,2-dioxygenase (homogenti	1.00	11.00
447388	AW630534	Hs.76277	Homo sapiens, clone MGC:9381, mRNA, comp	1.24	1.16
447532	AK000614	Hs.18791	hypothetical protein FLJ20607	1.23	1.63
448243	AW369771	Hs.52620	integrin, beta 8	15.84	1.00
448844	AI581519	Hs.177164	ESTs	1.00	31.00
449444	AW818436	Hs.23590	solute carrier family 16 (monocarboxylic	1.00	83.00
451807	W52854		hypothetical protein FLJ23293 similar to	1.55	35.00
452689	F33868	Hs.284176	transferrin	1.54	1.44
453392	U23762	Hs.32964	SRX (sex determining region Y)-box 11	1.00	16.00
453464	AI884911	Hs.32989	receptor (calcitonin) activity modifying	1.55	2.45
453735	AI065629	Hs.125073	ESTs	1.01	1.30

TABLE 11B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
410399	11995_1	BE068889 BE068882 AF044311 AF017256 NM_003087 AF037207 AF010126 AA633976 AA872836 BE298825 BE299889 AI016464 AI684600 AI936527 AA804675 AA394097 AI139933 AA946606 BE171313 AA722407 AA293803 AI468480 AA056035 AA055968 AW796957 AI637713 AA410737 H49348 AA486472 AA411094 AA235594 AA402624 AA443638 AW452137 AA421708 AW265211 AI493266 AA365132 AW966044 AU076704 T74854 T74860 T72098 T73265 T73873 T69180 T74658 T58786 T60385 T73410 T68781 T67845 T67593 T73952 T67864 T60630 T68367 T68401 T53959 T72360 T72099 T60377 T58961 T71712 T72821 T64738 T74845 T72037 T68688 T72063 T73258 T72826 T64242 T68220 T74673 T71800 T68355 T61227 T62738 T69317 T53850 T64692 T73768 T73962 T73382 T68914 T70975 T73400 T60631 T73277 T73203 T70498 T61409 T58925 NM_000508 M54982 T68301 T73729 T69445 T60424 T67922 T67736 T68716 T67755 T74765 T73819 T58719 T74756 T60477 T74863 T61109 T68329 T58850 T71857 T73425 T53736 T68607 T58898 T64309 T72031 T72079 T64305 T71908 T68107 T71916 T73787 T56035 T64425 T71870 T60476 T61376 T67820 T71895 T41006 T69441 T68170 T74617 T71958 T69440 T61875 R05796 H48353 T71914 T53939 T64121 AA693996 T72525 T67779 T68078 AA011465 AA345378 AV654847 AV654272 AV656001 AI064740 T82897 N33594 AA344542 AW805054 AI207457 T61743 AA026737 H94389 AA382695 AA918409 T68044 S82092 T39959 AI017721 AA312395 AA312919 T40156 H66239 AV652989 H38728 R98521 AV655200 R95790 W03250 W00913 AA344136 AV660126 R97923 AA343596 AW470774 AV651256 N54417 AA812862 AW182929 AI111192 H61463 H72060 AA344503 H38539 AI277511 AV661108 AI207625 T47810 AA235252 T27853 T47778 R95746 H70620 AA701463 AW827166 R98475 C20925 AV657287 T71959 T71313 T73920 T73333 T61618 T69293 T69283 T73931 T72178 T72456 AV645639 AV653476 T72957 T72300 T58906 T71457 T70494 T72956 T70495 T68267 T74407 T85778 AA344726 T27854 T74485 T74101 T73868 T71518 T72304 AA343853 T73909 T68070 T72065 H72149 T73493 T73495 AV645993 R02293 T70475 T64751 AA344441 AA343657 AA345732 AA344328 AI110639 AA344603 AF063513 T64696 T68516 T72223 T60507 T67633 R29500 T72517 R02292 T60599 T69206 T70452 T74677 R29366 T61277 T74914 T60352 R29675 T74843 AV645792 AA344408 T69197 T72057 T69368 T69358 T68258 AV650429 T73341 T61702 T74598 T40095 K02272 T40106 AA343045 AA341908 AA342807 AA341964 T53747 T72042 T62764 AI064899 AA343080 T67832 T72440 T71770 T68091 T69108 T72449 T69167 T71289 T68251 AV654844 T64375 AA345234 T67598 AA011414 T68036 H48262 AI207557 T68219 W86031 T69081 T64232 R93196 T62136 AV650539 H67459 T72978 AA344583 T60362 H58121 T95711 T72803 T68055 T71715 R29036 T72793 T69122 T64595 T62888 T69139 T68291 T64652 T67971 T46862 AA693592 AI248502 R29454 T64764 T57001 T73052 T71429 T51176 T58856 AV655414 H90426 AA342489 T73666 T67848 T72512 T53835 T67837 T73317 T74273 T69420 T68245 T74380 T67862 T74474 T56068 AI910275 X00474 X52003 X05030 NM_003225 AA314326 AA308400 AA506787 AA314825 AI571948 AA507595 AA614579 AA587613 R83818 AA568312 AA614409 AA307578 AI925552 AW950155 AI910083 M12075 BE074052 AW004668 AA578674 AA582084 BE074053 BE074126 BE074140 AA514776 AA588034 BE074051 BE074068 AW009769 AW050690 AA858276 R55389 AI001051 AW050700 AW750216 AA614539 BE074045 AI307407 AW602303 BE073575 AI202532 AA524242 AI970839 AI909751 BE076078 AI909749 R55292 AA156781 AW293839 U52054 AA024963 AA778446 BE073977 AW444904 AW602574 BE164040 BE164012 BE163972 BE163974 BE163992 AA837481 AW468444 BE185091 AW468002 AA687333 AA811830 AA581806 AI866686 AI572124 AA043777 AA040926 D02160 AI536733 AA812489 AW874142 AI471883 W84421 AA156850 W52854 AL117600 BE208116 BE208432 BE206239 BE082291 AW953423 AA351619 BE180648 BE140560 W80080 AA865478 N90291 AW450652 AW449519 AA93634 AI806539 AA351618 AW449522 AI827626 AA904788 AA380381 AA886045 AA774409 BE003229 Z41756

TABLE 11C

Pkey: Unique number corresponding to an Eos probeset.
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., *Nature* (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 N1_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	N1_position
403329	8516120	Plus	96450-96598
406399	9256288	Minus	63448-63554

TABLE 12A: Genes Distinguishing Squamous Cell Carcinoma from Other Lung Diseases and Normal Lung

Table 12A shows about 72 genes upregulated in squamous cell carcinomas of the lung relative to other lung tumors, non-malignant lung disease, and normal lung. These genes were selected from about 59680 probesets on the Eos/Affymetrix Hu03 Genechip array.

Table 12B show the accession numbers for those Pkey's lacking UnigenelD's for table 12A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Table 12C show the genomic positioning for those Pkey's lacking Unigene ID's and accession numbers in table 12A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Average of lung tumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatous and carcinoid tumors) divided by the average of normal lung samples
 R2: Average of non-malignant lung disease samples (including bronchitis, emphysema, fibrosis, atelectasis, asthma) divided by the average of normal lung samples

Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2
400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	132.45	4.00
400666			NM_002425:Homo sapiens matrix metallopro	3.26	3.22
401780			NM_005557*:Homo sapiens keratin 16 (foca	26.47	10.50
401781			Target Exon	10.33	4.61
401785			NM_002275*:Homo sapiens keratin 15 (KRT1	4.13	2.70
401994			Target Exon	61.84	47.00
402075			ENSP00000251056*:Plasma membrane calcium	1.00	1.00
404996			Target Exon	1.00	1.00
407839	AA045144	Hs.161566	ESTs	173.91	108.00
408000	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	151.17	8.00
408522	AI541214	Hs.46320	Small proline-rich protein SPRK (human,	1.98	1.24
410561	BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	10.04	1.00
415091	AL044872	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	1.00	30.00
415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	24.30	1.00
416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	53.29	51.00
417034	NM_006183	Hs.80962	neurotensin	1.00	1.00
417366	BE185289	Hs.1076	small proline-rich protein 1B (cornifin)	8.97	3.27
418663	AK001100	Hs.41690	desmocollin 3	112.17	19.00
418678	NM_001327	Hs.87225	cancer/testis antigen	1.18	1.10
419121	AA374372	Hs.89626	parathyroid hormone-like hormone	1.00	1.00
420783	AI659838	Hs.99923	lectin, galactoside-binding, soluble, 7	3.04	1.25
421773	W69233	Hs.112457	ESTs	1.12	1.14
421948	L42583	Hs.334309	keratin 6A	51.83	20.25
421978	AJ243662	Hs.110196	NICE-1 protein	1.01	0.91
422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	2.37	1.10
422440	NM_004812	Hs.116724	aldo-keto reductase family 1, member B10	47.53	32.00
423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	76.02	1.00
423725	AJ403108	Hs.132127	hypothetical protein LOC57822	4.20	1.00
423738	AB002134	Hs.132195	airway trypsin-like protease	10.14	51.00
424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	233.42	68.00
424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibito	1.00	1.00
424098	AF077374	Hs.139322	small proline-rich protein 3	137.82	54.00
424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	56.19	12.00
425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	33.45	1.00
427099	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	4.24	17.00
427335	AA448542	Hs.251677	G antigen 7B	51.83	4.00
428182	BE386042	Hs.293317	ESTs, Weakly similar to GGC1_HUMAN G ANT	1.00	1.00
428645	AA431400	Hs.98729	ESTs, Weakly similar to 2017205A dihydro	1.00	16.00
428748	AW593206	Hs.98785	Ksp37 protein	1.00	87.00
429259	AA420450	Hs.292911	ESTs, Highly similar to S60712 band-6-pr	2.01	1.18
429538	BE182592	Hs.11261	small proline-rich protein 2A	4.43	2.90
429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	11.80	1.00
430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	12.28	41.00
430890	X54232	Hs.2699	glypican 1	1.58	1.40
431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3	60.25	28.00
431846	BE019924	Hs.271580	uroplakin 1B	4.49	2.51
433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	1.20	1.09
434360	AW015415	Hs.127780	ESTs	40.98	27.00
434880	U02388	Hs.101	cytochrome P450, subfamily IVF, polypept	1.00	1.00
435505	AF200492	Hs.211238	interleukin-1 homolog 1	1.00	38.00
435793	AB037734	Hs.4993	KIAA1313 protein	23.68	42.00
436511	AA721252	Hs.291502	ESTs	16.76	14.00
438403	AA806607	Hs.292206	ESTs	1.00	1.00
439285	AL133916		hypothetical protein FLJ20093	46.23	139.00
439606	W79123	Hs.58561	G protein-coupled receptor 87	33.61	1.00
439670	AF088076	Hs.59507	ESTs, Weakly similar to AC004858 3 U1 sm	1.00	1.00
439706	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	86.55	11.00
440325	NM_003812	Hs.7164	a disintegrin and metalloproteinase doma	62.88	147.00
441525	AW241867	Hs.127728	ESTs	1.53	1.42
443162	T49951	Hs.9029	DKFZP434G032 protein	31.11	38.00
444378	R41339	Hs.12569	ESTs	1.00	1.00

	446292	AF081497	Hs.279682	Rh type C glycoprotein	1.55	1.26
	447078	AW885727	Hs.9914	ESTs	47.24	24.00
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	28.63	1.00
	449003	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o	1.00	1.00
5	449101	AA205847	Hs.23016	G protein-coupled receptor	2.58	27.00
	450832	AW970602	Hs.105421	ESTs	25.17	36.00
	452240	AI591147	Hs.61232	ESTs	13.42	1.00
	453317	NM_002277	Hs.41696	keratin, hair, acidic, 1	1.19	1.27
	453830	AA534296	Hs.20953	ESTs	24.92	25.00
10	454098	W27953	Hs.292911	ESTs, Highly similar to S60712 band-6-pr	1.26	1.11
	455601	AI368680	Hs.816	SRY (sex determining region Y)-box 2	206.11	1.00

TABLE 12B

15 Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

20 Pkey CAT Number Accession
 439285 47065_1 AL133916 N79113 AF086101 N76721 AW950828 AA364013 AW955684 AI346341 AI867454 N54784 AI655270 AI421279 AW014882
 AA775552 N62351 N59253 AA626243 AI341407 BE175639 AA456968 AI358918 AA457077

TABLE 12C

25 Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA
 sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 30 NI_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NI_position
400666	8118496	Plus	17982-18115,20297-20456
401780	7249190	Minus	28397-28617,28920-29045,29135-29296,29411-29567,29705-29787,30224-30573
35 401781	7249190	Minus	83215-83435,83531-83656,83740-83901,84237-84393,84955-85037,86290-86814
401785	7249190	Minus	165776-165996,166189-166314,166408-166569,167112-167268,167387-167469,168634-168942
401994	4153858	Minus	42904-43124,43211-43336,44607-44763,45199-45281,46337-46732
402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076
40 404996	6007890	Plus	37999-38145,38652-38998,39727-39872,40557-40674,42351-42450

TABLE 13A: Genes Distinguishing Non-Malignant Lung Disease from Lung Tumors and Normal lung

Table 13A shows about 23 genes upregulated in non-malignant lung disease relative to lung tumors and normal lung. These genes were selected from about 59680 probesets on the Eos/Affymetrix HuQ3 Genechip array.

Table 13B show the accession numbers for those Pkey's lacking UnigenelD's for table 13A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Table 13C show the genomic positioning for those Pkey's lacking UnigenelD's and accession numbers in table 13A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique Eos probeset identifier number
 ExAccon: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigenel number
 Unigenel Title: Unigenel gene title
 R1: Average of lung tumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatous and carcoid tumors) divided by the average of normal lung samples
 R2: Average of non-malignant lung disease samples (including bronchitis, emphysema, fibrosis, atelectasis, asthma) divided by the average of normal lung samples

Pkey	ExAccon	UnigenelD	Unigenel Title	R1	R2
408562	AA436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,	1.00	230.00
409031	AA376836	Hs.76728	ESTs	1.00	128.00
412372	R65998	Hs.285243	hypothetical protein FLJ22029	1.00	173.00
415910	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	1.00	145.00
417511	AL049176	Hs.82223	chordin-like	1.00	179.00
418819	AA228776	Hs.191721	ESTs	1.00	140.00
422060	R20893	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	1.00	156.00
424585	AA464840	Hs.131987	ESTs	1.00	167.00
426753	T89832	Hs.170278	ESTs	1.00	141.00
429496	AA453800	Hs.192793	ESTs	1.00	138.00
430719	AA488988	Hs.293796	ESTs	1.00	133.00
431089	BE041395		ESTs, Weakly similar to unknown protein	23.32	941.00
431385	BE178536	Hs.11090	membrane-spanning 4-domains, subfamily A	1.00	157.00
431728	NM_007351	Hs.268107	multimerin	1.00	157.00
436532	AA721522		gb:uv54h12.r1 NCI_CGAP_Ew1 Homo sapiens	1.00	218.00
437960	AI669586	Hs.222194	ESTs	1.00	147.00
438202	AW169287	Hs.22588	ESTs	1.00	141.00
441499	AW298235	Hs.101689	ESTs	1.00	167.00
444513	AL120214	Hs.7117	glutamate receptor, ionotropic, AMPA 1	1.00	151.00
448253	H25899	Hs.201591	ESTs	1.00	141.00
453636	R67837	Hs.169872	ESTs	1.00	116.00
458332	AI000341	Hs.220491	ESTs	1.00	192.00
459587	AA031956		gb:zk15e04.s1 Soares_pregnant_uterus_NbH	1.00	154.00

TABLE 13B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
431089	327825_1	BE041395 AA491826 AA621946 AA715980 AA666102
436532	421802_1	AA721522 AW975443 T93070

TABLE 13C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:469-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076

TABLE 14A: Preferred Utility and Subcellular Localization for Potential Lung Disease Targets

Table 14A shows the subcellular localization and preferred utility for the genes appearing in Tables 9A and 10A. mAb symbolizes monoclonal antibody, diag symbolizes diagnostic, s.m. symbolizes small molecule, and CTL symbolizes cytotoxic lymphocytic ligand. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array.

Table 14B show the accession numbers for those Pkey's lacking UnigenelD's for table 14A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Table 14C show the genomic positioning for those Pkey's lacking UnigenelD's and accession numbers in table 14A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique Eos probeset identifier number

ExAccn: Exemplar Accession number, Genbank accession number

UnigenelD: Unigenel number

Unigenel Title: Unigenel gene title

Pref.Utility: Preferred Utility

Pred.Loc: Predicted subcellular localization

Pkey	ExAccn	UnigenelD	Unigenel Title	Pref Utility	Pred. Loc
400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	mAb & diag & s.m.	extracellular
400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	mAb	plasma membrane
402075			ENSP00000251056:Plasma membrane calcium	mAb & diag	secreted
407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagonist	diag	secreted
408243	Y00787	Hs.624	interleukin 8	diag	secreted
408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	mAb & s.m.	plasma membrane
408908	BE296227	Hs.250822	serine/threonine kinase 15	s.m.	cytoplasm
409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	CTL & diag	secreted
409103	AF251237	Hs.112208	XAGE-1 protein	CTL	nuclear
409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini	diag	secreted
409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibitor	diag	secreted
409757	NM_001898	Hs.123114	cystatin SN	diag	extracellular
409893	AW247090	Hs.57101	minichromosome maintenance deficient (S.	CTL	nuclear
409956	AW103364	Hs.727	inhibin, beta A (activin A, activin AB a	diag	extracellular
410001	AB041036	Hs.57771	kallikrein 11	diag	extracellular
410407	X66839	Hs.63287	carbonic anhydrase IX	mAb & s.m.	plasma membrane
410418	D31382	Hs.63325	transmembrane protease, serine 4	mAb & diag & s.m.	plasma membrane
412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	s.m.	
412719	AW016610	Hs.816	ESTs	s.m.	nuclear
414774	X02419	Hs.77274	plasminogen activator, urokinase	diag	extracellular
414883	AA926960		CDC28 protein kinase 1	s.m.	
415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	CTL & diag	extracellular
415669	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibitor	mAb & diag & s.m.	secreted
415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	mAb & s.m.	plasma membrane
416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	diag	extracellular
417034	NM_006183	Hs.80962	neurotensin	diag	extracellular
417079	U65590	Hs.81134	Interleukin 1 receptor antagonist	diag	extracellular
417308	H60720	Hs.81892	KIAA0101 gene product	s.m.	mitochondrial
417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor	mAb & diag	secreted
417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	mAb	plasma membrane
417933	X02308	Hs.82962	thymidylate synthetase	s.m.	endoplasmic reticulum
418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	s.m.	cytoplasm
418506	AA084248	Hs.85339	G protein-coupled receptor 39	mAb & s.m.	plasma membrane
418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)	CTL	cytoplasmic
419121	AA374372	Hs.89626	parathyroid hormone-like hormone	diag	secreted
419171	NM_002846	Hs.89655	protein tyrosine phosphatase, receptor t	mAb & s.m.	plasma membrane
419183	U60669	Hs.89663	cytochrome P450, subfamily XXIV (vitamin	CTL & s.m.	mitochondrial
419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	diag	secreted
419235	AW470411	Hs.288433	neurotrimin	mAb & diag	plasma membrane
419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	mAb & s.m.	plasma membrane
419556	U29615	Hs.91093	chitinase 1 (chitotriosidase)	mAb & diag	extracellular*
420610	AJ683183	Hs.99348	distal-less homeo box 5	CTL	nuclear
421110	AJ250717	Hs.1355	cathepsin E	sm & diag	extracellular
421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	diag	secreted
421474	U76362	Hs.104637	solute carrier family 1 (glutamate trans	mAb & s.m.	plasma membrane
421552	AF026692	Hs.105700	secreted frizzled-related protein 4	diag	secreted
421753	BE314828	Hs.107911	ATP-binding cassette, sub-family B (MDR/	mAb & s.m.	plasma membrane
421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	mAb & s.m.	plasma membrane
422109	S73265	Hs.1473	gastrin-releasing peptide	diag	secreted
422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	diag	secreted
422282	AF019225	Hs.114309	apolipoprotein L	diag	secreted
422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	s.m.	nuclear
422424	AI186431	Hs.296638	prostate differentiation factor	diag	extracellular
422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	s.m.	cytoplasm
422809	AK001379	Hs.121028	hypothetical protein FLJ10549	s.m.	nuclear
422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	diag	extracellular
422956	BE545072	Hs.122579	ECT2 protein (Epithelial cell transformi	CTL & s.m.	
423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	diag	
423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	mAb & diag & s.m.	secreted
423961	D13666	Hs.136348	perostin (OSF-2os)	mAb & diag	extracellular
424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibitor	diag	secreted
424381	AA285249	Hs.146329	protein kinase Chk2	s.m.	nuclear

	424502	AF242388	Hs.149585	lengsin	s.m.	cytoplasmic
	424503	NM_002205	Hs.149609	integrin, alpha 5 (fibronectin receptor,	mAb & s.m.	plasma membrane
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	diag	extracellular
5	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	mAb & diag & s.m.	secreted
	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	s.m.	cytoplasmic
	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	mAb	plasma membrane
	425734	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxyg	s.m.	
	425776	U25128	Hs.159499	parathyroid hormone receptor 2	mAb & diag	plasma membrane
10	425852	AK001504	Hs.159651	death receptor 6, TNF superfamily member	mAb & s.m.	plasma membrane
	426215	AW963419	Hs.155223	stanniocalcin 2	mAb & diag	secreted
	426427	M86699	Hs.169840	TTK protein kinase	CTL & s.m.	nuclear
	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	mAb & diag	secreted
	427335	AA448542	Hs.251677	G antigen 7B	CTL	cytoplasmic
15	427747	AW411425	Hs.180655	serine/threonine kinase 12	s.m.	cytoplasmic
	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	diag	
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	mAb & diag & s.m.	extracellular
	428450	NM_014791	Hs.184339	KIAA0175 gene product	s.m.	nuclear
	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to	s.m.	nuclear
20	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	mAb & s.m.	plasma membrane
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	CTL & s.m.	nuclear
	428698	AA852773	Hs.334838	KIAA1866 protein	mAb	
	428748	AW593206	Hs.98785	Ksp37 protein	diag	extracellular
	428758	AA433988	Hs.98502	CA125 antigen; mucin 16	diag	mitochondria*
25	428969	AF120274	Hs.194689	artemin	diag	extracellular
	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	mAb & s.m.	plasma membrane
	429263	AA019004	Hs.198396	ATP-binding cassette, sub-family A (ABC1	mAb & s.m.	plasma membrane
	429547	AW009166	Hs.99376	ESTs	diag	secreted
	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas	mAb & diag	secreted
30	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	s.m.	
	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	mAb & s.m.	plasma membrane
	431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu	diag	extracellular
	431515	NM_012152	Hs.258583	endothelial differentiation, lysophospha	mAb & s.m.	plasma membrane
	431846	BE019924	Hs.271580	uroplakin 1B	mAb & diag	plasma membrane
35	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	mAb & diag	plasma membrane
	432201	AF538613	Hs.298241	Transmembrane protease, serine 3	mAb & diag & s.m.	plasma membrane
	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	s.m.	nuclear
	435505	AF200492	Hs.211238	interleukin-1 homolog 1	diag	secreted
	436481	AA379597	Hs.5199	HSPC150 protein similar to ublquitin-con	s.m.	
40	437016	AU076916	Hs.5398	guanine monophosphate synthetase	s.m.	cytoplasm
	437044	AL035864	Hs.69517	differentially expressed in Fanconi's an	CTL	ER
	437789	AF581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti	CTL	nuclear
	437852	BE001836	Hs.256897	ESTs, Weakly similar to dJ365012.1 [H.sa	mAb & s.m.	plasma membrane
	439223	AW238299	Hs.250618	UL16 binding protein 2	mAb	plasma membrane
45	439477	W69813	Hs.58042	ESTs, Moderately similar to GFR3_HUMAN G	mAb & s.m.	
	439606	W79123	Hs.58561	G protein-coupled receptor 87	mAb & s.m.	plasma membrane
	439738	BE246502	Hs.9598	sema domain, immunoglobulin domain (Ig),	mAb & s.m.	plasma membrane
	440006	AK000517	Hs.6844	NALP2 protein; PYRIN-Containing APAF1-li	s.m.	nuclear
	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	s.m.	
50	442117	AW664964	Hs.128899	ESTs; hypothetical protein for IMAGE:447	mAb & s.m.	plasma membrane
	443247	BE614387	Hs.333893	c-Myc target JPO1	CTL	extracellular*
	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	CTL	
	443859	NM_013409	Hs.9914	folistatin	diag	extracellular
55	444006	BE395085	Hs.10086	type I transmembrane protein Fn14	mAb	plasma membrane
	444371	BE540274	Hs.239	forkhead box M1	s.m.	nuclear
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	diag	secreted
	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote	mAb & diag	plasma membrane
	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	mAb & diag	secreted
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	diag	secreted
60	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	diag	extracellular
	447033	AF357412	Hs.157601	ESTs	CTL & diag	secreted
	447342	AF199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	CTL	
	448243	AW369771	Hs.52620	integrin, beta 8	mAb & s.m.	plasma membrane
	448844	AF581519	Hs.177164	ESTs	mAb & s.m.	
65	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	mAb	plasma membrane
	449722	BE280074	Hs.23960	cyclin B1	s.m.	cytoplasm
	450001	NM_001044	Hs.406	solute carrier family 6 (neurotransmitte	mAb & s.m.	plasma membrane
	450375	AA009647		a disintegrin and metalloproteinase doma	mAb & diag & s.m.	plasma membrane
	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-	mAb & diag	plasma membrane
70	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	diag	secreted
	451668	Z43948	Hs.326444	cartilage acidic protein 1	mAb & diag	plasma membrane
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	diag	
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	diag	extracellular
	452747	BE153855	Hs.61460	Ig superfamily receptor LNIR	mAb	plasma membrane
75	452838	U65011	Hs.30743	preferentially expressed antigen in mela	CTL	nuclear
	453968	AA847843	Hs.62711	High mobility group (nonhistone chromoso	CTL & s.m.	nuclear
	457489	AF693815	Hs.127179	cryptic gene	diag	secreted

TABLE 14B

80 Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey CAT Number Accession

414883 15024_1

AA926960 AA926959 W76521 W24270 W21526 AA037172 BE267636 H83186 AA469909 N86396 AA001348 BE535736 AA081745 BE566245
 AA082436 H72525 H77575 N49786 W80565 H78746 BE569085 W04339 R98127 T55938 BE279271 AW960304 T29812 AA476873 BE297387
 AA292753 AA177048 NM_001826 X54941 BE314366 AA908783 AI719075 BE270172 BE269819 AA889955 AI204630 W25243 AI935150
 AA872039 W72395 T99630 AI422691 H98460 N31428 BE255916 H03265 AI857576 AA776920 AA910644 AA459522 AA293140 AW514667
 R75953 AW662396 AA662522 AI865147 AI423153 AW262230 AA584410 AA583187 AW024595 AW069734 AI828996 AA282997 AA876046
 AW613002 AA527373 AW972459 AI831360 AA621337 AA100926 AA772418 AA594628 AI033892 W95096 AI034317 AA398727 AI085031
 N95210 AI459432 AI041437 AA932124 AA627684 AA935829 AI004827 AI423513 AI094597 H42079 R54703 AI630359 AA617681 AA978045
 AA643280 W44561 AI991988 AI537692 AI090262 AA740817 AI312104 AI911822 AA416871 AI185409 AA129784 AA701623 AI075239
 AI139549 AA633648 AI339996 AI336880 AA399239 AI078708 AI085351 AI362835 AI346618 AI146955 AI989380 AI348243 N92892 AA765850
 AI494230 AI278887 AA962596 AI492600 W80435 AA001979 R97424 AI129015 N24127 AA157451 AA235549 AA459292 AA037114 AA129785
 AI494211 AW059601 AW886710 R92790 N59755 AI361128 AW589407 H47725 H97534 H48076 H48450 T99631 AW300758 H03431 R76789
 AA954344 H77576 R96823 AI457100 N92845 N49682 H42038 BE220698 BE220715 H99552 AA701624 N74173 R54704 H79520 H72923
 H03266 BE261919 AA769633 AA480310 AA507454 AA910586 AI203723 AW104725 W25611 W25071 T88980 H03513 T77589 R99156
 W95095 R97470 AA702275 T77551 AA911952 H82956 N83673 AA283672
 AA009647 AA131254 AA374293 AW954405 H04410 AW606284 AA151166 BE157467 BE157601 H04384 W46291 AW663674 H04021 H01532
 AA190993 H03231 H59605 H01642 AA852876 AA113758 AA626915 AA746952 AI161014 AA099554 R69067

TABLE 14C

Pkey: Unique number corresponding to an Eos probaset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA
 sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
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402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076
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TABLE 15A: Information for all sequences in Table 16

Table 15A shows the Seq ID No, Pkey, ExAccn, UnigenelD, and Unigene Title for all of the sequences in Table 16.

Table 15B show the accession numbers for those Pkey's lacking UnigenelD's for table 15A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Table 15C show the genomic positioning for those Pkey's lacking Unigene ID's and accession numbers in table 15A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Seq ID No: Sequence ID number
 Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title

Seq ID No:	Pkey	ExAccn	UnigenelD	Unigene Title
Seq ID No: 1 & 2	410407	X66839	Hs.63287	carbonic anhydrase IX
Seq ID No: 3 & 4	412719	AW016610	Hs.816	ESTs
Seq ID No: 5 & 6	417034	NM_006183	Hs.80962	neurotensin
Seq ID No: 7 & 8	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam
Seq ID No: 9 & 10	407788	BE514982	Hs.38991	S100 calcium-binding protein A2
Seq ID No: 11 & 12	407788	BE514982	Hs.38991	S100 calcium-binding protein A2
Seq ID No: 13 & 14	407788	BE514982	Hs.38991	S100 calcium-binding protein A2
Seq ID No: 15 & 16	407788	BE514982	Hs.38991	S100 calcium-binding protein A2
Seq ID No: 17 & 18	439285	AL133916		hypothetical protein FLJ20093
Seq ID No: 19 & 20	413753	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin
Seq ID No: 21 & 22	120486	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog
Seq ID No: 23 & 24	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen
Seq ID No: 25 & 26	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines
Seq ID No: 27 & 28	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage
Seq ID No: 29 & 30	452838	U65011	Hs.30743	preferentially expressed antigen in mela
Seq ID No: 31 & 32	418663	AK001100	Hs.41690	desmocollin 3
Seq ID No: 33 & 34	418663	AK001100	Hs.41690	desmocollin 3
Seq ID No: 35 & 36	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibitor
Seq ID No: 37 & 38	429610	A8024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas
Seq ID No: 39 & 40	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad
Seq ID No: 41 & 42	431846	BE019924	Hs.271580	uroplakin 1B
Seq ID No: 43 & 44	418830	BE513731	Hs.88959	hypothetical protein MGC4816
Seq ID No: 45 & 46	424098	AF077374	Hs.139322	small proline-rich protein 3
Seq ID No: 47 & 48	443648	AI085377	Hs.143610	ESTs
Seq ID No: 49	311034	BE567130	Hs.311389	ESTs, Highly similar to NKGD_HUMAN NKG2-
Seq ID No: 50 & 51	408522	AI541214	Hs.46320	Small proline-rich protein SPRK (human,
Seq ID No: 52 & 53	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL
Seq ID No: 54 & 55	435505	AF200492	Hs.211238	interleukin-1 homolog 1
Seq ID No: 56 & 57	417366	BE185289	Hs.1076	small proline-rich protein 1B (cornifin)
Seq ID No: 58 & 59	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta
Seq ID No: 60 & 61	441020	W79283	Hs.35962	ESTs
Seq ID No: 62 & 63	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys
Seq ID No: 64 & 65	429538	BE182592	Hs.11261	small proline-rich protein 2A
Seq ID No: 66 & 67	448733	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitte
Seq ID No: 68 & 69	444371	BE540274	Hs.239	forkhead box M1
Seq ID No: 70 & 71	444371	BE540274	Hs.239	forkhead box M1
Seq ID No: 72 & 73	444371	BE540274	Hs.239	forkhead box M1
Seq ID No: 74 & 75	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias
Seq ID No: 76 & 77	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias
Seq ID No: 78 & 79	429259	AA420450	Hs.292911	Plakophilin
Seq ID No: 80 & 81	426440	BE382756	Hs.169902	solute carrier family 2 (facilitated glu
Seq ID No: 82 & 83	437044	AL035864	Hs.69517	differentially expressed in Fanconi's an
Seq ID No: 84 & 85	423662	AK001035	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro
Seq ID No: 86 & 87	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino
Seq ID No: 88 & 89	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3
Seq ID No: 90 & 91	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor
Seq ID No: 92 & 93	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr
Seq ID No: 94 & 95	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated
Seq ID No: 96 & 97	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E. coli Re
Seq ID No: 98 & 99	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic
Seq ID No: 100 & 101	449003	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o
Seq ID No: 102 & 103	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3
Seq ID No: 104 & 105	409103	AF251237	Hs.112208	XAGE-1 protein
Seq ID No: 106 & 107	417542	J04129	Hs.82269	progestagen-associated endometrial prote
Seq ID No: 108 & 109	428471	X57348	Hs.184510	stratiferin
Seq ID No: 110 & 111	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member
Seq ID No: 112 & 113	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2
Seq ID No: 114 & 115	418203	X54942	Hs.83758	CDC28 protein kinase 2
Seq ID No: 116	447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m
Seq ID No: 117 & 118	437016	AU076916	Hs.5398	guanine monophosphate synthetase
Seq ID No: 119 & 120	449230	BE613348	Hs.211579	melanoma cell adhesion molecule
Seq ID No: 121 & 122	446989	AK001898	Hs.16740	hypothetical protein FLJ11036
Seq ID No: 123 & 124	457819	AA057484	Hs.35406	ESTs, Highly similar to unnamed protein
Seq ID No: 125 & 126	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B

	Seq ID No: 127 & 128	414430	AI346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1
	Seq ID No: 129 & 130	418462	BE001596	Hs.85266	integrin, beta 4
	Seq ID No: 131 & 132	100668	L05424	Hs.169610	CD44 antigen (homing function and Indian
5	Seq ID No: 133 & 134	458933	AI638429	Hs.24763	RAN binding protein 1
	Seq ID No: 135 & 136	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me
	Seq ID No: 137 & 138	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me
	Seq ID No: 139 & 140	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me
	Seq ID No: 141 & 142	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me
10	Seq ID No: 143 & 144	446269	AW263155	Hs.14559	hypothetical protein FLJ10540
	Seq ID No: 145 & 146	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur
	Seq ID No: 147 & 148	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con
	Seq ID No: 149 & 150	440325	NM_003812	Hs.7164	a disintegrin and metalloproteinase doma
	Seq ID No: 151 & 152	439606	W79123	Hs.58561	G protein-coupled receptor 87
15	Seq ID No: 153 & 154	453884	AA355925	Hs.36232	KIAA0186 gene product
	Seq ID No: 155 & 156	453884	AA355925	Hs.36232	KIAA0186 gene product
	Seq ID No: 157 & 158	453884	AA355925	Hs.36232	KIAA0186 gene product
	Seq ID No: 159 & 160	453884	AA355925	Hs.36232	KIAA0186 gene product
	Seq ID No: 161 & 162	404877			NM_005365:Homo sapiens melanoma antigen,
	Seq ID No: 163 & 164	413129	AF292100	Hs.104613	RP42 homolog
20	Seq ID No: 165 & 166	413281	AA861271	Hs.222024	transcription factor BMAL2
	Seq ID No: 167 & 168	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote
	Seq ID No: 169 & 170	416819	U77735	Hs.80205	pim-2 oncogene
	Seq ID No: 171 & 172	451320	AW118072		diacylglycerol kinase, zeta (104kD)
	Seq ID No: 173 & 174	418543	NM_005329	Hs.85962	hyaluronan synthase 3
25	Seq ID No: 175 & 176	454034	NM_000691	Hs.575	aldehyde dehydrogenase 3 family, member
	Seq ID No: 177 & 178	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)
	Seq ID No: 179 & 180	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 181 & 182	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
30	Seq ID No: 183 & 184	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 185 & 186	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 187 & 188	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 189 & 190	419121	AA374372	Hs.89626	parathyroid hormone-like hormone
	Seq ID No: 191 & 192	448993	AI471630	Hs.8127	KIAA0144 gene product
35	Seq ID No: 193 & 194	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR
	Seq ID No: 195 & 196	430393	BE185030	Hs.241305	estrogen-responsive B box protein
	Seq ID No: 197 & 198	425057	AA826434	Hs.1619	achaeta-scute complex (Drosophila) homol
	Seq ID No: 199 & 200	420462	AF050147	Hs.97932	chondromodulin I precursor
	Seq ID No: 201 & 202	102963	X02404	Hs.274534	calcitonin-related polypeptide, beta
40	Seq ID No: 203 & 204	100576	X00356	Hs.37058	calcitonin/calcitonin-related polypeptid
	Seq ID No: 205 & 206	101175	U82671	Hs.36980	melanoma antigen, family A, 2
	Seq ID No: 207 & 208	429038	AL023513	Hs.194766	seizure related gene 6 (mouse)-like
	Seq ID No: 209 & 210	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)
	Seq ID No: 211 & 212	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)
45	Seq ID No: 213 & 214	131927	AJ003112	Hs.34780	doublecortin; lissencephaly, X-linked (d
	Seq ID No: 215 & 216	428182	BE386042	Hs.293317	ESTs, Weakly similar to GGC1_HUMAN G ANT
	Seq ID No: 217 & 218	427335	AA448542	Hs.251677	G antigen 7B
	Seq ID No: 219 & 220	409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini
	Seq ID No: 221 & 222	114346	AL137256	Hs.130489	ATPase, aminophospholipid transporter-II
50	Seq ID No: 223 & 224	438956	W00847	Hs.135056	Human DNA sequence from clone RP5-850E9
	Seq ID No: 225 & 226	404440			NM_021048:Homo sapiens melanoma antigen,
	Seq ID No: 227 & 228	415669	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibito
	Seq ID No: 229 & 230	103312	Y12642	Hs.3185	lysosomal
	Seq ID No: 231 & 232	320843	BE069288	Hs.34744	Homo sapiens mRNA; cDNA DKFZp547C136 (fr
55	Seq ID No: 233	429065	AI753247	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT
	Seq ID No: 234 & 235	446102	AW168067	Hs.317694	ESTs
	Seq ID No: 236 & 237	330495	U47924	Hs.71642	guanine nucleotide binding protein (G pr
	Seq ID No: 238	413573	AI733859	Hs.149089	ESTs
	Seq ID No: 239 & 240	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to
60	Seq ID No: 241 & 242	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to
	Seq ID No: 243 & 244	332180	AF134160	Hs.7327	claudin 1
	Seq ID No: 245	437915	AI637993	Hs.202312	Homo sapiens clone N11 NTERa2D1 teratoca
	Seq ID No: 246 & 247	441553	AA281219	Hs.121296	ESTs
	Seq ID No: 248 & 249	331692	AI683487	Hs.152213	wingless-type MMTV integration site fami
65	Seq ID No: 250 & 251	429413	NM_014058	Hs.201877	DESC1 protein
	Seq ID No: 252 & 253	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis
	Seq ID No: 254 & 255	448357	N20169	Hs.108923	RAB38, member RAS oncogene family
	Seq ID No: 256 & 257	446292	AF081497	Hs.279682	Rh type C glycoprotein
	Seq ID No: 258 & 259	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h
70	Seq ID No: 260 & 261	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1
	Seq ID No: 262 & 263	424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibito
	Seq ID No: 264 & 265	439223	AW238299	Hs.250618	UL16 binding protein 2
	Seq ID No: 266 & 267	429228	AI553633	Hs.326447	ESTs
	Seq ID No: 268 & 269	409757	NM_001898	Hs.123114	cystatin SN
75	Seq ID No: 270 & 271	411089	AA456454	Hs.214291	cell division cycle 2-like 1 (PITSLRE pr
	Seq ID No: 272 & 273	436511	AA721252	Hs.291502	ESTs
	Seq ID No: 274 & 275	428969	AF120274	Hs.194689	artemin
	Seq ID No: 276 & 277	428969	AF120274	Hs.194689	artemin
	Seq ID No: 278 & 279	428969	AF120274	Hs.194689	artemin
80	Seq ID No: 280 & 281	428969	AF120274	Hs.194689	artemin
	Seq ID No: 282	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen
	Seq ID No: 283 & 284	412723	AA648459	Hs.335951	hypothetical protein AF301222
	Seq ID No: 285 & 286	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-
	Seq ID No: 287 & 288	405770			NM_002362:Homo sapiens melanoma antigen,
	Seq ID No: 289 & 290	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13
85	Seq ID No: 291 & 292	414774	X02419	Hs.77274	plasminogen activator, urokinase

5	Seq ID No: 293 & 294	424629	M90656	Hs.151393	glutamate-cysteine ligase, catalytic sub
	Seq ID No: 295 & 296	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti
	Seq ID No: 297 & 298	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti
	Seq ID No: 299 & 300	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti
	Seq ID No: 301 & 302	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti
	Seq ID No: 303 & 304	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti
	Seq ID No: 305 & 306	453968	AA847843	Hs.62711	High mobility group (nonhistone chromoso
	Seq ID No: 307 & 308	403478			NM_022342Homo sapiens kinesin protein 9
10	Seq ID No: 309	441525	AW241867	Hs.127728	ESTs
	Seq ID No: 310 & 311	434105	AW952124	Hs.13094	presenilins associated rhomboid-like pro
	Seq ID No: 312 & 313	428810	AF068236	Hs.193788	nitric oxide synthase 2A (inducible, hep
	Seq ID No: 314 & 315	413691	AB023173	Hs.75478	ATPase, Class VI, type 11B
	Seq ID No: 316 & 317	423934	U89995	Hs.159234	forkhead box E1 (thyroid transcription f
15	Seq ID No: 318 & 319	409228	R16811	Hs.22010	ESTs, Weakly similar to 2109260A B cell
	Seq ID No: 320 & 321	425734	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxyg
	Seq ID No: 322 & 323	413582	AW295647	Hs.71331	hypothetical protein MGC5350
	Seq ID No: 324 & 325	438403	AA806607	Hs.292206	ESTs
	Seq ID No: 326 & 327	403329			unnamed protein product (Homo sapiens)
20	Seq ID No: 328 & 329	409893	AW247090	Hs.57101	minichromosome maintenance deficient (S.
	Seq ID No: 330 & 331	119073	BE245360	Hs.279477	v-ets erythroblastosis virus E26 oncogen
	Seq ID No: 332 & 333	113195	H83265	Hs.8881	ESTs, Weakly similar to S41044 chromosom
	Seq ID No: 334 & 335	102283	AW161552	Hs.83381	guanine nucleotide binding protein 11
	Seq ID No: 336 & 337	101345	NM_005795	Hs.152175	calcitonin receptor-like
25	Seq ID No: 338 & 339	103280	U84722	Hs.76206	cadherin 5, type 2, VE-cadherin (vascula
	Seq ID No: 340 & 341	102012	BE259035	Hs.118400	singed (Drosophila)-like (sea urchin fas
	Seq ID No: 342 & 343	105729	H46612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds
	Seq ID No: 344 & 345	134299	AW580939	Hs.97199	complement component C1q receptor
	Seq ID No: 346 & 347	412719	AW016610	Hs.816	ESTs
30	Seq ID No: 348 & 349	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL
	Seq ID No: 350 & 351	128924	BE279383	Hs.26557	plakophilin 3
	Seq ID No: 352 & 353	100486	T19006	Hs.10842	RAN, member RAS oncogene family
	Seq ID No: 354 & 355	419121	AA374372	Hs.89626	parathyroid hormone-like hormone
	Seq ID No: 356 & 357	409459	D86407	Hs.54481	low density lipoprotein receptor-related
35	Seq ID No: 358 & 359	330493	M27826		endogenous retroviral protease
	Seq ID No: 360 & 361	417866	AW067903	Hs.82772	collagen, type XI, alpha 1
	Seq ID No: 362 & 363	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4
	Seq ID No: 364 & 365	437016	AU076916	Hs.5398	guanine monophosphate synthetase
	Seq ID No: 366 & 367	429612	AF062649	Hs.252587	pituitary tumor-transforming 1
40	Seq ID No: 368 & 369	440704	M69241	Hs.162	insulin-like growth factor binding prote
	Seq ID No: 370 & 371	431221	AA449015	Hs.286145	SRB7 (suppressor of RNA polymerase B, ye
	Seq ID No: 372 & 373	431565	AF161470	Hs.260622	butyrate-induced transcript 1
	Seq ID No: 374 & 375	431565	AF161470	Hs.260622	butyrate-induced transcript 1
	Seq ID No: 376 & 377	132354	BE185289	Hs.1076	small proline-rich protein 1B (comifin)
45	Seq ID No: 378 & 379	424441	X14850	Hs.147097	H2A histone family, member X
	Seq ID No: 380 & 381	103768	AF086009	Hs.296398	gb:Homo sapiens full length insert cDNA
	Seq ID No: 382 & 383	417512	X76534	Hs.82226	glycoprotein (transmembrane) nmb
	Seq ID No: 384 & 385	425266	J00077	Hs.155421	alpha-fetoprotein
	Seq ID No: 386 & 387	424503	NM_002205	Hs.149609	integrin, alpha 5 (fibronectin receptor,
50	Seq ID No: 388 & 389	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin
	Seq ID No: 390 & 391	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial
	Seq ID No: 392 & 393	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial
	Seq ID No: 394 & 395	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino
	Seq ID No: 396 & 397	415138	C18356	Hs.295944	tissue factor pathway inhibitor 2
55	Seq ID No: 398 & 399	418506	AA084248	Hs.85339	G protein-coupled receptor 39
	Seq ID No: 400 & 401	423961	D13666	Hs.136348	perlestin (OSF-2os)
	Seq ID No: 402 & 403	414812	X72755	Hs.77367	monokine induced by gamma interferon
	Seq ID No: 404 & 405	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein
	Seq ID No: 406 & 407	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein
60	Seq ID No: 408 & 409	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse
	Seq ID No: 410 & 411	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy
	Seq ID No: 412 & 413	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti
	Seq ID No: 414 & 415	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated
	Seq ID No: 416 & 417	411789	AF245505	Hs.72157	Adican
65	Seq ID No: 418 & 419	428698	AA852773	Hs.334838	KIAA1866 protein
	Seq ID No: 420 & 421	450098	W27249	Hs.8109	hypothetical protein FLJ21080
	Seq ID No: 422 & 423	421552	AF026692	Hs.105700	secreted frizzled-related protein 4
	Seq ID No: 424 & 425	452747	BE153855	Hs.61460	lg superfamily receptor LNIR
	Seq ID No: 426 & 427	450375	AA009647		a disintegrin and metalloproteinase doma
70	Seq ID No: 428 & 429	426215	AW963419	Hs.155223	stanniocalcin 2
	Seq ID No: 430 & 431	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin
	Seq ID No: 432 & 433	432201	AI538613	Hs.298241	Transmembrane protease, serine 3
	Seq ID No: 434 & 435	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph
	Seq ID No: 436 & 437	442117	AW664964	Hs.128899	ESTs; hypothetical protein for IMAGE:447
75	Seq ID No: 438 & 439	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn
	Seq ID No: 440 & 441	447033	AI357412	Hs.157601	ESTs
	Seq ID No: 442 & 443	447033	AI357412	Hs.157601	ESTs
	Seq ID No: 444 & 445	447033	AI357412	Hs.157601	ESTs
	Seq ID No: 446 & 447	115522	BE614387	Hs.333893	c-Myc target JPO1
80	Seq ID No: 448 & 449	410418	D31382	Hs.63325	transmembrane protease, serine 4
	Seq ID No: 450 & 451	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119
	Seq ID No: 452 & 453	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119
	Seq ID No: 454 & 455	452461	N78223	Hs.108106	transcription factor
	Seq ID No: 456 & 457	412420	AL035668	Hs.73853	bone morphogenetic protein 2
85	Seq ID No: 458 & 459	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara
	Seq ID No: 460 & 461	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagonist

	Seq ID No: 462 & 463	437852	BE001836	Hs.256897	ESTs, Weakly similar to dJ365O12.1 [H.s]
	Seq ID No: 464 & 465	402075			ENSP00000251056*:Plasma membrane calcium
	Seq ID No: 466 & 467	421110	AJ250717	Hs.1355	cathepsin E
5	Seq ID No: 468 & 469	451668	Z43948	Hs.326444	cartilage acidic protein 1
	Seq ID No: 470 & 471	451668	Z43948	Hs.326444	cartilage acidic protein 1
	Seq ID No: 472 & 473	451668	Z43948	Hs.326444	cartilage acidic protein 1
	Seq ID No: 474 & 475	422282	AF019225	Hs.114309	apolipoprotein L
	Seq ID No: 476 & 477	425852	AK001504	Hs.159651	death receptor 6, TNF superfamily member
10	Seq ID No: 478 & 479	439738	BE246502	Hs.9598	sema domain, immunoglobulin domain (Ig),
	Seq ID No: 480 & 481	427747	AW411425	Hs.180655	serine/threonine kinase 12
	Seq ID No: 482 & 483	420281	AI623693	Hs.323494	Predicted cation efflux pump
	Seq ID No: 484 & 485	405932			C15000305:gi 3806122 gb AAC69198.1 (AF0
	Seq ID No: 486 & 487	405932			C15000305:gi 3806122 gb AAC69198.1 (AF0
15	Seq ID No: 488 & 489	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane
	Seq ID No: 490 & 491	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy
	Seq ID No: 492 & 493	417079	U65590	Hs.81134	Interleukin 1 receptor antagonist
	Seq ID No: 494 & 495	430890	X54232	Hs.2699	glypican 1
	Seq ID No: 496 & 497	419721	NM_001650	Hs.288650	aquaporin 4
20	Seq ID No: 498 & 499	444471	AB020684	Hs.11217	KIAA0877 protein
	Seq ID No: 500 & 501	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote
	Seq ID No: 502 & 503	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly
	Seq ID No: 504 & 505	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro
	Seq ID No: 506 & 507	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro
	Seq ID No: 508 & 509	450001	NM_001044	Hs.406	solute carrier family 6 (neurotransmitte
25	Seq ID No: 510 & 511	410407	X66839	Hs.63287	carbonic anhydrase IX
	Seq ID No: 512 & 513	309931	AW341683		gb:hd13d01.x1 Soares_NFL_T_GBC_S1 Homo s
	Seq ID No: 514 & 515	412719	AW016610	Hs.816	ESTs
	Seq ID No: 516 & 517	417034	NM_006183	Hs.80952	neurotensin
30	Seq ID No: 518 & 519	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam
	Seq ID No: 520 & 521	413753	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalin
	Seq ID No: 522 & 523	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen
	Seq ID No: 524 & 525	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage
	Seq ID No: 526 & 527	418663	AK001100	Hs.41690	desmocollin 3
35	Seq ID No: 528 & 529	418663	AK001100	Hs.41690	desmocollin 3
	Seq ID No: 530 & 531	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas
	Seq ID No: 532 & 533	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad
	Seq ID No: 534 & 535	431846	BE019924	Hs.271580	uroplakin 1B
	Seq ID No: 536 & 537	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL
40	Seq ID No: 538 & 539	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta
	Seq ID No: 540 & 541	437044	AL035864	Hs.69517	differentially expressed in Fanconi's an
	Seq ID No: 542 & 543	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino
	Seq ID No: 544 & 545	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3
	Seq ID No: 546 & 547	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor
	Seq ID No: 548 & 549	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3
45	Seq ID No: 550 & 551	417542	J04129	Hs.82269	progesterone-associated endometrial prola
	Seq ID No: 552 & 553	449230	BE613348	Hs.211579	melanoma cell adhesion molecule
	Seq ID No: 554 & 555	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma
	Seq ID No: 556 & 557	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma
	Seq ID No: 558 & 559	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B
50	Seq ID No: 560 & 561	418462	BE001596	Hs.85266	integrin, beta 4
	Seq ID No: 562 & 563	410274	AA381807	Hs.61762	hypoxia-inducible protein 2
	Seq ID No: 564 & 565	439606	W79123	Hs.58561	G protein-coupled receptor 87
	Seq ID No: 566 & 567	404877			NM_005365:Homo sapiens melanoma antigen,
55	Seq ID No: 568 & 569	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote
	Seq ID No: 570 & 571	418543	NM_005329	Hs.85962	hyaluronan synthase 3
	Seq ID No: 572 & 573	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 574 & 575	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 576 & 577	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
60	Seq ID No: 578 & 579	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 580 & 581	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 582 & 583	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 584 & 585	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR
	Seq ID No: 586 & 587	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)
65	Seq ID No: 588 & 589	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)
	Seq ID No: 590 & 591	409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini
	Seq ID No: 592 & 593	332180	AF134160	Hs.7327	claudin 1
	Seq ID No: 594 & 595	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,
	Seq ID No: 596 & 597	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,
70	Seq ID No: 598 & 599	439223	AW238299	Hs.250618	UL16 binding protein 2
	Seq ID No: 600 & 601	409757	NM_001898	Hs.123114	cystatin SN
	Seq ID No: 602 & 603	428969	AF120274	Hs.194689	artemin
	Seq ID No: 604 & 605	428969	AF120274	Hs.194689	artemin
	Seq ID No: 606 & 607	428969	AF120274	Hs.194689	artemin
75	Seq ID No: 608 & 609	428969	AF120274	Hs.194689	artemin
	Seq ID No: 610 & 611	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-
	Seq ID No: 612 & 613	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-
	Seq ID No: 614 & 615	414774	X02419	Hs.77274	plasminogen activator, urokinase
	Seq ID No: 616 & 617	407944	R34008	Hs.239727	desmocollin 2
	Seq ID No: 618 & 619	407944	R34008	Hs.239727	desmocollin 2
80	Seq ID No: 620 & 621	457489	AI693815	Hs.127179	cryptic gene
	Seq ID No: 622 & 623	429547	AW009166	Hs.99376	ESTs
	Seq ID No: 624 & 625	407242	M18728		gb:Human nonspecific crossreacting antig
	Seq ID No: 626 & 627	407242	M18728		gb:Human nonspecific crossreacting antig
	Seq ID No: 628 & 629	407242	M18728		gb:Human nonspecific crossreacting antig
85	Seq ID No: 630 & 631	444006	BE395085	Hs.10086	type I transmembrane protein Fn14

Seq ID No: 632 & 633	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase domain
Seq ID No: 634 & 635	422109	S73265	Hs.1473	gastrin-releasing peptide
Seq ID No: 636 & 637	419235	AW470411	Hs.288433	neurotrophin
Seq ID No: 638 & 639	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose inducible
Seq ID No: 640 & 641	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cyt)
Seq ID No: 642 & 643	431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precursor
Seq ID No: 644 & 645	448243	AW369771	Hs.52620	integrin, beta 8
Seq ID No: 646 & 647	426427	M86699	Hs.169840	TTK protein kinase
Seq ID No: 648 & 649	445537	AJ245671	Hs.12844	EGF-like domain, multiple 6
Seq ID No: 650 & 651	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6
Seq ID No: 652 & 653	428450	NM_014791	Hs.184339	KIAA0175 gene product
Seq ID No: 654 & 655	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin)
Seq ID No: 656 & 657	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11
Seq ID No: 658 & 659	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic)
Seq ID No: 660 & 661	425776	U25128	Hs.159499	parathyroid hormone receptor 2
Seq ID No: 662 & 663	425776	U25128	Hs.159499	parathyroid hormone receptor 2
Seq ID No: 664 & 665	431515	NM_012152	Hs.258583	endothelial differentiation, lysophosphatidylcholine
Seq ID No: 666 & 667	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7
Seq ID No: 668 & 669	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino acid
Seq ID No: 670 & 671	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino acid
Seq ID No: 672 & 673	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino acid
Seq ID No: 674 & 675	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino acid
Seq ID No: 676 & 677	410001	AB041036	Hs.57771	kallikrein 11
Seq ID No: 678 & 679	426501	AW043782	Hs.293616	ESTs
Seq ID No: 680 & 681	408369	R38438	Hs.182575	solute carrier family 15 (H ⁺ transport)
Seq ID No: 682 & 683	445413	AA151342	Hs.12677	CGI-147 protein
Seq ID No: 684 & 685	422424	AI186431	Hs.296638	prostate differentiation factor
Seq ID No: 686 & 687	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin)
Seq ID No: 688 & 689	420610	AI683183	Hs.99348	distal-less homeobox 5

TABLE 15B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
309931	AW341683	
330493	33264_5	M27826 R78416 AA307645 AW957879 AW957800 AA633529 H03662
439285	47065_1	AL133916 N79113 AF086101 N76721 AW950828 AA364013 AW955684 AI346341 AI867454 N54784 AI655270 AI421279 AW014882
		AA775552 N62351 N59253 AA626243 AI341407 BE175639 AA456968 AI358918 AA457077
450375	83327_1	AA009647 AA131254 AA374293 AW954405 H04410 AW606284 AA151166 BE157467 BE157601 H04384 W46291 AW663674 H04021 H01532
		AA190993 H03231 H59605 H01642 AA852876 AA113758 AA626915 AA746952 AI161014 AA099554 R69067
451320	86576_1	AW118072 AI631982 T15734 AA224195 AI701458 W20198 F26326 AA890570 N90552 AW071907 AI671352 AI375892 T03517 R88265
		AI124088 AA224388 AI084316 AI354686 T33652 AI140719 AI720211 T03490 AI372637 T15415 AW205836 AA630384 T03515 T33230
		AA017131 AA443303 T33623 AI222556 T33511 T33785 AI419606 D55612

TABLE 15C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
402075	8117407	Plus	121907-122035, 122804-122921, 124019-124161, 124455-124610, 125672-126076
403329	8516120	Plus	96450-96598
403478	9958258	Plus	116458-116564
404440	7528051	Plus	80430-81581
404877	1519284	Plus	1095-2107
405770	2735037	Plus	61057-62075
405932	7767812	Minus	123525-123713

Table 16

Seq ID NO: 1 DNA sequence
Nucleic Acid Accession #: NM_001216
Coding sequence: 43..1422

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1	11	21	31	41	51	
GCCCCGTACAC	ACCGTGTGCT	GGGACACCCC	ACAGTCAGCC	GCATGGCTCC	CCTGTGCCCC	60
AGCCCCCTGGC	TCCCTCTGTT	GATCCCGGCC	CCTGCTCCAG	GCCTCACTGT	GCAACTGCTG	120
CTGTCACTGC	TGCTTCTGAT	GCCTGTCCAT	CCCCAGAGGT	TGCCCGGAT	GCAGGAGGAT	180
TCCCCCTTGG	GAGGAGGCTC	TTCTGGGAA	GATGACCCAC	TGGGCGAGGA	GGATCTGCC	240
AGTGAAGAGG	ATTCAACCAG	AGAGGAGGAT	CCACCCGAG	AGGAGGATCT	ACCTGGAGAG	300
GAGGATCTAC	CTGAGAGGA	GGATCTACCT	GAAGTTAAGC	CTAAATCAGA	AGAAGAGGGC	360
TCCCTGAAGT	TAGAGGATCT	ACCTACTGTT	GAGGCTCCTG	GAGATCCTCA	AGAACCCAG	420
AATAATGCCC	ACAGGGACAA	AGAAGGGGAT	GACCAGAGTC	ATTGGCGCTA	TGGAGGCGAC	480
CGCCCTGGC	CCCGGGTGT	CCAGCCCTGC	GCGGGCCGCT	TCCAGTCCCC	GGTGGATATC	540
CGCCCCCAGC	TCGCGCCTT	CTGCGCGGCC	CTGCGCCCC	TGGAACCTCT	GGGCTTCCAG	600
CTCCCGCCGC	TCCAGAACT	GCGCCTGCGC	AACAATGGCC	ACAGTGTGCA	ACTGACCCCTG	660
CCTCCTGGGC	TAGAGATGGC	TCTGGGTCCC	GGGCGGGAGT	ACCGGCTCT	GCAGCTGCAT	720
CTGCACTGGG	GGGCTGCAGG	TCGTCCGGGC	TCGGAGCACA	CTGTGGAAGG	CCACCGTTTC	780
CCTGCGGAGA	TCCACGTGGT	TCACCTCAGC	ACCGCCTTTG	CCAGAGTTGA	CGAGGCCTTG	840
GGGCGCCGG	GAGGCTTGGC	CGTGTGGCC	GCCTTTCTGG	AGGAGGGCCC	GGAGAAAAC	900
AGTGCCTATG	AGCAGTTGCT	GTCTCGCTTG	GAAGAAATCG	CTGAGGAAGG	CTCAGAGACT	960
CAGGTCCAG	GACTGGACAT	ATCTGCACTC	CTGCCCTCTG	ACTTCAGCCG	CTACTTCCAA	1020
TATGAGGGGT	CTCTGACTAC	ACCGCCCTGT	GCCCAGGGTG	TCATCTGGAC	TGTGTTTAA	1080
CAGACAGTGA	TGCTGAGTGC	TAAGCAGCTC	CACACCTCT	CTGACACCCT	GTGGGGACCT	1140
GGTGAATCTC	GGCTACAGCT	GAATCTCCGA	GCGACGCAGC	CTTTGAATGG	GCGAGTGATT	1200
GAGGCTCTCT	TCCCTGCTGG	AGTGGACAGC	AGTCTCTGGG	CTGCTGAGCC	AGTCCAGCTG	1260
AATTCCTGCC	TGGCTGCTGG	TGACATCCTA	GCCCTGGTTT	TGGCCTCCT	TTTGTCTGTC	1320
ACCAGCGTCG	CGTTCCTTGT	GCAGATGAGA	AGGCAGCACA	GAAGGGGAAC	CAAGGGGGGT	1380
GTGAGCTACC	GCCAGCAGA	GGTAGCCGAG	ACTGGAGCCT	AGAGGCTGGA	TCTTGAGAAA	1440
TGTGAGAAGC	CAGCCAGAGG	CATCTGAGGG	GGAGCCGCTA	ACTGTCTCTG	CCTGCTCATT	1500
ATGCCACTTC	CTTTTAACCTG	CCAAGAAATT	TTTTAAATA	AATATTATA	AT	

Seq ID NO: 2 Protein sequence:
Protein Accession #: NP_001207

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1	11	21	31	41	51	
MAPLCPSPWL	PLLIPAPAPG	LTVQLLSLL	LLMPVHPQRL	PRMQEDSPLG	GGSSGEDDPL	60
GEEDLPSEED	SPREEDPPGE	EDLPGEEDLP	GEEDLPEVKP	KSEEEGSLKL	EDLPTVEAPG	120
DPQEPQNNAH	RDKEGDDQSH	WRYGGDPWP	RVSPACAGRF	QSPVDIRPQL	AAFCPALRPL	180
ELLGQLPPL	PELRLRNNGH	SVQTLPPGL	EMALGPGRY	RALQLHLHWG	AAGRPGSEHT	240
VEGHRFPABI	HVVHLSTAF	RVDEALGRPG	GLAVLAAFL	EGPEENSAYE	QLLSRLEBIA	300
EEGSETQVFG	LDISALLPSD	FSRYFYQEGS	LTPPPCAQGV	IWTFVNQTM	LSAKQLHTLS	360
DTLWGFGRDSR	LQLNFRATQP	LNGRVIEASF	PAGVDSSPRA	AEPVQLNSCL	AAGDILALVF	420
GLLFAVTSVA	FLVQMRQRH	RGTGKGVSYR	PAEVAETGA			

Seq ID NO: 3 DNA sequence
Nucleic Acid Accession #: BC013923
Coding sequence: 438-1391

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AGCGGGGTG	TCTATTAAC	TGTTCAAAAA	GTATCAGGAG	TTGTCAAGGC	AGAGAAGAGA	60
GTGTTTGCAA	AAGGGGGAAA	GATGTTTGCT	GCCTCTTTAA	GACTAGGACT	GAGAGAAAGA	120
AGAGGAGAGA	GAAAGAAAGG	GAGAGAAGTT	TGAGCCCCAG	GCTTAAGCCT	TTCAAAAAAA	180
TAATAATAAC	AATCATCGGC	GGCGGCAGGA	TCGGCCAGAG	GAGGAGGGAA	GCGCTTTTTT	240
TGATCCTGAT	TCCAGTTTGC	CTCTCTCTTT	TTTTCCCCCA	AATTATTCTT	CGCCTGATTT	300
TCTCTCGGGA	GCCCTGCGCT	CCCGACACCC	CCGCCCCGCT	CCCTCTCTCC	TCTCCCCCGG	360
CCCGCGGGCC	CCCAAGATC	CCGCGCGGCC	CGAGGTCGG	CGGCGCGCG	CGGGCGGGC	420
CGCGGCACAG	CGCCCGCATG	TACAACATGA	TGGAGACGGA	GCTGAAGCCG	CGGGCCCGC	480
AGCAAACTTC	GGGGGGCGGC	GGCGGCAACT	CCACCGGGC	GGCGGCGGC	GGCAACCAGA	540
AAAAACAGCC	GGACCGCGTC	AAGCGGCCCA	TGAATGCCTT	CATGGTGTGG	TCCCGCGGGC	600
AGCGGCGCAA	GATGGCCAG	GAGAAACCCA	AGATGCACAA	CTCGGAGATC	AGCAAGCGCC	660
TGGGCGCGGA	GTGAAAACCT	TTGTGCGAGA	CGGAGAACGG	GCCGTTCATC	GACGAGGCTA	720
AGCGGCTGCG	AGCGCTGCAC	ATGAAGGAGC	ACCGGATTA	TAAATACCGG	CCCGGCGGGA	780
AAACCAAGAC	GCTCATGAAG	AAGGATAAGT	ACACGCTGCC	CGGCGGGCTG	CTGGCCCCCG	840
GCGGCAATAG	CATGGCGAGC	GGGGTCGGGG	TGGCGCGCGG	CCTGGGCGCG	GGCGTGAACC	900
AGCGCATGGA	CAGTTACGCG	CACATGAACG	GCTGGAGCAA	CGGCAGCTAC	AGCATGATGC	960
AGGACCAGCT	GGGCTACCGG	CAGCACCCGG	GCCTCAATGC	GCACGCGCA	GCGCAGATGC	1020
AGCCCATGCA	CCGCTACGAC	GTGAGCGCCC	TGCAGTACAA	CTCCATGACC	AGCTCGCAGA	1080
CCTACATGAA	CGGCTCGCCC	ACCTACAGCA	TGTCTACTC	GCAGCAGGGC	ACCCCTGGCA	1140
TGGCTCTTGG	CTCCATGGGT	TCGGTGGTCA	AGTCCGAGGC	CAGCTCCAGC	CCCCCTGTGG	1200
TTACCTCTTC	CTCCACTTCC	AGGGCGCCCT	GCCAGGCGCG	GGACCTCCGG	GACATGATCA	1260
GCGTGTATCT	CCCCGCGCCT	GAGGTGCCGG	AACCGCGCGC	CCCCAGCAGA	CTTCACTGT	1320
CCCAGCACTA	CCAGAGCGGC	CCGGTGCCCG	GCACGGCCAT	TACCGCACA	CTGCCCTCT	1380
CACACATGTG	AGGGCCGAGC	AGCGAACTGG	AGGGGGGAGA	AATTTTCAAA	GAAAAACGAG	1440
GGAAATGGGA	GGGGTGCAAA	AGAGGAGAGT	AAGAAACAGC	ATGGAGAAAA	CCCGGTACGC	1500
TCAAAAAAAA	AAAAAAAATA	AAAATCCCAT	CACCCACAGC	AAATGACAGC	TGCAAAAGAG	1560
AACACCAATC	CCATCCACAG	TCACGCAAAA	ACCGCGATGC	CGACAAGAAA	ACTTTTATGA	1620
GAGAGATCCT	CGACTTCTTT	TKGGGGACT	ATTTTGTGAC	AGAGAAAAAC	TGGGAGGGT	1680
GGGGAGGGCG	GGGGAATGGA	CTTGTATAG	ATCTGGAGGA	AAGAAAGCTA	CGAAAACTT	1740
TTTAAAGATT	CTAGTGGTAC	GGTAGGAGCT	TTGCAGGAAG	TTTGCAAAAG	TCTTTACCAA	1800
TAATATTAG	AGATGCTTTC	CAACGACGCA	AAAAAATGTT	TTAATTTTGG	CAAGCAACTT	1860
TTGTACAGTA	TTTATCGAGA	TAAACATGCG	AATCAAAATG	TCCATTGTTT	ATAAGCTGAG	1920

AATTGCGCAA TATTTTTCAA GGAGAGGCTT CTTGCTGAAT TTTGATTCTG CAGCTGAAAT 1980
 TTAGGACAGT TGCAAAACGTG AAAAGAAGAA AATTATTCAA ATTTGGACAT TTTAATTGTT 2040
 TAAAAATTGT ACAAAGAGAA AAAATTAGAA TAAGTACTGG CGAACCATCT CTGTGGTCTT 2100
 GTTTAAAAAG GGCAAAAGTT TTAGACTGTA CTAAATTTTA TAACTTACTG TTTAAAGCAA 2160
 AAATGGCCAT GCAGGTTGAC ACCGTTGGTA ATTTATAATA GCTTTTGTTT GATCCCAACT 2220
 TTCCATTTTG TTCAGATAAA AAAAACCATG AAATTACTGT GTTTGAAATA TTTTCTTATG 2280
 GTTTGTAATA TTTCTGTAAA TTTATTGTGA TATTTTAAGG TTTTCCCCC TTTATTTTCC 2340
 GTAGTTGTAT TTTAAAAGAT TCGGCTCTGT ATTATTGAA TCAGTCTGCC GAGAATCCAT 2400
 GTATATATTT GAACTAATAT CATCCTTATA ACAGGTACAT TTTCAACTTA AGTTTCTTACT 2460
 CCATTATGCA CAGTTTGAGA TAAATAAATT TTTGAAATAT GGCACTGAA AAAAAAAAAA 2520
 AAAAAACCAA AACAAAAAAA CAAAAACAA AACACAAAAA AAAAAACAA 2580
 CACAACACAA AACAAAAAAA AAAAAAAGA AACAAACACA CAACACAACA CAACACAAAA 2640
 CCACAACACA AACACAACA CACAGAGGG

Seq ID NO: 4 Protein sequence:
 Protein Accession #: CAA83435.1

1 11 21 31 41 51
 MYNMMETELK PPGPQQTSGG GGNSTAAAA GGNQKNSPDR VKRPMNAFMV WSRGQRRKMA 60
 QENPKMHNSE ISKRLGAEWK LLSETEKRPF IDEAKRLRAL HMKEHPDYKY RPRRKTITLM 120
 KDKYTLPPG LLAPGGNSMA SGVGVGAGLG AGVNQRMSY AHMNGWSNGS YSMQDQLGY 180
 PQHPGLNAHG AAQMOPMHRV DVSALQYNSM TSSQTYMNGS PTYSMSYSQQ GTPGMALGSM 240
 GSVVKSEASS SPPVVTSSSH SRAPCQAGDL RDMISMYLPG AEVPEPAAPS RLHMSQHYQS 300
 GPVPGTAING TLPLSHM

Seq ID NO: 5 DNA sequence
 Nucleic Acid Accession #: U91618
 Coding sequence: 29-541

1 11 21 31 41 51
 CGGACTTGGC TTGTTAGAAG GCTGAAAGAT GATGGCAGGA ATGAAAATCC AGCTTGTATG 60
 CATGCTACTC CTGCTCTTCA GCTCCTGGAG TCTGTGCTCA GATTGAGAAG AGGAAATGAA 120
 AGCATTAGAA GCAGATTCTT TGACCAATAT GCATACATCA AAGATTAGTA AAGCACATGT 180
 TCCCTCTTGG AAGATGACTC TGCTAAATGT TTGCAGTCTT GTAAATAATT TGAACAGCCC 240
 AGCTGAGGAA ACAGGAGAAG TTCATGAAGA GGAGCTTGTT GCAAGAAGGA AACTTCCTAC 300
 TGCTTTAGAT GCCTTTAGCT TGAAGCAAT GTTGACAATA TACCAGCTCC ACAAATCTG 360
 TCACAGCAGG GCTTTTCAAC ACTGGGAGTT AATCCAGGAA GATATTCTTG ATACTGGAAA 420
 TGACAAAAAT GGAAAGGAAG AAGTCATAAA GAGAAAAATT CCTTATATTC TGAACCGCAA 480
 GCTGTATGAG AATAAACCCA GAAGACCCTA CATACTCAA AGAGATTCTT ACTATTACTG 540
 AGAGAATAAA TCATTATTTT ACATGTGATT GTGATTCAAT ATCCCTTAAT TAAATATCAA 600
 ATTATATTTG TGTGAAATAT TGACAAACAC ACTTATCTGT CTCTTCTACA ATTGTGGTTT 660
 ATTGAATGTG TTTTCTGCA CTAATAGAAA TTGACTAAG TGTTTTCAA TAAATCTAAA 720
 TCTTCAAAAA AAAAAAAAAA AAATGGGGCC GCAATT

Seq ID NO: 6 Protein sequence:
 Protein Accession #: AAB50564

1 11 21 31 41 51
 MMAGMKIQLV CMLLLAFSSW SLCSDSSEEM KALEADFLTN MHTSKISKAH VPSWKMTLLN 60
 VCSLVNNLNS PAETGEVHE EELVARRKLP TALDGFSLTA MLTIYQLHKI CHSRAFAQHWE 120
 LIQEDILDG NDKNGKEEVI KRKIPYILKR QLYENKPRRP YILKRDSYYY

Seq ID NO: 7 DNA sequence
 Nucleic Acid Accession #: NM_006536.2
 Coding sequence: 109-2940

1 11 21 31 41 51
 ACCTAAAACC TTGCAAGTTC AGGAAGAAAC CATCTGCATC CATATTGAAA ACCTGACACA 60
 ATGTATGCAG CAGGCTCAGT GTGAGTGAAC TGGAGGCTTC TCTACAACAT GACCCAAAGG 120
 AGCATTGCAG GTCCTATTG CAACCTGAAG TTTGTGACTC TCCTGGTTGC CTTAAGTTCA 180
 GAACTCCCAT TCCTGGGAGC TGGAGTACAG CTTCAGACA ATGGGTATAA TGGATTGCTC 240
 ATTGCAATTA ATCTCAGGT ACCTGAGAA CAGAACCCTA TCTCAAACAT TAAGGAAATG 300
 ATAACTGAAG CTTTCAATTTA CCTATTTAAT GCTACCAAGA GAAGAGTATT TTTGAGAAAT 360
 ATAAAGATTT TAATACCTGC CACATGGAAG GCTAATAATA ACAGCAAAAT AAAACAAGAA 420
 TCATATGAAA AGGCAATGT CATAGTGACT GACTGGTATG GGGCACATGG AGATGATCCA 480
 TACACCTTAC AATACAGAGG GTGTGGAAAA GAGGGAAAAAT ACATTCATTT CACACCTAAT 540
 TTCCTACTGA ATGATAACTT AACAGCTGGC TACGGATCAC GAGGCCGAGT GTTTGTCCAT 600
 GAATGGGCCC ACCTCCGTTG GGGTGTGTTT GATGAGTATA ACAATGACAA ACCTTCTTAC 660
 ATAAATGGGC AAAATCAAA TAAAGTGACA AGGTGTTTCA CTGACATCAC AGGCATTTT 720
 GTGTGTGAAA AAGGTCTCTG CCCCCAAGAA AACTGTATTA TTAGTAAGCT TTTTAAAGAA 780
 GGATGCACCT TTATCTACAA TAGCACCCAA AATGCAACTG CATCAATAAT GTTCATGCAA 840
 AGTTTATCTT CTGTGGTTGA ATTTTGTAAAT GCAAGTACCC ACAACCAAGA AGCACCAAAC 900
 CTACAGAACC AGATGTGCAG CCTCAGAAGT GCATGGGATG TAATCACAGA CTCTGCTGAC 960
 TTTACACACA GCTTCCCAT GAATGGGACT GAGCTTCCAC CTCTCCAC ATTCTCGCTT 1020
 GTACAGGCTG GTGACAAAGT GGTCTGTTTA GTGCTGGATG TGTCCAGCAA GATGGCAGAG 1080
 GCTGACAGAC TCCTTCAACT ACACAAGGCC GCAGAATTTT ATTTGATGCA GATTGTTGAA 1140
 ATTCACTCCT TCGTGGGACT TGCAGTTTTC GACAGCAAG GAGAGATCAG AGCCCGACTA 1200
 CACCAAAATTA ACAGCAATGA TGATCGAAAG TTGCTGGTTT CATATCTGCC CACCACTGTA 1260
 TCAGCTAAAA CAGACATCAG CATTTGTTCA GGGCTTAAGA AAGGATTTGA GGTGGTTGAA 1320
 AAACGAAATG GAAAGCTTA TGGCTCTGTG ATGATATTAG TGACCAGCGG AGATGATAAG 1380
 CTCTCTGGCA ATTGCTTACC CACTGTGCTC AGCAGTGGTT CAACAATTCA CTCCATTGCC 1440

	CTGGGTTTCAT	CTGCAGCCCC	AAATCTGGAG	GAATTATCAC	GTCTTACAGG	AGGTTTAAAG	1500
	TTCTTTGTTTC	CAGATATATC	AAACTCCAAT	AGCATGATTG	ATGCTTTTCAG	TAGAATTTCC	1560
	TCTGGAACCTG	GAGACATTTT	CCAGCAACAT	ATTTCAGCTTG	AAAGTACAGG	TGAAAAATGTC	1620
5	AAACCTCACC	ATCAATTGAA	AAACACAGTG	ACTGTGGATA	ATACTGTGGG	CAACGACACT	1680
	ATGTTTCTAG	TTACGTGGCA	GGCCAGTGGT	CCTCCTGAGA	TTATATTATT	TGATCCTGAT	1740
	GGACGAAAT	ACTACACAAA	TAATTTTATC	ACCAATCTAA	CTTTTCGGAC	AGCTAGTCTT	1800
	TGGATTCCAG	GAACAGCTAA	GCCTGGGCAC	TGGACTTACA	CCCTGAAACA	TACCCATCAT	1860
	TCTCTGCAAG	CCCTGAAAGT	GACAGTGACC	TCTCGGCGCT	CCAACCTCAGC	TGTGCCCCCA	1920
10	GCCACTGTGG	AAGCCTTTGT	GGAAAGAGAC	AGCCTCCATT	TTCTCATCC	TGTGATGATT	1980
	TATGCCAATG	TGAAACAGGG	ATTTTATCCC	ATTCCTTAATG	CCACTGTCAC	TGCCACAGTT	2040
	GAGCCAGAGA	CTGAGATGCC	TGTTACGCTG	AGACTCCTTG	ATGATGGAGC	AGGTGCTGAT	2100
	GTTATAAAAA	ATGATGGAAT	TTACTCGAGG	TA'TTTTCT	CCTTGTCTGC	AAATGGTAGA	2160
	TATAGCTTGA	AAGTGCATGT	CAATCACTCT	CCCAGCATAA	GCACCCCAAC	CCACTCTATT	2220
15	CCAGGGAGTC	ATGCTATGTA	TGTACCAAGT	TACACAGCAA	ACGGTAATAT	TCAGATGAAT	2280
	GCTCCAAGGA	AATCAGTAGG	CAGAAATGAG	GAGGAGCGAA	AGTGGGGCTT	TAGCCGAGTC	2340
	AGCTCAGGAG	GCTCCTTTTC	AGTGCTGGGA	GTTCAGCTG	GCCCCACCC	TGATGTGTTT	2400
	CCACCATGCA	AAATTATTGA	CCTGGAAAGT	GTAAAAGTAG	AAGAGGAATT	GACCCATATCT	2460
	TGGACAGCAC	CTGGAGAAGA	CTTTGATCAG	GGCCAGGCTA	CAAGCTATGA	AATAAGAAATG	2520
20	AGTAAAGATC	TACAGAATAT	CCAAGATGAC	TTTAACAATG	CTATTTTAGT	AAATACATCA	2580
	AAGCGAAATC	CTGAGCAAGT	TGGCATCAGG	GAGATATTTA	CGTTCTCACC	CCAGATTTCC	2640
	ACGAATGGAC	CTGAACATCA	GCCAAATGGA	GAAACACATG	AAAGCCACAG	AATTTATGTT	2700
	GCAATACGAG	CAATGGATAG	GAACCTCCTA	CAGTCTGCTG	TATCTAACAT	TGCCCAGGCG	2760
	CCTCTGTTTA	TTCCCCCAA	TTCTGATCCT	GTACCTGCCA	GAGATTATCT	TATATTGAAA	2820
25	GGAGTTTTAA	CAGCAATGGG	TTTGATAGGA	ATCATTTGCC	TTATTATAGT	TGTGACACAT	2880
	CATACTTTAA	GCAGGAAAAA	GAGAGCAGAC	AAGAAAGAGA	ATGGAACAAA	ATTATTATAA	2940
	ATAAATATCC	AAAGTGTCTT	CCTTCTTAGA	TATAAGACCC	ATGGCCTTCG	ACTACAAAAA	3000
	CATACTAACA	AAGTCAAAAT	AACATCAAAA	CTGTATTAAA	ATGCATTGAG	TTTTTGTACA	3060
	ATACAGATAA	GATTTTTTACA	TGGTAGATCA	ACAATTCCTT	TTGGGGGTAG	ATTAGAAAAAC	3120
30	CCTTACATT	TGGCTATGAA	CAAAATAATA	AAATTATTCT	TTAAAGTAAT	GTCTTTAAAG	3180
	GCAAAGGGAA	GGGTAAAGTC	GGACCAAGTG	CAAGGAAAGT	TTGTTTTATT	GAGGTGGAAA	3240
	AATAGCCCCA	AGCAGAGAAA	AGGAGGGTAG	GTCTGCATTA	TAAGTGTCTG	TGTGAAGCAA	3300
	TCATTTAGTT	ACTTTGATTA	ATTTTCTTT	TCTCCTTATC	TGTGCAGTAC	AGGTTGCTTG	3360
	TTTACATGAA	GATCATGCTA	TATTTTATAT	ATGTAGCCCC	TAATGCAAAG	CTCTTTACCT	3420
	TTTGCTATT	TGTTATATAT	ATTTTCAGATG	ACATCTCCCT	GCTAATGCTC	AGAGATCTTT	3480
35	TTTCACTGTA	AGAGGTAAAC	TTTAAACAATA	TGGGTATTAC	CTTTGTCTCT	TCATACCGGT	3540
	TTTATGACAA	AGGTCTATTG	AATTTATTG	TNTGTAAGTT	TCTACTCCCA	TCAAAGCAGC	3600
	TTTCTAAGTT	TATTGCCTTG	GGTTATTATG	GAATGATAGT	TATAGCCCN	TATAATGCCT	3660
	TACCTAGGAA	A					

Seq ID NO: 8 Protein sequence:
Protein Accession #: NP_006527.1

	1	11	21	31	41	51	
45	MTQRSIAGPI	CNLKFVTLIV	ALSSSELPFLG	AGVQLQDNGY	NGLLIAINPQ	VPEQNQLISN	60
	IKEMITEASF	YLFNATKRRV	FFRNKILIP	ATWKANNNSK	IKQESYEKAN	VIVTDWYGAAH	120
	GDDPYTLQVR	GCGKEGKVIH	FTPNFLNDN	LTAGYGSRRG	VFWHEWAHLR	WGVFDEYNND	180
	KPFYINGQNG	IKVTRCSSDI	TGIFVCEKGP	CPQENCIISK	LFKEGCTFIY	NSTQNATASI	240
	MFMSLSLVV	EFCNASTHNG	EAPNLQNMOC	SLRSAWDVIT	DSADFHHSFP	MNGTELPPPP	300
50	TFSLVQAGDK	VVCLVLDVSS	KMAEADRLLO	LQQAEEFYLM	QIVEIHTFVG	IASFDSKGEI	360
	RAQLHQINSN	DDRKLIVSYL	PTTVSAKTDI	SICSGLKKGF	EVVEKLNGKA	YGSVMILVTS	420
	GDDKLLGNCL	PTVLSGGSTI	HSIALGSSAA	PNLEELSRIT	GGLKPFVPDI	SNSNSMIDAF	480
	SRISSTGDI	FQHQIQUEST	GENVKPHQL	KNTVTVDNTV	GNDTMFLVTW	QASGPPEIIL	540
	FDPDGRKYIT	NNFITNLTFR	TASLWIPGTA	KPGHWYTYTLN	NTHSLQALK	VTVTSRASNS	600
55	AVPPATVEAF	VERDSLHFFH	PVMYIANVKQ	GFYPILNATV	TATVEPETGD	PVTLRLLLDDG	660
	AGADVIKNDG	IYSRYFFSFA	ANGRYSLKVH	VNHSFISIST	AHSIPGSHAM	YVPGYTANGN	720
	IQMNAPRKSV	GRNEEERKVG	FSRVSSGGSF	SVLGVPAAGPH	PDVFPCKII	DLEAVKVEEE	780
	LTLSTWAPGE	DFDQQAATSY	EIRMSKSLQN	IQDDFNNAIL	VNTSKRNPPQ	AGIREIFTFS	840
60	PQISTNGPEH	QPNGETHESH	RIVVAIRAMD	RNSLQSAVSN	IAQAPLFIPP	NSDPVPARDY	900
	LILKGVLTAM	GLIGIICLII	VVTHHTLSRK	KRADKKENG	T		

Seq ID NO: 9 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 336-632

	1	11	21	31	41	51	
70	CTCCCTCAC	CCCGGTCCAG	GATGCCCACT	CCCCACGACA	CCTCCCACTT	CCCACTGTGG	60
	CCTGGGTGGG	CTCAGGGGCT	GCCCTTGACC	TGGCCTAGAG	CCCTCCCCCA	GCTGGTGGTG	120
	GAGCTGGCAC	TCTCTGGGAG	GGAGGGGCT	GGGAGGGAAT	GAGTGGGAAT	GGCAAGAGGC	180
	CAGGGTTTGG	TGGGATCAGG	TTGAGGCAGG	TTTGGTTTCC	TTAAATGCC	AAGTTGGGGG	240
	CCAGTGGGGC	CCACATATAA	ATCCTCACCC	TGGGAGCCTG	GCTGCCTTGC	TCTCCTCTCT	300
	GGGTCTGTCT	CTGCACCTG	GTCTGCCACA	GATCCATGAT	GTGCAGTTCT	CTGGAGCAGG	360
75	CGCTGGCTGT	GCTGGTCACT	ACCTTCCACA	AGTACTCCTG	CCAAGAGGGC	GACAAGTTCA	420
	AGCTGAGTAA	GGGGGAAATG	AAGGAACTTC	TGCACAAGGA	GCTGCCACGC	TTTGTGGGGG	480
	AGAAAGTGGG	TGAGGAGGGG	CTGAAGAAGC	TGATGGGCAG	CCTGGATGAG	AACAGTGACC	540
	AGCAGGTGGA	CTTCCAGGAG	TATGCTGTTT	TCCTGGCACT	CATCACTGTC	ATGTGCAATG	600
	ACTTCTTCCA	GGGCTGCCCA	GACCGACCTT	GAAGCAGAAC	TCTTGACTTC	CTGCCATGGA	660
80	TCTCTTGGGC	CCAGGACTGT	TGATGCCCTT	GAGTTTGTGA	TTCAATAAAC	TTTTTTGTGC	720
	TGTTGATAAT	ATTTTAATTG	CTCAGTGATG	TTCCATAACC	CGGCTGGCTC	AGCTGGAGTG	780
	CTGGGAGATG	AGGGCCTCCT	GGATCCTGCT	CCCTTCTGGG	CTCTGACTCT	CCTGGAAATC	840
	TCTCAAGGC	CAGGACTATG	CTTTAGGTCT	CAATTTTGGG	ATTTCAAACA	CCAGCAAAAA	900
85	ATTGGAAATC	GAGATAGGTT	GCTGACTTTT	ATTTTGTCAA	ATAAGATAT	TAAAAAAGGC	960
	AAATACCA						

Seq ID NO: 10 Protein sequence:

Protein Accession #: NP_005969.1

1 11 21 31 41 51
 5 MMCSLEQAL AVLVTTFFHKY SCQEGDKFKL SKGEMKELLH KELPSFVGEK VDEEGLKKLM 60
 GSLDENSDQQ VDFQEYAVFL ALITVMCNDP FQGCPRDP

Seq ID NO: 11 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 336-626

1 11 21 31 41 51
 15 CTCCCTCAC CCCGCTCCAG GATGCCAGT CCCCAAGACA CCTCCCACTT CCCACTGTGG 60
 CCTGGGTGGG CTCAGGGGCT GCCCTTGACC TGGCCTAGAG CCCTCCCCCA GCTGGTGGTG 120
 GAGCTGGCAC TCTCTGGGAG GGAGGGGGCT GGGAGGGAAT GAGTGGGAAT GGCAAGAGGC 180
 CAGGGTTTGG TGGGATCAGG TTGAGGCAGG TTGGTTTCC TTAATAATGCC AAGTTGGGGG 240
 CCAGTGGGGC CCACATATAA ATCCTCACCC TGGGAGCCTG GCTGCCTTGC TCTCCTTCCT 300
 20 GGGTCTGTCT CTGCCACCTG GTCTGCCACA GATCCATGAT GTGCAGTTCT CTGGAGCAGG 360
 CGCTGGCTGT GCTGGTCACT ACCTTCACCA AGTACTCCTG CCAAGAGGGC GACAAGTTCA 420
 AGCTGAGTAA GGGGGAATG AAGGAACCTC TGCACAAGGA GCTGCCAGC TTTGTGGGGC 480
 ATTCAGAGA ACCATGTGCT GTGAGGGGCT TCCGAGTCCA TCTGTTAAT CCTGTCAATG 540
 GAGACTTGAG AAACCAGAGC CCAGAAGGGA AAAGTGATTG TCCCAAGATC ACACAGCACT 600
 25 GGAGAAAGTG GATGAGGAGG GGCTGAAGAA GCTGATGGGC AGCCTGGATG AGAACAGTGA 660
 CCAGCAGGTG GACTTCCAGG AGTATGCTGT TTTCTGGCCA CTCATCACTG TCATGTGCAA 720
 TGACTTCTTC CAGGGCTGCC CAGACCGACC CTGAAGCAGA ACTCTTGACT TCCTGCCATG 780
 GATCTCTTGG GCCCAGGACT GTTGATGCCT TTGAGTTTGG TATTCAATAA ACTTTTTTTG 840
 30 TCTGTTGATA ATATTTTAAT TGCTCAGTGA TGTTCATAA CCGGGCTGGC TCAGCTGGAG 900
 TGCTGGGAGA TGAGGGCCTC CTGGATCCTG CTCCTTCTG GGTCTGACT CTCCTGAAA 960
 TCTCTCCAG GCCAGAGCTA TGCTTTAGGT CTCATTTTG GAATTTCAA CACCAGCAA 1020
 AAATTGAAA TCGAGATAGG TTGCTGACTT TTATTTTGTC AAATAAAGAT ATTAATAAAG 1080
 GCAATACCA

Seq ID NO: 12 Protein sequence:
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 40 MMCSLEQAL AVLVTTFFHKY SCQEGDKFKL SKGEMKELLH KELPSFVGHS REPCA VRAFR 60
 VHLFNEVIGD LRNQSPGKGS DCPKITQHRW KWMRRG

Seq ID NO: 13 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 58-354

1 11 21 31 41 51
 50 GTGAGTCAC CATGTGGGGG TGAGGCTGAG AGAAAACAAG TACACAGCCA CAGATCCATG 60
 ATGTGCAGTT CTCTGGAGCA GGCCTGGCT GTGCTGGTCA CTACCTTCCA CAAGTACTCC 120
 TGCCAAGAGG GCGACAAGTT CAAGCTGAGT AAGGGGGAAA TGAAGGAACT TCTGCACAAG 180
 GAGCTGCCCA GCTTTGTGGG GGAGAAAGTG GATGAGGAGG GGCTGAAGAA GCTGATGGGC 240
 55 AGCCTGGATG AGAACAGTGA CCAGCAGGTG GACTTCCAGG AGTATGCTGT TTTCTGGCA 300
 CTCATCACTG TCATGTGCAA TGACTTCTTC CAGGGCTGCC CAGACCGACC CTGAAGCAGA 360
 ACTCTTGACT TCCTGCCATG GATCTCTTGG GCCCAGGACT GTTGATGCCT TTGAGTTTGG 420
 TATTCAATAA ACTTTTTTTG TCTGTTGATA ATATTTTAAT TGCTCAGTGA TGTTCATAA 480
 CCGGCTGGC TCAGCTGGAG TGCTGGGAGA TGAGGGCCTC CTGGATCCTG CTCCTTCTG 540
 60 GGCTCTGACT TCCTGGAAA TCTCTCCAAG GCCAGAGCTA TGCTTTAGGT CTCATTTTGG 600
 GAATTTCAA CACCAGCAA AAATTGAAA TCGAGATAGG TTGCTGACTT TTATTTTGTC 660
 AAATAAAGAT ATTAATAAAG GCAATACCA

Seq ID NO: 14 Protein sequence:
 Protein Accession #: NP_005969.1

1 11 21 31 41 51
 65 MMCSLEQAL AVLVTTFFHKY SCQEGDKFKL SKGEMKELLH KELPSFVGEK VDEEGLKKLM 60
 GSLDENSDQQ VDFQEYAVFL ALITVMCNDP FQGCPRDP

Seq ID NO: 15 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 62-358

1 11 21 31 41 51
 75 GGAGGGTGTG CCGCTGAGTC ACTGCCTGGG CATCTGGGCC TGGAACTCG GCCACAGATC 60
 CATGATGTGC AGTTCTCTGG AGCAGGCGCT GGCTGTGCTG GTCCTACCT TCCACAAGTA 120
 CTCCTGCCAA GAGGCGGACA AGTTCAAGCT GAGTAAGGGG GAAATGAAGG AACTTCTGCA 180
 80 CAAGGAGCTG CCCAGCTTTG TGGGGGAGAA AGTGGATGAG GAGGGCTGTA AGAAGCTGAT 240
 GGGCAGCCTG GATGAGAACA GTGACCAGCA GGTGGACTTC CAGGAGTATG CTGTTTTCCT 300
 GGCATCTATC ACTGTCTATG GCAATGACTT CTTCCAGGGC TGCCAGAGC GACCTTGAAG 360
 CAGAACTCTT GACTTCTTGC CATGGATCTC TTGGGCCAG GACTGTTGAT GCCTTTGAGT 420
 85 TTTGTATTCA ATAACTTTT TTTGTCTGTT GATAATATTT TAATTGCTCA GTGATGTTCC 480
 ATAACCCGCG TGGCTCAGCT GGAGTGCTGG GAGATGAGGG CCTCTGGAT CCTGCTCCCT 540
 TCTGGGCTCT GACTCTCTG GAAATCTCTC CAAGGCCAGA GCTATGCTTT AGGTCTCAAT 600
 TTTGGAATTT CAAACACCAG CAAAAAATG GAAATCGAGA TAGGTTGCTG ACTTTTATT 660

Seq ID NO: 16 Protein sequence:
Protein Accession #: NP_005969.1

1	11	21	31	41	51	
MMCSSLEQAL	AVLVTTTFHKY	SCQEGDKPKL	SKGEMKELLH	KELPSFVGEK	VDEEGLKKLM	60
GSLDENSDQQ	VDFQEYAVFL	ALITVMCNDF	FQGCPCDRP			

Seq ID NO: 17 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 939-2372

1	11	21	31	41	51	
AAGACGGATT	CTCAGACAAG	GCTTGCAAAT	GCCCCGCAGC	CATCATTTAA	CTGCACCCGC	60
AGAATAGTTA	CGGTTTGTC	CCCGACCCCTC	CCGGATCGCC	TAATTTGTCC	CTAGTGAGAC	120
CCCGAGGCTC	TGCCCGCGCC	TGGCTTCTTC	GTAGCTGGAT	GCATATCGTG	CTCCGGCGCAG	180
CGCGGGCGCA	TGGCAGCGGT	TGCGGCACAC	CCTAGCACAC	ATGAACACGC	GCAAGAGCTG	240
AACCAAGCAC	GGTTTCCATT	TCAAAAAGGG	AGACAGCCTC	TACCGCGATT	GTAGAAGAGA	300
CTGTGGTGTG	AATTAGGAGC	CGGGAGGCGT	CGAACCGAGG	AACGGTTTAT	CTTAGAGACT	360
AATTTTCTGG	AGTTTCTGCC	CTGCTCTGTC	GTACGCCCTC	ACGTCACTTC	GCCAGCAGTA	420
GCAGAGGCGG	CGGCGGCGGC	TCCCGGAATT	GGGTTGGAGC	AGGAGCCTCG	CTGGCTGCTT	480
CGCTCGCGCT	CTACGCGCTC	AGTCCCGGCG	GGTAGCAGGA	GCCTGGACCC	AGGCGCGCGC	540
GGCGGGCGTG	AGGCGCGCGA	GCCCGGCCTC	GAGGTGCATA	CCGGACCCCC	ATTCCGATCT	600
AACAAGGAAT	CTGCGCCCCA	GAGAGTCCCG	GGAGCGCCGC	CGGTCCGTGC	CCGGCGCGCC	660
GGGCCATGCA	GCGACGCGCG	CCGCGGAGCT	CCGAGCAGCG	GTAGCGCCCC	CCTGTAAAGC	720
GGTTCGTAT	CCCGGGGCGC	CTGTGAACCC	TGCCGCCTGC	CGGAACACTC	TTCGCTCCGG	780
ACCAGCTCAG	GCTCTGATAA	GCTGGACTCG	GCACGCCCGC	AACAAGCACC	GAGGAGTTAA	840
GAGAGCCGCA	AGCGCAGGGA	AGGCCTCCCC	GCACGGGTGG	GGGAAAGCGG	CCGGTGCAGC	900
GCGGGGACAG	GCACCTCGGC	TGGCACTGGC	TGCTAGGGAT	GTCTCTCTGG	ATAAGSTGGC	960
ATGGACCCGC	CATGGCGCGG	CTCTGGGGCT	TCTGCTGGCT	GGTTGTGGGC	TTCTGGAGGG	1020
CCGCTTTTCG	CTGTCCACAG	TCCTGCAAAAT	GCAGTGCCCT	TCGGATCTGG	TGCAGCGACC	1080
CTTCTCCTGG	CATCGTGGCA	TTTCCGAGAT	TGGAGCCTAA	CAGTGTAGAT	CCTGAGAACA	1140
TCACCGAAAT	TTTCATCGCA	AACCGAGAAA	GGTTAGAAAT	CATCAACGAA	GATGATGTTG	1200
AAGCTTATGT	GGGACTGAGA	AATCTGACAA	TTGTGGATTC	TGGATTAAAA	TTTGTGGCTC	1260
ATAAAGCATT	TCTGAAAAAC	AGCAACCTGC	AGCACATCAA	TTTTACCGGA	AACAACTGA	1320
CGAGTTTGTG	TAGGAAACAT	TTCCGTCAAC	TTGACTTGTG	TGAACTGATC	CTGGTGGGCA	1380
ATCCATTATC	ATGCTCCTGT	GACATTATGT	GGATCAAGAC	TCCTCAAGAG	GCTAAATCCA	1440
GTCCAGACAC	TCAGGATTGT	TACTGCTGTA	ATGAAAGCAG	CAAGAATATT	CCCCTGGCAA	1500
ACCTGCAGAT	ACCGAATTGG	GGTTTGCCAT	CTGCAAAATC	GGCCGCACCT	AACCTCACTG	1560
TGGAGGAAGG	AAAGTCTATC	ACATTATCCT	GTAGTGTGGC	AGGTGATCCG	GTTCTTAATA	1620
TGTATTGGGA	TGTTGGTAAC	CTGGTTTCCA	AACATATGAA	TGAAACAAGC	CACACACAGG	1680
GCTCCTTAAG	GATAACTAAC	ATTTCATCCG	ATGACAGTGG	GAGACAGATC	TCTTGTGTGG	1740
CGGAAATCT	TGTAGGAGAA	GATCAAGATT	CTGTCAACCT	CACTGTGCAT	TTTGACACAA	1800
CTATCACATT	TCTCGAATCT	CCAACCTCAG	ACCACCACTG	GTGCATTCCA	TTCACTGTGA	1860
AAGCAACACC	GAAACAGATT	CTTCAGTGGT	TCTATAACGG	GGCAATATTG	AATGAGTCCA	1920
AATACATCTG	TACTAAAATA	CATGTTACCA	ATCACACGGA	GTACCACGGC	TGCCTCCAGC	1980
TGGATAATCC	CACTCACATG	AACAATGGGG	ACTACACTCT	AATAGCCAAG	AATGAGTATG	2040
GGAGAGGATG	GAAACAGATT	TCTGCTCACT	TCATGGGCTG	GCCTGGAAAT	GACGATGGTG	2100
CAAAACCCAA	TTATCCTGAT	GTAATTTATG	AAGATTATGG	AATGACAGCG	AATGACATCG	2160
GGGACACCAC	GAACAGAAGT	AATGAAATCC	CTTCCACAGA	CGTCACTGAT	AAAACCGGTC	2220
GGGAACATCT	CTCGGTCTAT	GCTGTGGTGG	TGATTGCGTC	TGTGGTGGGA	TTTTGCCTTT	2280
TGGTAATGCT	GTTTCTGCTT	AAGTTGGCAA	GACACTCCAA	GTTTGGCATG	AAAGGTTTTG	2340
TTTTGTTTCA	TAAGATCCCA	CTGGATGGGT	AGCTGAAATA	AAGGAAAGGA	CAGAGAAAGG	2400
GGCTGTGGTG	CTTGTGTGTT	GATGCTGCCA	TGTAAGCTGG	ACTCCTGGGA	CTGCTGTGGG	2460
CTTATCCCGG	GAAGTGCTGC	TTATCTGGGG	TTTTCTGGTA	GATGTGGGCG	GTGTTTGGAG	2520
GCTGTACTAT	ATGAAGCCTG	CATATACTGT	GAGCTGTGAT	TGGGGAACAC	CAATGCAGAG	2580
GTAACCTCTA	CGCAGCTAAG	CAGCACCTCA	AGAAAACATG	TTAAATTAAT	GCTTCTCTTC	2640
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GTCCAAATGT	TTAGCTTAGG	TCTGAGAGTC	AAACAATGTT	AAGGATTGTC	TTAAAGTTCC	3060
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AAGAAAAAAA	ACAAGAACAA	GCAGCAACAG	CTGTTTGTGT	GGGGCTATAG	ATTTAAGTTA	3180
GGCATAGTCA	ATTTCAGAAAT	AACTAAGAGT	GGAATATATG	CATATGGTGA	AATTATAACC	3240
TTGCCCTTTT	TTATTGCGCC	TCTGCGATCC	ACCTGCTTTT	TAGAAGTCTG	CCGAGTGAGC	3300
AGGCCACAGT	ATCTTGCATT	GTTTGCATTA	CAGAACTGCA	GCTTTTCTAC	TCTGAAAAGG	3360
CCTGGGAGCA	GAATGGCTGG	CCTGCTGTGA	GCAGGAGAGG	AGATTCTAAG	AAGGATAGTC	3420
CCCCCTACAA	CATACTGTCA	TACTGCTGGG	TTTTCATGGG	TAGGAAAGCT	TGCTCTGACC	3480
CCAGCAGCAA	AGAGTGTGCA	GGTCGCTAAT	GAATATATGC	TTTATAATGT	CCTTCTTCAT	3540
TGCTGAGAGG	GCAGCCTTAG	AGCTGTGGAT	TTCTGCATCC	CCCCTGAGTC	TGACCCATGG	3600
ACACCTGTTT	CATTCACTTT	AGCATCACAG	TGACCTTTGT	ATGCTCTGTT	CAGTCTGTGT	3660
CAGGCAGTAT	GCTTGTCTTG	AAGAGAGGTT	TGGCTATCCC	CACCCACCCC	CACCCACCCC	3720
TGTTCTCTTT	TTATCAGGAG	GACTTCAGAG	CCAGGCCTGC	AGCATTTTGT	TTGAAAACAC	3780
AATCAGCTCT	GACAGTTAGA	CATGCACACA	GACGCCATAG	CTGGATTGGA	AACATTGATG	3840
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TCTATAGATT	TTAACTAGT	CCAACACAGT	CAGAAACATT	GTTTGAATC	CTCTGTAAC	3960
CAAGGCATTA	ATCTTAATAA	ACCAGGATCC	ATTTAGGTAC	CACCTTGATAT	AAAAAGGATA	4020
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 10 TTTAAATGG AGAGAAGTGG ACAGATAAGG CCATTTAATA TATCAAAGAT CAGTTGACAT 4680
 CTCCTAGGGA ATGATGAAAA CAGCAGGCTA T

Seq ID NO: 18 Protein sequence:
 Protein Accession #: CAA53571

15 1 11 21 31 41 51
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 20 NFRNKLTS SRKHFRHLDL SELILVGNPF TCSCDIMWIK TLQEAQSSPD TQDLYCLNES 180
 SKNIPLANLQ IPNCGLPAN LAENLITVEE GKSITLSCSV AGDPVFNMYW DVGNLVSKHM 240
 NETSHTQSL RITNISSDDS GKQISCVAEN LVGEDQDSVN LTVHFAPTIT FLESPTSDDH 300
 WCIPTVKGN PKPALQWFM GAILNESKYI CTKIHVTNHT EVHGCLQLDN PTHMNGDYT 360
 LIAKNEYGKD EKQISAHPMG WPGIDDGANP NYPDVIYEDY GTAANDIGDT TNRSNEIPST 420
 25 DVTDKTGREH LSVYAVVVIA SVVGFCLLVM LFLKLARHS KFGMKGFVLF HKIPLDG

Seq ID NO: 19 DNA sequence
 Nucleic Acid Accession #: NM_000228
 Coding sequence: 82-3600

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 35 CTGTGTTGGA GGACCCGGT TCTCCGAGCT TCATCTACCT GTGGACTGAC CAAGCCTGAG 240
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 CAGTCCCTGC CTCAGAGGCC TAATGCACGC CTAAATGGGG GGAAGGTCCA ACTTAACCTT 660
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 55 CCAGTGACCG GGCAGTGTGT GTGCAAGGAG CATGTGCAGG GAGAGCGCTG TGACCTATGC 1320
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 CTGCCCAAG TGGTGGGTCC CAAATGTGAC CAGTGTGCTC CCTACCACTG GAAGCTGGCC 1500
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 85 AGGTTTGTG AGGTTTCAAG GGTACTGCGG CCAGCAGAAA AGCTGGTGAC AAGCATGACC 3180
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 AAAATCTTTG G

Seq ID NO: 20 Protein sequence:
 Protein Accession #: NP_000219

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 MEFQGPMPAG MLIERSSDFG KTWVYQYLA ADCTSTFPRV RQGRPQSWQD VRCQSLPQRP 180
 NARLNGGKVQ LNLMDLVSGI PATQSQKIQE VGEITNLRVN FTLLAPVPQR GYHPPSAYYA 240
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 PWRPAEQDRA HECQRCDNCG HSETCHFDPV VFAASQGAYG GVDCNCRDHT EGNKNCERCQL 360
 HYFRNRPGA SIQETCISCE CDDPGAVPGA PCDPVTGQCV CKEHVQGERC DLCKPGFTGL 420
 TYANPQGGHR CDCNLLGSRV DMPDDEESGR CLCLPNVVG P KCDQCAPYHW KLASGGGCEP 480
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 AYEQSAQAAQ QVSDSSRLLD QLRDSRREAE RLVQAGGGG GTGSPKLVAL RLEMSSLPDL 780
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Seq ID NO: 21 DNA sequence
 Nucleic Acid Accession #: NM_003722
 Coding sequence: 145-1491

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Seq ID NO: 22 Protein sequence:
 Protein Accession #: NP_003713

1 11 21 31 41 51
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 FEARICACPG RDRKADEDSI RKQVSDSTK NGDGTKRPF RQNTHQIMTS IKRRSPDDE 360
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Seq ID NO: 23 DNA sequence
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 CTGGGTCTGT CCAGCCAGCT GTTTCCATCC CTGACCTCT GCAGCATGGT AACTATTAG 2880
 TAACGGAGAC TTAACGCTCT TCTGGTCTCC TCGTGCAACC TTCCACTGCA GGCTTTGATC 2940
 CACTTCTCAC ACAAATGTG ATAGTGACAG AAAGGGTGAT CTGTCCCAT TCCAGTGTTC 3000
 CTGGCAACCT AGCTGGCCCA ACGCAGCTAC GAGGGTCACA TACTATGCTC TGTACAGAGG 3060
 ATCCTTGCTC CGTCTAATA TGACCAGAA GAGCTGGAAT ACCCACTGTA CCAATCTGG 3120
 ATCTTTGGAC TAAAGTATTC AAAATAGCAT AGCAAAGCTC ACTGTATTGG GCTAATAATT 3180
 TGGCACTTAT TAGCTTCTCT CATAACTGA TCACGATTAT AAATTAATG TTTGGGTTCA 3240
 TACCCCAAAA GCAATATGTT GTCATCTCTA ATTCTCAAGT ACTATTCAAA TTGTAGTAAA 3300
 TCTTAAAGTT TTTCAAAACC CTAATATCAT ATTCGC

Seq ID NO: 24 Protein sequence:
 Protein Accession #: NP_001935.1

1 11 21 31 41 51

	MMGLFPRTTG	ALAIFVVVIL	VHGLRIETK	QYDEEEMTM	QQAQRQKRE	WVKFAKPCRE	60
	GEDNSKRNPI	AKITSYQAT	QKITRYISGV	GIDQPPFGIF	VVDKNTGDIN	ITAIVDREET	120
5	PSFLITCRAL	NAQGLDVEKP	LILTVKILDI	NDNPPVPSQ	IFMGEIEENS	ASNSLVMILN	180
	ATDADEPNHL	NSKIAFKIVS	QEPAGTMMFL	LSRNTGEVRT	LTNSLDREQA	SSYRLVVSQA	240
	DRDGBGLSTQ	CECNKVKVDV	NDNFPMFRDS	QYSARIEENI	LSSELLRFQV	TDLDEEYTDN	300
	WLAVYFFTS	NEGNWFIEQT	DPRTNEGILK	VVKALDYBQL	QSVKLSIAVK	NKAEFHQSVI	360
	SRYRVQSTPV	TIQVINVRG	IAPRPASKTF	TVQKGISSKK	LVYIILGTQY	AIDEDTNKAA	420
10	SNVKYVMGRN	DGGYLMWDSK	TAEIKFVKNM	NRDSTFIVNK	TITAEVLAI	EYTGKTSTGT	480
	VYVRVPDFND	NCPTAVLEKD	AVCSSSPSVV	VSARTLNNRY	TGPTTFALD	QPVKLPVWS	540
	ITTLNATSAL	LRAQEQIPEG	VYHISLVLT	SQNNRCMPR	SLTLEVQCQD	NRGICGTSYP	600
	TTSPGTRYGR	PHSGRLGPA	IGLLLLGLLL	LLLAFLLLLT	CDCGAGSTGG	VTGGFIPVPD	660
	GSEGTIHQWG	IEGAHPEDKE	ITNICVPPVT	ANGADFMBESS	EVCTNTYARG	TAVEGTSME	720
15	MTTKLGAATE	SGCAAGFATG	TVSGAASGFG	AATGVGICSS	QSGTMRTRH	STGGTNKDYA	780
	DGAISMNPLD	SYFSQKAFAC	AEEDDQGEAN	DCLLIYDNEG	ADATGSPVGS	VGCCSFIAAD	840
	LDDSFLLSLG	PKFKKLAEIS	LGVDGEGKEV	QPPSKDSGYG	IESCGHPIEV	QQTGFVKCQT	900
	LSGSQGSAL	SAGSVQAPAV	SIPDPLQHGN	YLVETYSAS	GSLVQPSSTAG	FDPLLTQNV	960
	VERTVICPIS	SVPGNLAGPT	QLRGSHTMLC	TEDPCSRLLI			

Seq ID NO: 25 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 56-1642

	1	11	21	31	41	51	
25	AGTATCCCG	GAGGAGCAAG	TGGCAGCTCT	TCGGACCTAG	GCTGCCCTG	CCGTCATGTC	60
	GCAAGGGATC	CTTTCTCCGC	CAGCGGGCTT	GCTGTCCGAT	GACGATGTCG	TAGTTTCTCC	120
	CATGTTTGAG	TCCAAGCTCG	CAGATTGGGG	GTCTGTGGTA	CGCAAGAAC	TGCTATCAGA	180
	CTGCTCTGTC	GTCTCTACCT	CCCTAGAGGA	CAAGCAGCAG	GTTCCATCTG	AGGACAGTAT	240
30	GGAGAAGGTG	AAAGTATACT	TGAGGGTTAG	GCCCTTGTTA	CCCTCAGAGT	TGGAACGACA	300
	GGAAGATCAG	GGTTGTGTCC	GTATTGAGAA	TGTGGAGACC	CTGTCTTAC	AAGCACCCAA	360
	GGAATCTTTT	GCCCTGAAGA	GCAATGAACG	GGGAATTGGC	CAAGCCACAC	ACAGGTTTAC	420
	CTTTTCCCG	ATCTTTGGGC	CAGAAGTGGG	ACAGGCATCC	TTCTTCAACC	TAAGTGTGAA	480
	GGAGATGGTA	AAGGATGTAC	TCAAAGGGCA	GAATGGGCTC	ATCTATACAT	ATGGAGTCAC	540
35	TAACTCAGGG	AAAACCCACA	CGATTCAAGG	TACCATCAAG	GATGGAGGGA	TTCTCCCCCG	600
	GTCCCTGGCG	CTGATCTTCA	ATAGCCTCCA	AGGCCAATCT	CATCCAACAC	CTGATCTGAA	660
	GCCTTGTCTC	TCCAATGAGG	TAATCTGGCT	AGACAGCAAG	CAGATCCGAC	AGGAGGAAAT	720
	GAAGAAGCTG	TCCCTGCTAT	ATGGAGGCCT	CCAAGAGGAG	GAGCTGTCCA	CTTCTTGAA	780
40	GAGGAGTGTC	TACATCGAAA	GTCGGATAGG	TACCAGCACC	AGCTTCGACA	GTGGCATTGC	840
	TGGGCTCTCT	TCTATCAGTC	AGTGTACCAG	CAGTAGCCAG	CTGGATGAAA	CAAGTCATCG	900
	ATGGGCACAG	CCAGACATCG	CCCCACTACC	TGTCCTGGCA	AACATTGCTC	TCTCCATCTG	960
	GATCTCATTC	TTTGAGATCT	ACAACGAATC	GCTTTATGAC	CTATTAGAAC	GCCTAGCCA	1020
	ACAGCGCAAG	AGGCAGACTT	TGCGGCTATG	CGAGGATCAA	AATGGCAATC	CCTATGTGAA	1080
	AGATCTCAAC	TGGATTCTAT	TGCAAGATGC	TGAGGAGGCG	TGGAAGCTCC	TAAAGTGGG	1140
45	TCGTAAGAAC	CAGAGCTTTG	CCAGCACCCA	CCTCAACCAG	AACTCCAGCC	GCAGTCACAG	1200
	CATCTTCTCA	ATCAGGATCC	TACACCTTCA	GGGGGAAGGA	GATATAGTCC	CCAAGATCAG	1260
	CGAGCTGTCA	CTCTGTGATC	TGGCTGGCTC	AGAGCGCTGC	AAAGATCAGA	AGAGTGGTGA	1320
	ACGGTTGAAG	GAAGCAGGAA	ACATTAACAC	CTCTCTACAC	ACCCTGGGCC	GCTGTATTGC	1380
	TGCCCTTCGT	CAAAACCCAG	AGAACCGGTC	AAAGCAGAAC	CTGGTTCCCT	TCCGTGACAG	1440
50	CAAGTTGACT	CGAGTGTTCC	AAGGTTTCTT	CACAGGCCGA	GGCCGTTCCT	GCATGATTGT	1500
	CAATGTGAAT	CCCTGTGCAT	CTACCTATGA	TGAAACTCTT	CATGTGGCCA	AGTTCTCAGC	1560
	CATTGTCTAGC	CAGGTGACTT	GTGCTATGCC	CACCTATGCA	ACTGGGATTC	CCATCCCTGC	1620
	ACTCGTTCAT	CAAGGAACAT	AGTCTTCAGG	TATCCCCCAG	CTTAGAGAAA	GGGGCTAAGG	1680
55	CAGACACAGG	CCTTGATGAT	GATATTGAAA	ATGAAGCTGA	CATCTCCATG	TATGGCAAAG	1740
	AGGAGCTCCT	ACAAGTTGTG	GAAGCCATGA	AGACACTGCT	TTTGAAGGAA	CGACAGGAAA	1800
	AGCTACAGCT	GGAGATGCAT	CTCCGAGATG	AAATTGTCAA	TGAGATGGTA	GAACAGATGC	1860
	AACAGCGGGA	ACAGTGGTGC	AGTGAACATT	TGGACACCCA	AAAGGAACCT	TTGGAGGAAA	1920
	TGTATGAAGA	AAAACATAAT	ATCCTCAAGG	AGTCACTGAC	AAGTTTTTAC	CAAGAAGAGA	1980
60	TTCAGGAGCG	GGATGAAGA	ATTGAAGAGC	TAGAAGCTCT	CTTGACAGAA	GCCAGACAAC	2040
	AGTCAGTGGC	CCATCAGCAA	TCAGGGTCTG	AATTGGCCCT	ACGGCGGTCA	CAAAGTTTGG	2100
	CAGCTTCTGC	CTCCACCCAG	CAGCTTCAGG	AGGTTAAAGC	TAAATTACAG	CAGTGCAAAG	2160
	CAGAGCTAAA	CTCTACCACT	GAAGAGTTGC	ATAAGTATCA	GAAATGTGTA	GAACCCACAC	2220
	CCTCAGCCAA	GCCCTTACAC	ATTGATGTGG	ACAAGAAGTT	AGAAGAGGGC	CAGAAGAATA	2280
	TAAGGCTGTT	GGCGACAGAG	CTTCAGAAAC	TTGGTGAGTC	TCTCCAATCA	GCAGAGAGAG	2340
65	CTTGTGCGCA	GCCTTTTGGC	GCAGGAAAC	TTCTGCAAGC	CTTGACCACT	TGTGATGACA	2400
	TCTTAATCAA	ACAGGACCAG	ACTCTGGCTG	AACTGCAGAA	CAACATGGTG	CTAGTGAAC	2460
	TGGACCTTCG	GAAGAAGGCA	GCATGTATTG	CTGAGCAGTA	TCATACTGTG	TTGAAACTCC	2520
	AAGGCCAGGT	TTCTGCCAAA	AAGCGCCTTG	GTACCAACCA	GGAAAATCAG	CAACCAACCC	2580
70	AACAACCACC	AGGGAAGAAA	CCATTCCCTC	GAAATTTACT	TCCCCGAACA	CCAACCTGCC	2640
	AAAGCTCAAC	AGACTGCAGC	CCTTATGCCC	GGATCCTACG	CTCACGGCGT	TCCCTTTTAC	2700
	TCAAATCTGG	GCCTTTTGGC	AAAAAGTACT	AAGGCTGTGG	GGAAAGAGAA	GAGCAGTCAT	2760
	GGCCCTGAGG	TGGGTCAGCT	ACTCTCCTGA	AGAAATAGGT	CTCTTTTATG	CTTTACCATA	2820
	TATCAGGAAT	TATATCCAGG	ATGCAATACT	CAGACACTAG	CTTTTCTCTC	ACTTTTGTAT	2880
75	TATAACCACC	TATGTAATCT	CATGTTGTTG	TTTTTTTTTA	TTTACTTATA	TGATTTCTAT	2940
	GCACACAAAA	ACAGTTATAT	TAAAGATATT	ATTGTTTACA	TTTTTTTATTG	AATTCCAAAT	3000
	GTAGCAAAAT	CATTAAAAA	AATTATAAAA	GGGACAGAAA	AA		

Seq ID NO: 26 Protein sequence:
Protein Accession #: Eos sequence

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80	MSQILSPPA	GLLSDDDVVV	SPMFESTAAD	LGSVVRKNLL	SDCSVVSTSL	EDKQVPSSE	60
	SMEKVKVYLR	VRPLLPSELE	RQEDQGCVR	ENVETLVLA	PKDSFALKSN	ERGIGQATHR	120
85	FTFSQIFGPE	VQASPFNL	VKEMVKDVLK	QGNWLIYTYG	VTNSGKTHTI	QGTIKDGGIL	180
	PRSLALIFNS	LQQLHPTPD	LKPLLSNEVI	WLDKQIRQE	EMKLSLNLG	GLQEELSTS	240
	LKRSVYIESR	IGTSTSFDSG	IAGLSSISQC	TSSSQLDETS	HRWAQPDTP	LPVPANIRFS	300

IWISFFEIYN ELLYDLLEPP SQQRKRQTLR LCEQNGNPNY VKDLNWIHVQ DAEAWKLLK 360
 VGRKNQSPAS THLNQNSRSR HSIFSIIRILH LQEGDIVPK ISELSLCDLA GSERCKDQKS 420
 GERLKEAGNI NTSLHTLGRC IAAALRQNNQ RSKQNLVFFR DSKLTRVFQ FFGTRGRSCM 480
 IVNVNFCAS YDETLHVAKF SAIASQVTCA CPTYATGIPI PALVHQGT

Seq ID NO: 27 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 13-1424

10 1 11 21 31 41 51
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 TAGAAGTTTA CAATGAAGTT TCTTCTAATA CTGCTCCTGC AGGCCACTGC TTCTGGAGCT 60
 CTTCCTCTGA ACAGCTCTAC AAGCCTGGAA AAAAATAATG TGCTATTGG TGAAGATAC 120
 15 TTAGAAAAAT TTTATGGCCT TGAGATAAAC AAACCTCCAG TGACAAAAAT GAAATATAGT 180
 GGAAACTTAA TGAAGGAAAA AATCCAAGAA ATGCAGCACT TCTTGGGTCT GAAAGTGACC 240
 GGGCAACTGG ACACATCTAC CCTGGAGATG ATGCACGCAC CTCGATGTGG AGTCCCGAT 300
 GTCCATCATT TCAGGGAATG GCCAGGGGGG CCCGTATGGA GGAACATTA TATCATCTAC 360
 AGAATCAATA ATTACACACC TGACATGAAC CGTGAGGATG TTGACTACGC AATCCGAAAA 420
 GCTTTCCAAG TATGGAGTAA TGTATACCCC TTGAAATTCA GCAAGATTAA CACAGGCATG 480
 20 GCTGACATTT TGGTGGTTT TGCCCGTGGG GCTCATGGAG ACTTCCATGC TTTTGATGGC 540
 AAAGTGGAA TCCTAGCCCA TGCTTTTGGG CCTGGATCTG GCATTGGAGG GGATGCACAT 600
 TTCGATGAGG ACGAATCTG GACTACACAT TCAGGAGGCA CAAACTTGTT CCTCACTGCT 660
 GTTACGAGA TTGGCCATT CTTAGGTCTT GGCCATTCTA GTGATCCAAA GGCCGTAATG 720
 25 TTCCCCACCT ACAATATGT TGACATCAAC ACATTTCGCC TCTCTGCTGA TGACATACGT 780
 GGCAATCAGT CCTGTATGAG AGACCCAAAA GAGAACCAAC GCTTGCCAAA TCCTGACAAT 840
 TCAGAACCA CTTCTGTGTA CCCCAATTG AGTTTGTATG CTGTCACTAC CGTGGGAAAT 900
 AAGATCTTTT TCTTCAAGA CAGGTTCTTC TGGCTGAAGG TTTCTGAGAG ACCAAAGACC 960
 AGTGTAAAT TAAATTTCTT CTTATGGCCA ACCTTGCCAT CTGGCATTGA AGCTGCTTAT 1020
 30 GAAATTGAAG CAGAGAAATCA AGTTTCTT TTTAAAGATG ACAAATCATG GTTAATTAGC 1080
 AATTTAAGAC CAGAGCCAAA TTATCCCAAG AGCATACATT CTTTGTGTTT TCCTAACTTT 1140
 GTGAAAAAAA TTGATGCAGC TGTTTTAAAC CCACGTTTTT ATAGGACCTA CTTCTTTGTA 1200
 GATAACCACT ATTGGAGGTA TGATGAAAGG AGACAGATGA TGGACCTGG TTATCCCAA 1260
 CTGATTACCA AGAATCTCCA AGGAATCGGG CCTAAAATTG ATGCAGTCTT CTACTCTAAA 1320
 AACAAATACT ACTATTTCTT CCAAGGATCT AACCAATTG AATATGACTT CTACTCTCAA 1380
 35 CGTATACCA AACACTGAA AAGCAATAGC TGGTTTGGTT GTTGAAAAATG GTGTAATTAA 1440
 TGGTTTGTGT TAGTTCACTT CAGCTTAATA AGTATTTATT GCATATTGTC TATGTCTCTA 1500
 GTGTACCACT ACTTAGAGAT ATGTATCATA AAAATAAAAT CTGTAAACCA TAGGTAATGA 1560
 TTATATAAAA TACATAATAT TTTTCAATTT TGAAAACTCT AATTGTCCAT TCTTGCTTGA 1620
 CTCTACTATT AAGTTTGAAA ATAGTTACCT TCAAAGCAAG ATAATTCTAT TTGAAGCATG 1680
 40 CTCTGTAAGT TGCTTCTTAA CATCCTTGGG CTGAGAAATT ATACTTACTT CTGGCATAAC 1740
 TAAATTAAG TATATATATT TTGGCTCAA TAAATTTG

Seq ID NO: 28 Protein sequence:
 Protein Accession #: Eos sequence

45 1 11 21 31 41 51
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 MKFLLILLQ ATASGALPLN SSTSLKNNV LFGERYLEKF YGLEINKLPV TKMKYSGNLM 60
 KEKIQEMQHF LGLKVTGQLD TSTLEMHAP RCGVPDVHFF REMPGGPVWR KHYITYRINN 120
 50 YTPDMNREDF VAIKRAFCV WSNVTPLKFS KINTGMADIL VVFARGAHGD FHFADGKGGI 180
 LAHAFPGSGS IGGDAHFDEE EFWTTHSGGT NLFLTAVHEI GHSLGLGHSS DPKAVMFPTY 240
 KYVDINTFRL SADDIRIGQS LYGDPKENQR LPNPDNSEPA LCDPNLSFDA VTTVGNKIFF 300
 KDRFFWLKV SERPKTSVNL ISSLWPTLPS GIEAAYEIEA RNQVFLFKDD KYWLISNLRP 360
 55 EPNYPKSIHS FGFPNFVKKI DAAVFNPRFY RTYFFVDNQY WRYDERRQMM DPGYPKLITK 420
 NFGGIGPKID AVFYSKNKY YFFQGSNQFE YDFLLQRITK TLKSNNSWFGC

Seq ID NO: 29 DNA sequence
 Nucleic Acid Accession #: NM_006115.1
 Coding sequence: 236..1765

60 1 11 21 31 41 51
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 GCTTCAGGGT ACAGCTCCCC CGCAGCCAGA AGCCGGGCTT GCAGCCCTC AGCACGCTC 60
 CGGGACACCC CACCCGCTTC CCAGGCGTGA CCTGTCAACA GCAACTTCGC GGTGTGGTGA 120
 65 ACTCTCTGAG GAAAAACFAT TTTGATTATT ACTCTCAGAC GTGCGTGGCA ACAAGTGACT 180
 GAGACCTAGA AATCCAAGCG TTGGAGGTCC TGAGGCCAGC CTAAGTCGCT TCAAAATGGA 240
 ACGAAGGCGT TTGTGGGGTT CCATTGAGAG CCGATACATC AGCATGAGTG TGTGGACAAG 300
 CCCACGGAGA CTTGTGGAGC TGGCAGGGCA GAGCCTGCTG AAGGATGAGG CCTGGCCAT 360
 70 TGCCGCCCTG GAGTTGCTGC CCAGGGAGCT CTTCCCGCCA CTCTTCATGG CAGCCTTTGA 420
 CGGGAGACAC AGCCAGACCC TGAAGGCAAT GGTGCAGGCC TGGCCCTTCA CTGCTCTCCC 480
 TCTGGGAGTG CTGATGAAGG GACAACTCT TCACCTGGAG ACCTTCAAAG CTGTGCTTGA 540
 TGGACTTGAT GTGCTCCTTG CCCAGGAGGT TCGCCCCAGG AGGTGGAAC TTCAAGTGCT 600
 GGATTACCGG AAGAACTCTC ATCAGGACTT CTGGACTGTA TGGTCTGGAA ACAGGGCCAG 660
 75 TCTGTACTCA TTTCCAGAGC CAGAAGCAGC TCAGCCCATG ACAAAGAAGC GAAAAGTAGA 720
 TGGTTTGAGC ACAGAGGCAG AGCAGCCCTT CATTCAGTA GAGGTGCTCG TAGACCTGTT 780
 CCTCAAGGAA GGTGCTGTG ATGAATTGTT CTCCTACCTC ATTGAGAAAG TGAAGCGAAA 840
 GAAAAATGTA CTACGCTGTG GCTGTAAGAA GCTGAAGATT TTTGCAATGC CCATGCAGGA 900
 TATCAAGATG ATCCTGAAAA TGGTGCAGCT GGAATCTATT GAAGATTGG AAGTGACTTG 960
 TACCTGGAAG CTACCCACTT TGGCGAAATT TTCTCCTTAC CTGGGCCAGA TGATTAATCT 1020
 80 GCGTAGACTC CTCCTCTCCC ACATCCATGC ATCTTCTTAC ATTTCCCCCG AGAAGGAAGA 1080
 GCAGTATATC GCCCAGTTCA CCTCTCAGTT CCTCAGTCTG CAGTGCCTGC AGGCTCTCTA 1140
 TTGGGACTCT TTAATTTTCC TTAGAGGCCG CCTGGATCAG TTGCTCAGGC ACGTGAATGA 1200
 CCCCTTGGAA ACCCTCTCAA TAACATACTG CCGGCTTTCG GAAGGGGATG TGATGCATCT 1260
 85 GTCCAGAGT CCCAGCGTCA GTCAGCTAAG TGTCTGAGT CTAAGTGGGG TCATGCTGAC 1320
 CGATGTAAGT CCGAGGCCCT TCCAAGCTCT GCTGGAGAGA GCCTCTGCCA CCTCCAGGA 1380
 CCTGGTCTTT GATGAGTGTG GGATCACGGA TGATCAGCTC CTGCCCCTCC TGCCTTCCCT 1440
 GAGCCACTGC TCCCAGCTTA CAACCTTAAG CTTCTACGGG AATTCCATCT CCATATCTGC 1500

CTTGCAGAGT CTCTCGCAGC ACCTCATCGG GCTGAGCAAT CTGACCCACG TGCTGTATCC 1560
 TGTCCCCCTG GAGAGTTATG AGGACATCCA TGGTACCCCTC CACCTGGAGA GGCTTGCCTA 1620
 TCTGCATGCC AGGCTCAGGG AGTTGCTGTG TGAGTTGGGG CGGCCACGCA TGGTCTGGCT 1680
 TAGTGCCAAC CCTGTCTCTC ACTGTGGGGA CAGAACCTTC TATGACCCGG AGCCCATCCT 1740
 GTGCCCCGTG TTCATGCCTA ACTAGCTGGG TGCACATATC AAATGCTTCA TTCTGCATAC 1800
 TTGGACACTA AAGCCAGGAT GTGCATGCAT CTGTAAGCAA CAAAGCAGCC ACAGTTTCAG 1860
 ACAAAATGTT AGTGTGAGTG AGGAAAACAT GTTCAGTGAG GAAAAAACAT TCAGACAAAT 1920
 GTTCAGTGAG GAAAAAAGG GGAAGTTGGG GATAGGCAGA TGTGACTTGA AGGAGTTAAT 1980
 GTGATCTTTG GGGAGATACA TCTTATAGAG TTAGAAATAG AATCTGAATT TCTAAAGGGA 2040
 GATTCTGGCT TGGGAAGTAC ATGTAGGAGT TAATCCCTGT GTAGACTGTT GTAAAGAAAC 2100
 TGTTGAAAT AAGAGAGAGC AATGTGAAGC AAAAAAAAAA AAAAAAAAAA

Seq ID NO: 30 Protein sequence:
 Protein Accession #: NP_006106.1

1 11 21 31 41 51
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 GCTTCAGGGT ACAGCTCCCC CGCAGCCAGA AGCCGGGCGT GCAGCGCCTC AGCACCCTC 60
 CGGGACACCC CACCCGCTTC CCAGGCGTGA CCTGTCAACA GCAACTTCGC GGTGTGGTGA 120
 ACTCTCTGAG GAAAAACCAT TTTGATTATT ACTCTCAGAC GTGCGTGGCA ACAAGTGAAT 180
 GAGACCTAGA AATCCAAGCG TTGGAGGTCC TGAGGCCAGC CTAAGTCTCG TCAAAATGGA 240
 ACGAAGGCGT TTGTGGGGTT CCATTGAGAG CCGATACATC AGCATGAGTG TGTGGACAAG 300
 CCCACGGAGA CTTGTGGAGC TGGCAGGGCA GAGCCTGCTG AAGGATGAGG CCCTGGCCAT 360
 TGCCGCGCTG GAGTTGTGTC CCAGGGAGCT CTTCCCGCCA CTCTTCATGG CAGCCTTTGA 420
 CGGGAGACAC AGCCAGACCC TGAAGGCAAT GGTGACGGCC TGGCCCTTCA CCTGCCTCCC 480
 TCTGGGAGTG CTGATGAAGG GACAAACATCT TCACCTGGAG ACCTTCAAG CTGTGCTTGA 540
 TGGACTTGAT GTGCTCCTTG CCCAGGAGGT TCGCCCCAGG AGGTGGAAAC TTCAAGTGCT 600
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 TCTGTACTCA TTTCCAGAGC CAGAAGCAGC TCAGCCCATG ACAAAGAAGC GAAAAGTAGA 720
 TGGTTTGAGC ACAGAGGCAG AGCAGCCCTT CATTCCAGTA GAGGTGCTCG TAGACCTGTT 780
 CCTCAAGGAA GGTGCCTGTG ATGAATTGTT CTCCTACCTC ATTGAGAAAG TGAAGCGAAA 840
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 CGATTAAGT CCCGAGCCCC TCCAGGCTCT GCTGGAGAGA GCCTCTGCCA CCCTCCAGGA 1380
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 GAGCCACTGC TCCCAGCTTA CAACCTTAAG CTTCTACGGG AATTCCATCT CCATATCTGC 1500
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 TGTCCCCCTG GAGAGTTATG AGGACATCCA TGGTACCCCTC CACCTGGAGA GGCTTGCCTA 1620
 TCTGCATGCC AGGCTCAGGG AGTTGCTGTG TGAGTTGGGG CGGCCACGCA TGGTCTGGCT 1680
 TAGTGCCAAC CCTGTCTCTC ACTGTGGGGA CAGAACCTTC TATGACCCGG AGCCCATCCT 1740
 GTGCCCTGTG TTCTGCTCTA CTAGCTGGG TGACATATC AAATGCTTCA TTCTGCATAC 1800
 TTGGACACTA AAGCCAGGAT GTGCATGCAT CTTGAAGCAA CAAAGCAGCC ACAGTTTCAG 1860
 ACAAAATGTT AGTGTGAGTG AGGAAAACAT GTTCAGTGAG GAAAAAACAT TCAGACAAAT 1920
 GTTCAGTGAG GAAAAAAGG GGAAGTTGGG GATAGGCAGA TGTGACTTGA AGGAGTTAAT 1980
 GTGATCTTTG GGGAGATACA TCTTATAGAG TTAGAAATAG AATCTGAATT TCTAAAGGGA 2040
 GATTCTGGCT TGGGAAGTAC ATGTAGGAGT TAATCCCTGT GTAGACTGTT GTAAAGAAAC 2100
 TGTTGAAAT AAGAGAGAGC AATGTGAAGC AAAAAAAAAA AAAAAAAAAA

Seq ID NO: 31 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 64-2754

1 11 21 31 41 51
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 CCGATGGCCG CCGCTGGGCC CCGGCGCTCC GTGCGCGGAG CCGTCTGCCT GCATCTGCTG 120
 CTGACCCCTG TGATCTTCAG TCGTGATGGT GAAGCCTGCA AAAAGGTGAT ACTTAATGTA 180
 CCTTCTAAAC TAGAGGCAGA CAAAATAATT GGCAGAGTTA ATTTGGAAGA GTGCTTCAGG 240
 TCTGCAGACC TCATCCGGTC AAGTGATCCT GATTTCAGAG TTCTAAATGA TGGGTCAGTG 300
 TACACAGCCA GGGCTGTGTC GCTGTCTGAT AAGAAAAGAT CATTACCCTT ATGGCTTTCT 360
 GACAAAAGGA AACAGACACA GAAAGAGGTT ACTGTGCTGC TAGAACATCA GAAGAAGGTA 420
 TCGAAGACAA GACACACTAG AGAAACTGTT CTCAGGCGTG CCAAGAGGAG ATGGGCACCT 480
 ATTCCTTGCT CATGTGCAAG GAATTCCTTG GGCCTTTTCC CATTGTTTCT TCAACAAGTT 540
 GAATCTGATG CAGCAGAGAA CTATCTGTC TTTACTCAA TAAGTGAGC TGGAGTTGAT 600
 AAAGAACCTT TAAATTTGTT TTATATAGAA AGAGACACTG GAAATCTATT TTGCACTCGG 660
 CCTGTGGATC GTGAAGAATA TGATGTTTTT GATTGATTG CTTATGCTC AACTGCAGAT 720
 GGATATTCAG CAGATCTGCC CCTCCACTA CCTCATAGG TAGAGGATGA AAATGACAAC 780
 CACCTCTGTT TCACAGAAGC AATTTATAAT TTTGAAGTTT TGGAAAGTAG TAGACCTGGT 840
 ACTACAGTGG GGGTGGTTTG TGCCACAGAC AGAGATGAAC CGGACACAAT GCATACGCGC 900
 CTGAAATACA GCAATTTGCA GCAGACACCA AGGTCACTGT GGCTCTTTTC TGTGCATCCC 960
 AGCACAGGCG TAATCACCAC AGTCTCTCAT TATTTGGACA GAGAGTTGTT AGACAAGTAC 1020
 TCATTGATAA TGAAAGTACA AGACATGGAT GGCAGTTTTT TTGATTGAT AGGCACATCA 1080
 ACTTGATACA TAACAGTAAC AGATTCAAAT GATAATGCAC CCACTTTCAG ACAAATGCT 1140
 TATGAAGCAT TTGTAGAGGA AAATGCATTC AATGTGGAAT TCTTACGAAT ACCTATAGAA 1200
 GATAAGGATT TAATTAAACAC TGCCAAATGG AGAGTCAATT TTACCAATTT AAAGGGAAAT 1260
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 GTAAAGCCAC TGAATTATGA AGAAAACCGT CAAGTGAACC TGGAAATTGG AGTAAACAAT 1380
 GAAGCGCCAT TTGCTAGAGA TATTTCCAGA GTGACAGCCT TGAACAGAGC CTTGGTTACA 1440
 GTTCATGTGA GGGATCTGGA TTAGGGGCGCT GAATGCACTC CTCAGGCCCA ATATGTGCGG 1500
 ATTAAGAAA ACTTAGCAGT GGGGTCAAAG ATCAACGGCT ATAAGGCATA TGACCCCGAA 1560

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	ATTGATGAAA	TTTCAGGGTC	AATCATAACT	TCCAAAATCC	TGGATAGGGA	GGTTGAAACT	1680
	CCCAAAATG	AGTTGTATAA	TATTACAGTC	CTGGCAATAG	ACAAAGATGA	TAGATCATGT	1740
5	ACTGGAACAC	TTGCTGTGAA	CATTGAAGAT	GTAAATGATA	ATCCACCAGA	AATACTTCAA	1800
	GAATATGTAG	TCATTTGCAA	ACCAAAAATG	GGGTATACCG	ACATTTTAGC	TGTTGATCCT	1860
	GATGAACCTG	TCCATGGAGC	TCCATTTTAT	TTCACTTTGC	CCAATACTTC	TCCAGAAATC	1920
	AGTAGACTGT	GGAGCCTCAC	CAAAGTTAAT	GATACAGCTG	CCCGTCTTTC	ATATCAGAAA	1980
	AATGCTGGAT	TTCAAGAATA	TACCATTCTC	ATTACTGTAA	AAGACAGGGC	CGGCCAAGCT	2040
10	GCAACAAAAT	TATTTAGAGT	TAATCTGTGT	GAATGTACTC	ATCCAACTCA	GTGTCTGTGG	2100
	ACTTCAAGGA	GTACAGGAGT	AATACTTGGG	AAATGGGCAA	TCCTTGCAAT	ATTACTGGGT	2160
	ATAGCACTGC	TCTTTCTCTG	ATTGCTAACT	TTAGTATGTG	GAGTTTTTGG	TGCAACTAAA	2220
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	CCTGGAGACG	ATAGAGTGTG	CTCTGCCAAT	GGATTTATGA	CCCAAACTAC	CAACAACCTCT	2340
15	AGCCCAAGTT	TTTGTGGTAC	TATGGGATCA	GAATGAAAA	ATGGAGGGCA	GGAAACCAT	2400
	GAAATGATGA	AAGGAGGAAA	CCAGACCTTG	GAATCCTGCC	GGGGGGCTGG	GCATCATCAT	2460
	ACCCTGAGCT	CCTGCAGGGG	AGGACACACG	GAGGTGGACA	ACTGCAGATA	CACCTACTCG	2520
	GAGTGGCACA	TTTCTTACTC	ACCCCGTCTC	GGTGAAAAAT	TGCATCGATG	TAATCAGAA	2580
	GAAGACCGCA	TGCCATCCCA	AGATTATGTC	CTCACTTATA	ACTATGAGGG	AAGAGGATCT	2640
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	CCAAATTTATA	TTTTTAAAGC	CAGTTGTTGC	TTATCTTTTC	CAAAAAGTGA	AAAAATGTTAA	2940
25	AACAGACAAC	TGGTAAATCT	CAAACTCCAG	CACCTGGAAT	AAGGTCTCTA	AAGCATCTGC	3000
	TCTTTTTTTT	TTTTACGGAT	ATTTTAGTAA	TAAATATGCT	GGATAAATAT	TAGTCCAACA	3060
	ATAGCTAAGT	TATGCTAATA	TACATTATT	ATGTATTAC	TTTAAGTGAT	AGTTTAAAAA	3120
	ATAAACAAGA	AATATTGAGT	ATCACTATGT	GAAGAAAGTT	TTGGAAAAGA	AACAATGAAG	3180
	ACTGAATTA	ATTAATAATG	TTGCAGCTCA	TAAAGAATTG	GGACTCACCC	CTACTGCACT	3240
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	GTAAATAAAT	TAACTTTTTC	TGGTTTCTGT	GGGAAGGAAA	TAGGGAATCC	AATGGAACAG	3600
35	TAGCTTTGCT	TTTGCAGCTG	TTTCAAGATT	TCTGCATCCA	CAAGTTAGTA	GCAAACTGGG	3660
	GAATACTGCG	TGCAGCTGGG	GTTCCCTGCT	TTTTGGTAGC	AAGGGTCCAG	AGATGAGGTG	3720
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	CTGAATCAAG	GAAGGCCAGG	CCTTGTGGGC	CCCCTTCTTT	CGGCTTCTG	CTAAAGCAAC	4080
	ACCTCCAGCA	GAGATTCCCT	TAAGTGACTC	CAGGTTTCTC	ACCATCCTTC	AGCGTGAATT	4140
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	AAGCAGCCCA	AGTAGGTTAT	TTGTACAGTC	AGAGGGCAAC	AGGAAGATGC	AGGCCCTCAA	4320
	GGGCAAGGAG	AGGCCCAAG	GAATATGGGT	GGGAGTAAAA	GCAACATCGT	CTGCTTCATA	4380
	CTTTTTCTTA	GGCTTGGCAC	TGCCCTTTCC	TTTCTCAGGC	CAATGGCAAC	TGCCATTGTA	4440
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	CCCCCCCCCT	TTTTTTTTTG	AGACGGAGTC	TCGCTCTGAC	GCACAGGCTG	GAGTGCAGTG	4800
55	GCTCCGATCT	CTGCTCACTG	AAAGCTCCGC	CTCCCGGGTT	CATGCCATTTC	TCCTGCCTCA	4860
	GCCTCCTGAG	TAGCTGGGAC	TACAGGCGCC	CACCACCAAG	CCCGGCTAAT	TTTTTGTATT	4920
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	ATCCGCGCTG	CTCGGCTTCC	CAAGAGTCTG	GGATTACAGG	CATGACCCAC	CGCTCCCGGC	5040
	CTTGTTTTCC	GTTTAAAGTC	GTCTTCTTTT	AATGTAATCA	TTTTGAACAT	GTGTGAAAGT	5100
60	TGATCATACG	AATTTGGATCA	ATCTTGAAT	ACTCAACCAA	AAGACAGTCG	AGAAGCCAGG	5160
	GGGAGAAAAG	ACTCAGGGCA	CAAAATATTG	GTCTGAGAAT	GGAATTTCTC	GTAAGCCTAG	5220
	TTGCTGAAAT	TTCTGCTGTG	AACCCAGAGC	CAGTTTTATC	TAACGGCTAC	TGAACACCCC	5280
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	CTAGTGCCGA	TAACTTTTCT	CAAGAGCAAA	CCAGTATCAC	TTCCCTGTTT	ATAAAACCTC	5400
65	TAACCATCTG	TTTTGTCTTT	GAACATGCTG	AAAACCACTT	GGTCTGCATG	TATGCCCGAA	5460
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	CATATGTAGT	ATTATTTATT	CCTTATATGT	GTAAGGTGAA	ATTTATGGTA	TTTGAGTGTG	5580
	CAAGAAAATA	TATTTTAAAG	GCTTTCATTT	TTCCCCCACT	GAATGATTTA	GAATTTTATA	5640
	TGTAATATATA	CAGAATGTTT	TTTCTTACTT	TTATAAGGAA	GCAGCTGTCT	AAAAATGCAGT	5700
70	GGGGTTTGT	TTGCAATGTT	TTAAACAGAG	TTTTAGTATT	GCTATTAAAA	GAAATTAATT	5760
	TGCTTTTAAA	GAAACTTGGC	TGCTTAAAT	AAGCAAAAAT	TGGATGCATA	AAGTAATATT	5820
	TACAGATGTG	GGGAGATGTA	ATAAAACAAT	ATTAACCTGG	TTTCTTGT	TTGCTGTATT	5880
	TAGAGATTAA	ATAATTTCTA	GATGATCACT	TTGCAAAATT	ATGCTTATGG	CTGGCATGGA	5940
	AATAGAAAATA	CTCAATTTATG	TCTTTTGTGT	ATTAATGGGG	AATATTTTGG	ACAATGTTTC	6000
75	ATTATCAAA	TGTCGACATC	ATTAATATAT	ATTGTAATGT	TGGGAAGAGA	TCATATTTT	6060
	GAAGCACAGC	TTTACAGATG	AGTATCTATG	ATACATATGT	ATAATAAATT	TTGATCGGGT	6120
	ATTAAGGATA	TAGAAAGGTG	GTTATAATTG	CAGAGTATTC	CATGAATAGT	ACACTGCAC	6180
	AGGGGTTTTA	CTTTGAGGAC	CAGTGTAGTC	AAGGGAAAAC	ATGAGTTAAA	AAGAAAAGCA	6240
80	GGCAATATTG	CAGTCTTGAT	TCTGCCACTT	ACAGGATAGA	TAATGCCTGA	ACTTTAATGA	6300
	CAAGATGATC	CAACCATAAA	GGTGCTCTGT	GCTTCAAGT	GAATCTTTTC	CCCATGCAGG	6360
	AGTGTGCTCC	CCTACAAACG	TTAAGACTGA	TCATTTCAAA	AATCTATTAG	CTATATCAAA	6420
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	CATTATTTT	TGTATGTCT	TCATGAATGT	TCATTTGATT	TTTGTGTTGA	ATAGTAAAT	6540
	ACCGGATACA	TTTCACGTGT	CCTTCAGTAT	TGATTTGGTT	GAATATTTGG	TCATAATGGT	6600
85	TGAGAAGCAT	GGACACTAGA	GCCAGAATGC	TTGGATATGA	ATCCTGGATC	TGTCACCTAC	6660
	TTCTGTGTGA	CCCTTGTAAAG	GCTACTTATT	TCCTCTCTTA	GCTTTCTCAT	TAAATCAAT	6720
	GAACAAATGCC	AGCCTCATGG	GGTTGTTGAA	TGATTAATTA	AGTTAATATA	CCTAAAGTAC	6780

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Seq ID NO: 32 Protein sequence:
Protein Accession #: NP_001932.1

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KTRHRTRETVL	RRAKRRWAPI	PCSMQENSIG	PFPLFLQQVE	SDAAQNYTVF	YSISGRGVDK	180
EPLNLFYIER	DTGNLFCTRP	VDREEDVDFD	LIAYASTADG	YSADLPLPLP	IRVEDENDNH	240
PVFTEAIYNF	EVLESSRPGT	TVGVVVCATDR	DEPDTMHTRL	KYSILQQTFR	SPGLFSVHPS	300
TGVITTVSHY	LDRREVVDKYS	LIMKVQDMDG	QFFGLIGTST	CIITVTDSND	NAPTFRQNAV	360
EAFVEENAFN	VEILRIPIED	KDLINTANWR	VNFTILKGNE	NGHFKISTDK	ETNEGVLSVV	420
KPLNVEENRQ	VNLEIGVNE	APFARDIPRV	TALNRALVTV	HVRDLDEGPE	CTPAAQYVRI	480
KENLAVGSKI	NGYKAYDPEN	RNGNGLRYKK	LHDPKGWITI	DEISGSIITS	KILDREVETP	540
KNELYNITVL	ALDKDRDST	GTLAVNIEDV	NDNPPEILQE	YVVICKPKMG	YTDILAVDPD	600
EPVHGAPPYF	SIDPTSPBIS	RLWSLTQVND	TAARLSYQKN	AGFQEYTIPI	TVKDRAGQAA	660
TKLLRVNLCE	CTHPTQCRAT	SRSTGVILGK	WAILAILLGI	ALLFSVLLTL	VCGVFGATKG	720
KRFPEDLAQQ	NLIISNTEAP	GDDRVCSANG	FMTQTNNSS	QGFCGTMSGG	MKNGGQETIE	780
MMKGGNQMLE	SCRAGHHHT	LDSCRGGHTE	VDNCRYTYSE	WHSFTQPRLG	EKLHRCNQNE	840
DRMPSQDYVL	TYNVEGRGSP	AGSVGCCSEK	QEEDGLDFLN	NLEPKFITLA	EACTKR	

Seq ID NO: 33 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 64-2583

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 TCATTATCAA ATTGTCGACA TCATTAATAT ATATTGTAAT GTTGGGAAGA GATCACTATT 6180
 50 TTGAAGCACA GCTTTACAGA TGAGTATCTA TGATACATAT GTATAATAAA TTTTGATCGG 6240
 GTATTAAAG TTTATAAGGA TGGTTATAAT TGCAGAGTAT TCCATGAATA GTACACTGAC 6300
 ACAGGGGTTT TACTTTGAGG ACCAGTGTAG TCAAGGAAA ACATGAGTTA AAAAGAAAAG 6360
 CAGGCAATAT TGCAGCTTG ATTCTGCCAC TTACAGGATA GATAATGCCT GAACCTTAAT 6420
 GACAAGATGA TCCAACCTA AAGGTGCTCT GTGCTTACA GTGAATCTTT TCCCATGCA 6480
 55 GGAGTGTGCT CCCCTACAAA CGTTAAGACT GATCATTTCA AAAATCTATT AGCTATATCA 6540
 AAAGCCTTAC ATTTTAAAT AGGTTGAACC AAAATTTCAA TTCCAGTAAC TTCTATTGTA 6600
 ACCATTATT TTTGTATGTT CTTCAGAAAT GTTCATTGGA TTTTGTGTTG TAATAGTAAA 6660
 ATACCGGATA CATTTACGT GTCTTTCAGT ATTTGATTGG TTGAATATTG GGTGATAATG 6720
 GTTGAGAAGC ATGAGACATA GAGGCAGAAAT GCTTGGATAT GAATCCTGGA TCTGTCACTT 6780
 60 ACTTCTGTGT GACCTTTGAA AGGCTACTTA TTTCTCTCT TAGCTTCTC ATTAATAATCA 6840
 ATGAACAATG CCAGCTCAT GGGGTTGTTG AATGATTTAA TTAGTTAATA TACCTAAAGT 6900
 ACATAGAACA CTGCTGCAC ATAGTAAAG AATTATAAGT GTGAGGTAGT TGGTAAATTT 6960
 ATGTAGTTGG ATATACTACC GAACAAATATC TAATCTCTTT TTAGGGAAAT AAGTTTGTG 7020
 CATATATATA ATCCGAAAC ATG

Seq ID NO: 34 Protein sequence:
 Protein Accession #: NP_07741.1

1	11	21	31	41	51	
MAAAGPRRSV	RGAVCLHLLL	TLVIFSRDGE	ACKKVILNVP	SKLEADKIIG	RVNLEECFRS	60
ADLIRSSDPD	FRVLNDGSVY	TARAVALSDK	KRSFTINLSD	KRKQTKQKEV	VLLHQQKQVS	120
KTRHRTRETVL	RRAKRRWAPI	PCSMQENSLG	PFPLFLQQVE	SDAAQNYTVF	YSISGRGVDK	180
EPLNLFYIER	DTGNLFCTRP	VDREYDVDF	LIAYASTADG	YSADLPLPLP	IRVEDENDNH	240
PVFTEAIYNF	EVLESSRPGT	TVGVVCATDR	DEPDTMHTRL	KYSILQOTPR	SPGLFSVHPS	300
TGVITTVSHY	LDREVVDKYS	LIMKVQMDMG	QFFGLIGTST	CIITVDSND	NAPTFRQNAY	360
EAPVEENAFN	VEILRIPIED	KDLINTANWR	VNFITLKGNE	NGHFKISTDK	ETNEGVLVSV	420
KPLNVEENRQ	VNLBEIGVNE	APFARDIPRV	TALNRALVTV	HVRDLDEGPE	CTPAAQYVRI	480
KENLAVGSKI	NGYKAYDPEN	RNGNGLRYKK	LHDPKGWITI	DEISGSIITS	KILDREVETP	540
KNELYNITVL	AIDKDRSCT	GTLAVNIEDV	NDNPPEILQE	YVVICPKPMG	YTDILAVDPD	600
BPVHGAPPFY	SLPNTSPBIS	RLWSLTKVND	TAARLSYQKN	AGFQEYTIPI	TVKDRAGQAA	660
TKLLRVNLCE	CTHPTQCRAT	SRSTGVILGK	WAILAILLGI	ALLFSVLLTL	VCGVFGATKG	720
KRFPPEDLAQ	NLIISNTBAP	GDDRVCSANG	FMTQTTNNSS	QGFCTGMSG	MKNGGQETIE	780
MMKGGNQTL	SCRGAGHHT	LDSCRGGHTE	VDNCRYTYS	WHSFTQPRLG	EESIRGHTG	

Seq ID NO: 35 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 146-1273.

	1	11	21	31	41	51	
5	GGGAGTGGGC	GTGGCGGTGC	TGCCCAGGTG	AGCCACCGCT	GCTTCTGCCC	AGACACGGTC	60
	GCCTCCACAT	CCAGGCTCTT	GTGCTCCTCG	CTTGCTCTGT	CCTTTTCCAC	GCAATTTTCA	120
	GGATAACTGT	GACTCCAGGC	CCGCAATGGA	TGCCCTGCAA	CTAGCAAAAT	CGGCTTTTGC	180
	CGTTGATCTG	TTCAAAACAAC	TATGTGAAAA	GGAGCCACTG	GGCAATGTCC	TCTTCTCTCC	240
	AATCTGTCTC	TCCACCTCTC	TGTCACCTTC	TCAAGTGGGT	GCTAAAGGTG	ACACTGCAAA	300
10	TGAAATTTGA	CAGGTTCTTC	ATTTTGAAAA	TGTCAAAGAT	ATACCCCTTG	GATTTCAAAC	360
	AGTAACATCG	AGTGTAAACA	AACTTAGTTC	CTTTTACTCA	CTGAAACTAA	TCAAGCGGCT	420
	CTACGTAGAC	AAATCTCTGA	ATCTTTCTAC	AGAGTTCATC	AGCTCTACGA	AGAGACCTTA	480
	TGCAAAAGGAA	TTGGAAACTG	TTGACTTCAA	AGATAAATTG	GAAGAAACGA	AAGGTCAGAT	540
	CAACAACCTCA	ATTAAGGATC	TCACAGATGG	CCACTTTGAG	AACATTTTAG	CTGACAACAG	600
	TGTGAACGAC	CAGACCAAAA	TCCTTGTTGG	TAATGCTGCC	TACTTTGTTG	GCAAGTGGAT	660
15	GAAGAAATTT	CCTGAATCAG	AAACAAAAGA	ATGTCCTTTC	AGACTCAACA	AGACAGACAC	720
	CAAAACAGTG	CAGATGATGA	ACATGGAGGC	CACGTTCTGT	ATGGGAAACA	TTGACAGTAT	780
	CAATTGTAA	ATAAGTCTGA	TTCTTTTCA	AAATAAGCAT	CTCAGCATGT	TCATCCTACT	840
	ACCCAAGGAT	GTGGAGGATG	AGTCCACAGG	CTTGGAGAAG	ATTGAAAAAC	AACTCAACTC	900
	AGAGTCACTG	TCACAGTGGG	CTAATCCCAG	CACCATGGCC	AATGCCAAGG	TCAAACCTCT	960
20	CATTCCAAAA	TTAAAGTGTG	AAAAGATGAT	TGATCCCAAG	GCTTGTCTGG	AAAACTAGG	1020
	GCTGAAACAT	ATCTTCACTG	AAGACACATC	TGATTTCTCT	GGAATGTCTG	AGACCAAGGG	1080
	AGTGGCCCTA	TCAATGTGTA	TCCACAAAAG	GTGCTTAGAA	ATAACTGAAG	ATGGTGGGGA	1140
	TTCCATAGAG	GTGCCAGGAG	CACGGATCCT	GCAGCACCAAG	GATGAATTGA	ATGCTGACCA	1200
25	TCCCTTTTAT	TACATCATCA	GGCACAACAA	AACTCGAAAC	ATCATTTTCT	TTGGCAAAAT	1260
	CTGTTCTCCT	TAAAGTGGAT	AGCCCCATGT	AAGTCTCTCC	TGACTTTTCT	GTGGATGCGG	1320
	ATTTCTGTAA	ACTCTGCATC	CAGAGATTCA	TTTTCTAGAT	ACAATAAAT	GCTAATGTTG	1380
	CTGGATCAGG	AAGCCGCCAG	TACTTGTCTG	ATGTAGCCTT	CACACAGATA	GACCTTTTCT	1440
	TTTTTCCAA	TCTATCTTTT	GTTCCTTTT	TTCCCATAG	ACAATGACAT	ACGCTTTTAA	1500
30	TGAAAAGGAA	TCAAGTGTGA	GGAAAAATAT	TTATTCATTA	TTTGTCAAAT	TGTCGGGGT	1560
	AGTTGGCAGA	AATACAGTCT	TCCACAAAGA	AAATTCCTAT	AAGGAAGATT	TGGAAGCTCT	1620
	TCTTCCAGC	ACTATGCTTT	CCTTCTTTGG	GATAGAGAAT	GTTCAGAGCA	TCTCGCTTC	1680
	CCTGAAGAGC	TGAAGAAAGT	GTAGTGATCG	GGACCCACGA	AACTGCCCTG	GCTCCAGTGA	1740
	AACTTGGGCA	CATGCTCAGG	CTACTATAGG	TCCAGAAGTC	CTTATGTTAA	GCCCTGGCAG	1800
35	GCAGGTGTTT	ATTAATAATC	TGAATTTTGG	GGATTTTCAA	AAGATAATAT	TTTACATACA	1860
	CTGTATGTTA	TAGAACTTCA	TGGATCAGAT	CTGGGGCAGC	AACTTATAAA	TCAACACCTT	1920
	AATATGCTGC	AACAAAATGT	AGAATATTCA	GACAAAATGG	ATACATAAAG	ACTAAGTAGC	1980
	CCATAAGGGG	TCAAAATTTG	CTGCCAAATG	CGTATGCCAC	CAACTTACAA	AAACACTTCG	2040
	TTCCGAGAGC	TTTTTCAGATT	GTGGAATGTT	GGATAAGGAA	TTATAGACCT	CTAGTAGCTG	2100
40	AAATGCAAGA	CCCCAAGAGG	AAGTTCAGAT	CTTAATATAA	ATTCACTTTC	ATTTTGTGATA	2160
	GCTGTCCCAT	CTGTCTATGT	GGTTGGCACT	AGACTGGTGG	CAGGGGCTTC	TAGCTGACTC	2220
	GCACAGGAT	TCTCACAATA	GCCGATATCA	GAATTTGTGT	TGAAGGAACT	TGTCTCTTCA	2280
	TCTAATATGA	TAGCGGGAAA	AGGAGAGGAA	ACTACTGCCT	TTAGAAAATA	TAGTAAAGT	2340
	GATTAAAGTG	CTACCGTTAC	CTTGACACAT	AGTTTTTCAG	TCTATGGGTT	TAGTTACTTT	2400
45	AGATGGCAAG	CATGTAACCT	ATATTAATAG	TAATTTGTAA	AGTTGGGTGG	ATAAGCTATC	2460
	CCTGTGCGG	GTTTCATGGT	TACTTCTCTA	TAAAAAATAT	ATATTTACCA	AAAAATTTTG	2520
	TGACATTCTT	TCTCCCATCT	CTTCCTTGAC	ATGCATTGTA	AATAGGTTCT	TCTTGTCTCG	2580
	AGATTCAATA	TTGAATTTCT	CCTATGCTAT	TGACAATAAA	ATATTATTGA	ACTACC	

Seq ID NO: 36 Protein sequence:
Protein Accession #: NP_002630.1

	1	11	21	31	41	51	
55	MDALQLANSA	FAVDLPKQLC	EKEPLGNVLF	SPICLSTSL	LAQVGAKGDT	ANEIGQVLHF	60
	ENVKDIPIPGF	QTVTSDVNKL	SSPYSLKLIK	RLYVDKSLNL	STEFISSTKR	PYAKELETVD	120
	FKDKLEETKG	QINNSIKDLT	DGFENILAD	NSVNDQTKIL	VVNAAYFVKG	WMKKFPSEET	180
	KECPFRINKT	DTKPVQMMNM	EATFCMGNID	SINCKIIELP	FQNKHLSMFI	LLPKDVEDES	240
	TGLEKIEKQL	NSESLSQWTN	PSTMANAKVK	LSIPKFKVEK	MIDPKACLEN	LGLKHIFSED	300
60	TSDFSGMSET	KGVALSNVIH	KVLEITEEDG	GDSIEVFGAR	ILQHKDELNA	DHPFIYIIRH	360
	NKTRNIIFPG	KFCSP					

Seq ID NO: 37 DNA sequence
Nucleic Acid Accession #: NM_0168583
Coding sequence: 72-842

	1	11	21	31	41	51	
70	GGAGTGGGGG	AGAGAGAGGA	GACCAGGACA	GCTGCTGAGA	CCTCTAAGAA	GTCCAGATAC	60
	TAAGAGCAAA	GATGTTTCAA	ACTGGGGGCC	TCATTGTCTT	CTACGGGCTG	TTAGCCGAGA	120
	CCATGGCCCA	GTITGGAGGC	CTGCCCGTGC	CCCTGGACCA	GACCCCTGCC	TTGAATGTGA	180
	ATCCAGCCCT	GCCCTTGAGT	CCACACGGTC	TTGCAGGAAG	CTTGACAAAT	GCCCTCAGCA	240
	ATGGCCTGCT	GTCTGGGGGC	CTGTTGGGCA	TTCTGGAAAA	CCTTCCGCTC	CTGGACATCC	300
75	TGAAGCCTGG	AGGAGGTACT	TCTGGTGGCC	TCCTTGGGGG	ACTGCTTGGA	AAAGTGACGT	360
	CAGTGATTCC	TGGCCTGAAC	AACATCATTC	ACATAAAGGT	CACTGACCCC	CAGCTGCTGG	420
	AACTTGGCCT	TGTGCAGAGC	CCTGATGGCC	ACCGTCTCTA	TGTCAACATC	CCTCTCGGCA	480
	TAAAGCTCCA	AGTGAATACG	CCCTGGTTCG	GTGCAAGTCT	GTGAGGCTG	GCTGTGAAGC	540
	TGGACATCAC	TGCAGAAATC	TTAGCTGTGA	GAGATAAGCA	GGAGAGGATC	CACCTGGTCC	600
80	TTGGTGACTG	CACCCATTCC	CCTGGAAGCC	TGCAAAATTC	TCTGCTTGAT	GGACTTGGCC	660
	CCCTCCCAT	TCAAGGTCTT	CTGGACAGCC	TCACAGGGAT	CTTGAATAAA	GTCCGCTGCT	720
	AGTTGGTTCA	GGGCAACGTG	TGCCCTCTGG	TCAATGAGGT	TCTCAGAGGC	TTGGACATCA	780
	CCCTGGTGCA	TGACATTGTT	AACATGCTGA	TCCACGGACT	ACAGTTTGTG	ATCAAGGTCT	840
	AAGCCTTCCA	GGAAGGGGCT	GGCCTCTGCT	GAGCTGCTTC	CCAAGTCTCA	CAGATGGCTG	900
85	GCCCATGTGC	TGGAAGATGA	CACAGTTGCC	TTCTCTCCGA	GGAACCTGCC	CCCTCTCCTT	960
	TCCCACCAGG	CGTGTGTAAC	ATCCCATGTG	CCTCACCTAA	TAAATGGCT	CTTCTTCTGC	1020
	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA				

Seq ID NO: 38 Protein sequence:
Protein Accession #: NP_057667

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5      1      11      21      31      41      51
      |      |      |      |      |      |
      MFQTGGGLIVF YGLLAQTMQAQ FGGLFVPLDQ TLPLNVNPAI PLSPTGLAGS LTNALSNGLL 60
      SGGLLGILEN LPLLDILKPG GGTSGGLLGG LLGKVTSVIP GLNNIIDIIV TDPQLLELGL 120
      VQSPDGHRLY VTPLPLGKLQ VNTPLVGASL LRLAVKLDIT AEILAVRDKQ ERIHLVLGDC 180
10     THSPGSLQIS LLDGLGLPLI QGLLDSLTI LNKVLPVLVQ GNVCPVNEV LRGLDITLVH 240
      DIVNMLIHGL QFVIKV

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Seq ID NO: 39 DNA sequence
Nucleic Acid Accession #: NM_004363.1
Coding sequence: 115-2223

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15     1      11      21      31      41      51
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      CTCAGGGCAG AGGGAGGAAG GACAGCAGAC CAGACAGTCA CAGCAGCCTT GACAAAACGT 60
20     TCCTGGAACCT CAAGCTCTTC TCCACAGAGG AGGACAGAGC AGACAGCAGA GACCATGGAG 120
      TCTCCCTCGG CCCCTCCCA CAGATGTGTC ATCCCCCTGGC AGAGGCTCCT GCTCACAGCC 180
      TCACCTCTAA CCTTCTGGAA CCCGCCACCC ACTGCCAAGC TCACTATTGA ATCCACGCCG 240
      TTCAATGTCC CAGAGGGGAA GGAGGTGCTT CTACTTGTCC ACAATCTGCC CCAGCATCTT 300
25     TTTGGCTACA GCTGGTACAA AGGTGAAAGA GTGGATGGCA ACCGTCAAAT TATAGGATAT 360
      GTAATAGGAA CTCACCAAGC TACCCAGGG CCCGCATACA GTGGTCGAGA GATAATATAC 420
      CCCAATGCAT CCCTGCTGAT CCAAGAACATC ATCCAGAATG ACACAGGATT CTACACCCCTA 480
      CACGTCATAA AGTCAGATCT TGTGAATGAA GAAGCAACTG GCCAGTTCCG GGTATACCCG 540
      GAGCTGCCCA AGCCCTCCAT CTCCAGCAAC AACTCCAAAC CCGTGGAGGA CAAGGATGCT 600
      GTGGCCTTCA CCTGTGAACC TGAGACTCAG GACGCAACCT ACCTGTGGTG GGTAAACAAT 660
30     CAGAGCCTCC CGTTCAGTCC CAGGCTGCAG CTGTCCAATG GCAACAGGAC CCTCACTCTA 720
      TTCAATGTCA CAAGAAATGA CACAGCAAGC TACAAATGTG AAACCCAGAA CCCAGTGAGT 780
      GCCAGGCGCA GTGATTCAGT CATCTGAAT GTCCTCTATG GCCCGGATGC CCCCACCAT 840
      TCCCCTCTAA ACACATCTTA CAGATCAGGG GAAATCTGA ACCTCTCTCG CCACGCAGCC 900
      TCTAACCCAC CTCGACAGTA CTCTTGGTTT GTCAATGGGA CTTTCCAGCA ATCCACCCAA 960
35     GAGCTCTTTA TCCCAACAT CACTGTGAAT AATAGTGGAT CCTATACGTG CCAAGCCCAT 1020
      AACTCAGACA CTGGCCTCAA TAGGACCACA GTCACGACGA TCACAGTCTA TGCAGAGCCA 1080
      CCCAAACCCCT TCATCACCAG CAACAACCTCC AACCCCGTGG AGGATGAGGA TGCTGTAGCC 1140
      TTAACCTGTG AACCTGAGAA TCAGAACACA ACCTACCTGT GGTGGGTAAA TAATCAGAGC 1200
      CTCCCGGTCA GTCCAGGCT GCAGCTGTCC AATGACAACA GGACCCCTAC TCTACTCAGT 1260
40     GTCACAAGGA ATGATGTAGG ACCCTATGAG TGTGGAATCC AGAACGAATT AAGTGTGAC 1320
      CACAGCGACC GAGTGTAGAT GAATGCTCTC TATGGCCGAG ACGACCCAC CATTTCCTCC 1380
      TCATACACCT ATTACCGTCC AGGGGTGAAC CTCAGCCTCT CCTGCCATGC AGCCTCTAAC 1440
      CCACCTGCAC AGTATCTTGG GCTGATTGAT GGGAAACATCC AGCAACACAC ACAAGAGCTC 1500
      TTTATCTCCA AACTCACTGA GAAGAACAGC GGAATCTATA CTTGCCAGGC CAATAACTCA 1560
45     GCCAGTGGCC ACAGCAGGAC TACAGTCAAG ACAATCACAG TCTCTCGGGA GCTGCCCAAG 1620
      CCCTCCATCT CCAGCAACAA CTCCAAACCC GTGGAGGACA AGGATGCTGT GGCCTTCACC 1680
      TGTGAACCTG AGGTGAGTGA CACAACCTAC CTGTGGTGGG TAAATGGTCA GAGCCTCCCA 1740
      GTCAGTCCCA GGCTGCAGCT GTCCAATGGC AACAGGACCC TCACTCTATT CAATGTACA 1800
      AGAAATGAGC CAAGAGCCTA TGTATGTGGA ATCCAGAACT CAGTGAGTGC AAACCCGAGT 1860
50     GACCCAGTCA CCCTGATGGT CCTCTATGGG CCGACACCCC CCATCATTTT CCCCCAGAC 1920
      TCGTCTTACC TTTCCGGAGC GAACCTCAAC CTCTCCTGCC ACTCGGCTC TAAACCATCC 1980
      CCGCAGTATT CTGGCGTAT CAATGGGATA CCGCAGCAAC ACACACAAGT TCTCTTTATC 2040
      GCCAAATATA CGCCAAATAA TAACGGGACC TATGCCTGTT TTGTCTCTAA CTTGGCTACT 2100
      GGCCGCAATA ATTCCATAGT CAAGAGCATC ACAGTCTCTG CATCTGGAAC TTCTCCTGGT 2160
55     CTCTCAGCTG GGGCCACTGT CGGCATCATG ATTGGAGTGC TGTTTGGGGT TGCTCTGATA 2220
      TAGCAGCCTT GGTGTAGTGT CTTCAATTCA GGAAGACTGA CAGTTGTTTT GCTTCTCTCT 2280
      TAAAGCATTT GCAACAGCTA CAGTCTAAAA TTGCTTCTTT ACCAAGGATA TTTACAGAAA 2340
      AGACTCTGAC CAGAGATCGA GACCATCCTA GCCAACATCG TGAACCCCA TCTCTACTAA 2400
      AAATACAAAA ATGAGCTGGG CTTGTGGCG CGCACTGTGA GTCCCGGTTA TCGGGAGGCC 2460
60     TGAGGCAGGA GAATCGCTTG AACCCGGGAG GTGGAGATTG CAGTGAGCCC AGATCGCACC 2520
      ACTGCACTCC AGTCTGGCAA CAGAGCAGAA CTCCTACTCA AAAAGAAAAG AAAAGAAGAC 2580
      TCTGACCTGT ACTCTTGAAT ACAAGTTTCT GATACCACTG CACTGTCTGA GAATTTCCAA 2640
      AACTTTAATG AACTAACTGA CAGCTTCATG AAAGTGTCCA CCAAGATCAA GCAGAGAAAA 2700
      TAATTAATTT CATGGGACTA AATGAACATA TGAGGATTGC TGATTCTTTA AATGTCTTGT 2760
65     TTCCAGATT TCAGGAAACT TTTTCTCTTT TAAGCTATCC ACTCTTACAG CAATTGATA 2820
      AAATATACCT TTGTGAACAA AAATTGAGAC ATTTACATTT TCTCCCTATG TGGTCGCTCC 2880
      AGACTTGGGA AACTATTTCAT GAATATTAT ATTGTATGGT AATATAGTTA TTGCACAAGT 2940
      TCAATAAAAA TCTGCTCTTT GTATAACAGA AAAA

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Seq ID NO: 40 Protein sequence:
Protein Accession #: NP_004354.1

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75     1      11      21      31      41      51
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      MESPSAPPHR WCIPWQRLLL TASLLTFWNP PTTAKLTIES TPFNVAEGKE VLLLHVNLPO 60
      HLFEGYSWYKG ERVDGNRII GYVIGTQQAT PGPAYSGREI IYPNASLLIQ NIIQNDTGFY 120
      TLHVIKSDLV NEATGQFRV YPELPKPSIS SNNKPVEDK DAVAFTEPE TQDATYLVWV 180
      NNQSLPVSPR LQLSNGNRTL TLFNVTRNDT ASYKCETQNP VSARRSDSVI LNVLYGPDAP 240
      TISPLNTSYR SGENLNLSCH AASNPQAQYS WFNVTGTFQS TQELFIPNIT VNNSGSYTCQ 300
80     AHSNDTGLNR TVTITIYVA EPPKPFITSN NSNPVEDEDA VALTCEPEIQ NTTYLWVWNN 360
      QSLPVSPRLQ LSNDNRTLTL LSVTRNDVGP YECGIQNELS VDHSDPVILN VLYGPDPTI 420
      SPSYTYRPG VNLSLSCHAA SNPPAQYSWL IDGNIQQHTQ ELFISNITEK NSGLYTCQAN 480
      NSAGHSRRTT VKTITVSAL PKPSISSNNS KPVEDKDAVA FTCEPEAQNT TYLWVWNGQS 540
      LPVSPRLQLS NGNRTLTLFN VTRNDARAYV CGIQNSVSAN RSDPVTLDVL YGPDTPIIISP 600
85     PDSSYLSGAN LNLSCHSASN PSPQYSWRIN GIPQHTQVL FIAKITPNNN GTYACFVSNL 660
      ATGRNNSIVK SITVSASGTS PGLSAGATVG IMIGVLVGVA LI

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Seq ID NO: 41 DNA sequence
Nucleic Acid Accession #: NM_006952.1
Coding sequence: 11-793

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20

1	11	21	31	41	51	
AATCCGACA	ATGGCGAAG	ACAACTCAAC	TGTTCTGTTGC	TTCCAGGGCC	TGCTGATTTT	60
TGGAATGTG	ATTATTGGTT	GTTCGGGCAT	TGCCCTGACT	GCGAGTGCA	TCTTCTTGT	120
ATCTGACCA	CACAGCCTCT	ACCACTGCT	TGAAGCCACC	GACAACGATG	ACATCTATGG	180
GGCTGCTGG	ATCGGCATAT	TTGTGGGCAT	CTGCCTCTTC	TGCTGTCTG	TTCTAGGCAT	240
TGTAGGCATC	ATGAAGTCCA	GCAGGAAAAT	TCTTCTGGCG	TATTTCAATC	TGATGTTTAT	300
AGTATATGCC	TTTGAAGTGG	CATCTTGAT	CACAGCAGCA	ACACAACGAG	ACTTTTTCAC	360
ACCCAACCTC	TTCTTGAAGC	AGATGCTAGA	GAGGTACCAA	AACAACAGCC	TTCCAAACAA	420
TGATGACCAG	TGGAAAAACA	ATGGAGTCAC	CAAAACCTGG	GACAGGCTCA	TGCTCCAGGA	480
CAATTGCTGT	GGCGTAAATG	GTCCATCAGA	CTGGCAAAAA	TACACATCTG	CCTTCCGGAC	540
TGGAATAAAT	GATGCTGACT	ATCCCTGGCC	TCGTCAATGC	TGTGTTATGA	ACAATCTTAA	600
AGAACCTCTC	AACCTGGAGG	CTTGTAAGT	AGGCGTGCTT	GGTTTTATC	ACAATCAGGG	660
CTGCTATGAA	CTGATCTCTG	GTCCAATGAA	CCGACAGGCC	TGGGGGGTTG	CCTGGTTTGG	720
ATTGCCATT	CTCTGCTGGA	CTTTTGGGT	TCTCTGGGT	ACCATGTTCT	ACTGAGCAG	780
AATTGAATAT	TAAGAA					

Seq ID NO: 42 Protein sequence:
Protein Accession #: NP_008883.1

25
30

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MAKDNSTVRC	FQGLLIFGNV	IIGCCGIALT	AECIFFVSDQ	HSLYPLEEAT	DNDIYGAAW	60
IGTFVGICLF	CLSVLGIIVI	MKSSRKILLA	YFILMFIVYA	FEVASCITAA	TQRDFFTPNL	120
FLKQMLERYQ	NNSPPNDDQ	WKNNGVTKTW	DRLMLQDNCC	GVNGPSDWQK	YTSAPRTENN	180
DADYFPWRQC	CVMNNLKEPL	NLEACKLGVP	GFYHNQGCYE	LISGPMNRHA	WGVANWFGPAI	240
LCWTFNVLG	TMFYWSRIEY					

Seq ID NO: 43 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 83-2605

35
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1	11	21	31	41	51	
GCCGGACAGA	TCTGCGCGTA	TCCTGGAGCC	GGCCCAAGTTG	TGAAGTAGGA	GAGCTTTGGG	60
ACCTCTGTCC	CAAGCAAGAG	AGATGAATGG	AGAGTATAGA	GGCAGAGGAT	TTGGACGAGG	120
AAGATTTCAA	AGCTGGAAAA	GGGGAAGAGG	TGGTGGGAAC	TTCTCAGGAA	AATGGAGAGA	180
AAGAGAACAC	AGACCTGATC	TGAGTAAAAC	CACAGGAAAA	CGTACTTCTG	AACAACCCCC	240
ACAGTTTTTG	CTTTCAACAA	AGACCCACAC	GTCAATGCAG	TCAACATTGG	ATCGATTTCAT	300
ACCATATAAA	GGCTGGAAGT	TTTATTTCTC	TGAAGTTTAC	AGCGATAGCT	CTCCTTTGAT	360
TGAGAAGATT	CAAGCATTTG	AAAAATTTT	CACAAGGCAT	ATTGATTTGT	ATGACAAGGA	420
TGAAATAGAA	AGAAAGGGAA	GTATTTTGGT	AGATTTTAAA	GAAGTGACAG	AAGGTGGTGA	480
AGTAACATA	TTGATACCA	ATATAGCAAC	TGAAGTAAAG	GATGCACCTG	AGAAAACCTT	540
GGCTTGATG	GGTTTGGCAA	TACATCAGGT	GTTAACTAAG	GACCTTGAAA	GGCATGCAGC	600
TGAGTTACAA	GCCCAGGAAG	GATTGTCTAA	TGATGGAGAA	ACAATGGTAA	ATGTGCCACA	660
TATTCATGCA	AGGGTGTACA	ACTATGAGCC	TTTGACACAG	CTCAAGAAATG	TCAGAGCAAA	720
TTACTATGGA	AAATCAATTC	CTCTAAGAGG	GACAGTGGTT	CGTGTCACTA	ATATAAGGCC	780
TCTTTGCACC	AAGATGGCTT	TTCTTTGTGC	TGCATGTGGA	GAAATTCAGA	GCTTTCTCT	840
TCAGATGGA	AAATACAGTC	TTCCACAAAA	GTGTCCTGTG	CCTGTGTGTC	GAGGCAGGTC	900
ATTTACTGCT	CTCCGAGCT	CTCCTCTCAC	AGTTACGATG	GACTGGCAGT	CAATCAAAAT	960
CCAGGAATTG	ATGCTGATG	ATCAGAGAGA	AGCAGGTCGG	ATTCCACGAA	CAATAGAAATG	1020
TGAGCTTGTT	CATGATCTTG	TGGATAGCTG	TGTCGCGGGA	GACACAGTGA	CTATTACTGG	1080
AATTGTCAAA	GTCTCAATGG	CGGAAGAAAG	TTCTCGAAAT	AAGAATGACA	AGTGATATGT	1140
CCTTTGTAT	ATTGAAGCAA	ATTCTATTAG	TAATAGCAAA	GGACAGAAAA	CAAAGAGTTC	1200
TGAGGATGGG	TGTAAGCATG	GAATGTTGAT	GGAGTTCTCA	CTTAAAGACC	TTTATGCCAT	1260
CCAAGAGATT	CAAGCTGTA	AAAACCTGTT	TAAACTCATT	GTCAACTCGC	TTTGCCCTGT	1320
CATTTTGGT	CATGAACCTG	TAAAGCAGG	TTTGGCATT	GCACTCTTTG	GAGGAAGCCA	1380
GAAATACGCA	GATGACAAAA	ACAGAAATCC	AAATCGGGGA	GACCCCAACA	TCCTTGTGT	1440
TGGAGATCCA	GGCCTAGGAA	AAAGTCAAAAT	GCTACAGGCA	GCGTGCAATG	TTGCCCAAG	1500
TGGCGTGTAT	GTTTGTGGTA	ACACCACGAC	CACCTCTGGT	CTGACGGTAA	CTCTTTCAAA	1560
AGATAGTCC	TCTGGAGATT	TTGCTTTGGA	AGCTGGTGCC	CTGGTACTTG	GTGATCAAGG	1620
TATTTGTGGA	ATCGATGAAT	TTGATAAGAT	GGGGAATCAA	CATCAAGCCT	TGTTGGAAGC	1680
CATGGAGCAG	CAAAGTATTA	GTCTTGCTAA	GGCTGGTGTG	GTTTGTAGCC	TTCTTGCAAG	1740
AACCTCCATT	ATTGCTGCTG	CAATCCAGT	TGGAGGACAT	TACAATAAAG	CCAAAACAGT	1800
TTCTGAGAAAT	TAAAAATGG	GGAGTGCACT	ACTATCCAGA	TTTGATTGG	TCTTTATCCT	1860
GTTAGATACT	CCAAATGAGC	ATCATGATCA	CTTACTCTCT	GAACATGTGA	TTGCAATAAG	1920
AGCTGGAAG	CAGAGAACCA	TTAGCAGTGC	CACAGTAGCT	CGTATGAATA	GTCAAGATTTC	1980
AAATACTTCC	GTACTTGAAG	TAGTTTCTGA	GAAGCCATTA	TCAGAAAGAC	TAAAGTGGT	2040
TCCTGGAGAA	ACAATAGATC	CCATTCCCA	CCAGCTATTG	AGAAAGTACA	TTGGCTATGC	2100
TGCGCAGTAT	GTGTACCCAA	GGCTATCCAC	AGAAGCTGCT	CGAGTTCTTC	AAGATTTTFA	2160
CCTTGAGCTC	GCGAAACAGA	GCCAGAGGTT	AAATAGCTCA	CCAATCACTA	CCAGGCAGCT	2220
GGAATCTTTG	ATTCGTCTGA	CAGAGGCACG	AGCAAGGTTG	GAATTGAGAG	AGGAAGCAAC	2280
CAAGAAGAC	GCTGAGGATA	TAGTGGAAAT	TATGAAATAT	AGCATGCTAG	GAATCTACTC	2340
TGATGAATTT	GGGAACCTAG	ATTTGAGCG	ATCCACGATC	GGTTCTGGAA	TGAGCAACAG	2400
GTCAACAGCG	AAAAGATTTA	TTTCTGCTCT	CAACAACGTT	GCTGAAAGAA	CTTATAATTA	2460
TATATTTCAA	TTTCATCAAC	TTGGGCAGAT	TGCCAAAGAA	CTAAACATTC	AGGTTGCTGA	2520
TTTTGAAAT	TTTATGGAT	CACATAATGA	CCAGGGTTAC	CTCTTGAAAA	AAGGCCCAAA	2580
AGTTTACCAG	CTTCAAACTA	TGTAAGAGGA	CTTCAACCAAG	TTAGGGCTTC	CTGGGTTTAT	2640
TGCAGATTAA	AGCCATCTCA	GTGAGATAT	GCGTGCACGC	ACAGACAGAC	AGACACACAC	2700
ACACACACAC	ACACACACAC	ACACACAGTC	AAATACTGTT	CTCTGAAAAA		2760
TGATGTCCTCA	AAAGTATTAT	AATAGGAAAA	AAGCATTAAA	TATAATAAAC	TAATTTAAGA	2820

AGTGATAAAG TCTCCAGATG CAGTAGCTCA CACTGTAACT ACAGTGACTC AGGAGGCTGA 2880
 GGTGAGAGGA TTCCTTGAGG CCAGGGTTCG AGACCAACCT TGGGCAACAT AGCAAGACCC 2940
 CATTCTCTAA AAAAAAAAAA AAAAAATTAA AACTTAGCTG GGTATGGTGG CACATGCTTA 3000
 TAGTCTCAGC TACTTGTGAG GCTGAGGCAG GAGGATTCTT TGAGCCCAGG AGTTTGAGGT 3060
 TACAGTGAGC CACAATCACA CCAATCCTG CACTCCAGCC TGGGCAATAA AGTAACTCTT 3120
 GACTCAAAAA AATAAAAAAA ATTGTAGTGG TAGCCATGTG TTAATTGTGA AATAAATTCT 3180
 CCAAGGGGCT AAAAGTAAAT TACTTATAAA TTTTATATAG TTGTATTTT GACCTGCTTT 3240
 TTATATGTAT GAATATTTC AATGTTTGA TAGTTTTCGA TATCAGATGT AGGCATACAG ACAAATACAT 3300
 AAACCAATGA ATATATTACA TATTCTGTGT TCCAATAAAA CTTTATTTAT GGACACTAAA 3360
 ATTTGAATTT CATAAAATTT TCCCATGTCA AGAATACAAA ATACTTGAGT TTTGTTTTTA 3420
 GCTATTTAAT AATAGGCTCTC ATTTATTCCA CAGGCTGTAG TTTGTAGTCT TGCTTGAAAC 3480
 AATAGAAACA GACTGATTAA GCAGGAGAAG TTTTGTGAAA GAATTTTGT TGGCTCACGG 3540
 AATTATTAGA AGGCAGGTGA ACCAGGAGGG TAAGCTTCCA GCAGCAATTT GTAAAAACCAT 3600
 GCCTTAGAAT TGGACTAAGG AAGAAGCTGC TGACACTCCA CTGCCACACA GGGCACTGGA 3660
 AGAAAGTGCT GCTGCCTCCC TGCCCCACCT TTGCCACTTC TGCAAGAGGA ATAGGTAGAA 3720
 GAATGCCCCC ACCCGCACCG GAACAGCAAC AAAAGGATTC TGCATGAGAT GCCTCCCTAA 3780
 ATTGCTGAAT TCAAAAAAGA AGTTGCATAC AAGACATCT GATTGAAAAA GGGTATGTGA 3840
 TATGCCCCCT TCATAGGCTG CTAGGGAGTT TTCCTGGTTC TACTTTCAGG TGGTGGGATC 3900
 AATAAGACCA GAATTTCTCA TATGTTGTGA GAGGATTCAA ATGTTACAGG GTTGCCAGCC 3960
 AAACATCAAA TCAATGATAA ATCCAAACAA CACTTTGTAA CATAACAAGA CTCAGGAAAT 4020
 GTGAACCAT GTTGAGAAAT CTACTAAAT ACGGCTTCCC GCAACGAAG ATGAATGGAA 4080
 AATGTAAATA AAAAGAATCG GCAGTGTATA TCAGATGTTT AACTATAGGA CCAGAACTAA 4140
 GATGTGGAGA CTATTTGCCAT AGACCACAAT GTAAATTTT AAGTGAGGAA GGAAAAATCA 4200
 GGAATCAAAA GGGGCCAGGT GCAGTGGCTC ACATCTATAA TCCAGAGCT TTGGGAGTTC 4260
 GAGGCAGGAG GATCACTTGA AGCCAGTTT GAGACCAGCC TATGCAACAC ATTGAGACCC 4320
 TATCTCTACA AAAATGAGCT TAGCTGGGCA CGGTGGTGA TGCCTATTGT CCTACCTACT 4380
 GTGGAGGCTG AAGTAGGAAA TCACCTGAGC CCGAGAGTTT GAGGTTACAG TGAGCTATGA 4440
 TTATACCACT GCATCCAGC CTGGCAAGA GAGCAAGACC TTGTCTCTT

Seq ID NO: 44 Protein sequence:
 Protein Accession #: CAB55276.2

1 11 21 31 41 51
 MNGEYRGRGF GRGRFQSWKR GRGGGNFSGK WREREHRPDL SKTTGKRTSE QTPQFLLSTK 60
 TPQSMQSTLD RFIPYKWKGL YFSEVYSDSS PLIEKIQAPE KFFTRHIDLY DXDEIERKGS 120
 ILVDFKELTE GGEVTNLIPD IATELRDAPE KTLACMGLAI HQVLT KDOLER HAAELQAQEG 180
 LSNDGETMVN VPHIHARVYN YEPITQLKNV RANYYGKYIA LRGTVVRVSN IKPLCTKMAF 240
 LCAACGEIQS FPLPDGKYSL PTKCPVPVCR GRSFTALRSS PLTVTMDWQS IKIQELMSDD 300
 QREAGRIPRT IECBLVHDLV DSCVPDGTVT ITGIVKVSNA EEGSRNKNDK CMFLLYIEAN 360
 SISNSKGQKT KSSBDGCKHG MLMEFSLKDL YAIQEIQAEE NLFKLI VNSL CPVIFGHELV 420
 KAGLALALFPG GSKYADDKN RPIRGDPHI LVVGDPLGK SQMLQAACNV APRGVYVCGN 480
 TTTTSGLTVT LSKDSSSDGF ALEAGALVLG DQIGCGIDEF DKMGNOHQAL LEAMEQQSIS 540
 LAKAGVVCSL PARTSIIAAA NFVGGHYNKA KTVSENLMKG SALLSRFDLV FILLDT PNEH 600
 HDHLLSEHVI AIRAGKQRTI SSATVARMNS QDSNTSVLEV VSEKPLSERL KVPVGETIDP 660
 IPHQLLRKYI GYARQYVYPR LSTEAARVLQ DFYLELRKQS QRLNSSPITT RQLESILRLT 720
 EARARLELR EATKEDAEDI VEIMKYSMLG TYSDEFNLD FERSQHGSGM SNRSTAKRFI 780
 SALINVAERT YNNIFQFHQL RQIAKELNIQ VADPFENFIGS LNDQGYLLKK GPKVYQLQTM

Seq ID NO: 45 DNA sequence
 Nucleic Acid Accession #: NM_005416.1
 Coding sequence: 149..658

1 11 21 31 41 51
 ACCAGATCCC AGAGGCTGAA CACCTCGACC TTCTCTGCAC AGCAGATGAT CCCTGAGCAG 60
 CTGAAGACCA GAAAGGCCAC TAAGACTTTC TGCTTAATTC AGGAGCTTAG AGGATTCTTC 120
 AAAGAGTGTG TCCAGCATCC TTTGAAGCAT GAGTTCTTAC CAGCAGAAGC AGACCTTTAC 180
 CCCACCACCT CAGCTTCAAC AGCAGCAGGT GAAACAACCC AGCCAGCCTC CACCTCAGGA 240
 AATATTTGTT CCCACAACCA AGGAGCCATG CCACTCAAAG GTTCCACAAC CTGGAACAC 300
 AAAGATTCCA GAGCCAGGCT GTACCAAGGT CCCTGAGCCA GGCTGTACCA AGGTCCCTGA 360
 GCCAGGCTGT ACCAAGGTCC CTGAGCCAGG TTGTACCAAG GTCCCTGAGC CAGGCTGTAC 420
 CAAAGTCCCT GAGCCAGGTT GTACCAAGGT CCCTGAGCCA GGCTACACCA AGGTCCCTGA 480
 ACCAGGCAGC ATCAAGGTCC CTGACCAAGG CTTATCAAG TTTCTGAGC CAGGTGCCAT 540
 CAAAGTCTCT GAGCAAGGAT ACACCAAGT TCCTGTGCCA GGCTACACAA AGGTACACGA 600
 GCCATGTCTCT TCAACGGTCA CTCCAGGCCC AGCTCAGCAG AAGACCAAGC AGAAGTAATT 660
 TGGTGCACAG ACAAGCCCTT GAGAAGCCAA CCACCATGAT CTGGACACCC TCTTCCCATC 720
 TGTCTCTGTG TCTTAATTGT CTGTAGACCT TGTAAATCAGC ACATTGTAC CCAAGCCAT 780
 AGTCTCTCTC TTATTTGTAT CCTAAAATA CGTACTATAA AGCTTTTGT CACACACACT 840
 CTGAAGAATC CTGTAAGCCC CTGAATTAAG CAGAAAGTCT TCATGGCTTT TCTGGTCTTC 900
 GGCTGCTCAG GGTTCATCTG AAGATTCGAA TGAAAAGAAA TGCATGTTTC CTGCTCTTCC 960
 CTCATTAAAT TGCTTTTAAAT TCCA

Seq ID NO: 46 Protein sequence:
 Protein Accession #: NP_005407.1

1 11 21 31 41 51
 MSSYQQKQTF TPPPQLQQQQ VKQPSQPPPP EIFVPTTKEP CHSKVPQPGN TKIPEPGCTK 60
 VPEPGCTKVP EPGCTKVPEP GCTKVPEPGC TKVPEPGCTK VPEPGYTKVP EPGSIKVPDQ 120
 GFIKFPEPGA IKVPEQGYTK VPVPGYTKLP EPCPSTVTPG PAQKQTKQK

Seq ID NO: 47 DNA sequence
 Nucleic Acid Accession #: Eos sequence

1 11 21 31 41 51
 5 GCGTCGTGTG CAGGCGTCCC CGGGCTGTGG ATAATTAGAC ACGTTCCTCC CTCATTGCC 60
 AAGGCTCGTT AGAATTCGCC CTAGAGCTGT ATCATGTATT TTCTTTCAAA TTAACCTTGC 120
 TTGCAATTAA GCTTAGGGAA CCAGCAACAA AAGCAAACCT GGGCCGAGGT CGTTCACCGC 180
 GAAAAATGGAT TAGAGAACT TCTTCCCAGA TTTAAGGGGA AAGATTCCTG CGGCCAGCGC 240
 TTTGGGGAAG GTGCCCGGAC CGCAGAGGCG ACGACAGGGG AGCAGGAAGC TGCTCACGGT 300
 AGTCGGCGTT GGGCGCAGCG GTGGCCTTCC TCATCTGGGC GATGTGGGCT CCTAGAAGAG 360
 10 TAAGGATAAC ATCCTGGAAA TGACTTCTGT ACGGTTTGAG CCCAACTGCA CACTCATGAC 420
 TTGGAGCTGC CCGTGGAGT TACAGTTTAC CAAACACATT CATGAACATA ATCTCATTTA 480
 CTAAAAAATT TCTGAGAATT TTCTTTTACT AAAATTTTTT CTTATTACAA A

Seq ID NO: 48 DNA sequence:

Nucleic Acid Accession #: CAT cluster

1 11 21 31 41 51
 20 TTCCAAATTT TTTTCTTGT AATAAGAAAA AATTTTAGTA AAAGAAAATT CTCACAAAGT 60
 TTTTAGTAAA TGAGATTATG TTCATGAATG TGTTTGGTAA ACTGTAATC CACAGGGCAG 120
 CTCCAAGTCA TGAGTGTGCA GTTGGGCTCA AACCGTACAG AAGTCATTTC CAGGATGTTA 180
 TCCTTACTCT TCTCGAGGCC CACATCGCCC AGATGAGGAA GGCACCGCT CGGCCAACG 240
 CCGACTACCG TGAGCAGCTT CCTGCTCCCC TGTGCTCGCC TCTGCGGTG GGGCACTTTC 300
 25 CCCAAAGCGC TGGCGCAGG AATCTTTCCC CTTAAATCGG GGAAGAAATT TCTCTAATCC 360
 ATTTTCGCGG TGAACGACCT CGGGCCAAGT TTGCTTTTGT TGCTGTTTCC CTAAGCTTAA 420
 TTGCAAGCAA AGTTAATTGT AAAGAAAAATA CATGATACAG CTCTAGGGCG AATTCTAACG 480
 AGCCTTGGGC AATGAGGAA GAACGTGTCT AGTTATCCAC AGCCCGGGGA CGCCTGCACA 540
 CGACGCT

Seq ID NO: 49 DNA sequence

Nucleic Acid Accession #: CAT cluster

1 11 21 31 41 51
 35 TCTTCTTCT GCTGCTCGTT TGTCTCTCT GTGCTCTTCT TCTTCTTTC CTGCGCGCT 60
 CCTGCGGACC TCTGTGTCT CTCTCTGAT GGCAGGGGGC GGGAGAAGCT GACCGGTGAG 120
 ACCGTAGACC CGAAACCAT GGGGTGCACA AGCCGGTCCG CGGCTTTTTT GGGAGAAGCC 180
 GACACATGCA GACCACTTTT CCTGGAAACNG CATGACCATG TTATTACTAT GGGCCGCTTC 240
 40 CCCAACCAAA GTGTTTAAA CTTTTTAGGG CACCCCAAAA ATTTTTTTTT TTTTTTTTTT 300
 TTCAATTAAA AAACCTAAT ATTTATATTA AATACAAAGA TACCCAAACC CTTTATGCTT 360
 CTTTCTCTGA TCTGTGTCTT TTTTCTTTGA CAGCATCTCC ATTTTTTTTC TGCTGCTTCA 420
 TCGCTGTAGC CATGGGAATC CGTTTCAITA TTATGGTAGC AATATGGAGT GCTGTATTCC 480
 TAAAGAACT GACACAGGAG AATCACTTGA ACTTGGGAGG CAGAGTTTGC AGTGAGCCGA 540
 GATTGAACCA GTGCACTCCA GCCTTGGCAG CGGAGCAAGA TTCTGTCAAC GTTCTGAAG 600
 45 TGCTGGTATC GTCTGCAGC CCCATCCTCG GTTCCATTGC GCTGCCAGGC AGGGTGCTGG 660
 GACGTGGGGA GAGCTGGTCT ATATATCCCG GTGAAGCTCA GCTGTGGCAC ACCTTGGATG 720
 CCGGCTCTCT CTTGGCCCGC GGGACCTAGT ATTTTGTCCA CGAGTGTACA CCAACCAAG 780
 GAGACAGCAT CATTATGAG CCTGCAGCAT CCACCCTACT GCTGTATCCA GTTCCATTG 840
 ACTG

Seq ID NO: 50 DNA sequence

Nucleic Acid Accession #: L05187

Coding sequence: 1991..2260

1 11 21 31 41 51
 55 CTGCAGGGAG GCAGGTAGAA AAGGCTTTTG GGTTTTCAGG TGGGGGGCAG TCTAGCCTGA 60
 TCAGAAAGGA GGAAGAGGCC AGGGCAGATG TCTGGGTGGA GTGAAGGGAA AAAGTGATCC 120
 60 CAGAAGAAGG ATTAGCCCTT GAAAGTCCCT GAAAGTAGGAG AAGGGTAAAG GTGTGGTTGG 180
 TGAAGGAAAG CAGGTTTTCC CAGATTAGCA ACCAGTCAGG GGGAGGAAGG TGAGAGTGGG 240
 AGAGTCATAA GTAAATTATT CTGAATGTGT GTAGTTTAAT GGAATTGGGA AAAAGATGGG 300
 GGAATATGGAT GGAAGGTTCT GGAAGGTTCT GGAAGGTTCT TATAATCAGT CCATTTCATT 360
 ATTTCTAGCT TCCACCTTCA CCAAGGCAGA CAAGGAGGGC CCACCTCAGC TCCTCTGCTC 420
 65 CCCCTCCCTT TCCACCTTAT TCATGTGTGC AAGAGTGGCC TGTCCACAG AACACGGGGA 480
 ACAACCATCT CAATGACAAG GACAGCAGGT GGCAGGCTC AACAGGACTC AGATGTCCCC 540
 CCAGGGTTAA CTCATGAAAC CCTCCATGAA GCCTGCTGCT CACCCCTCCC TCAAGGCAAG 600
 CCTGCACTCT GGGTCTGAGG ATGAGGGTGG CAGTGAAAT TAGGCCAGTG ACATCATTTT 660
 CAGCCAGCTA GTGCCAAAAA ATATCAGGTG GTGTTTCATCA AATAAGCCGA GCCAACCGGT 720
 70 GATGAGGATG GTAGTGTGAG TCATGTGTGA CAGGTGAGGA ATGAAAACAG AGTGCCCGAG 780
 AGCTTCTATT TCCTTGAGGC AGGGCTCATT CATCTTATAA AAGCCAGCTG GCCATTGCCT 840
 TCACACCAAA CCCAAGGGAC CACACAGCCC ATTCTGCTCC GTATACCAGG TAAGTCTCTG 900
 ATTGCAACAA ACTGGCAATT CTAGTGTACT TTTTCATTAT TAGAAATTAG CTAAGGCAA 960
 ATATGTGTAA GCAGGTAAAT CCAGGGTTTC AATGGGAGAT AGAGAATAGT GGAATATCTT 1020
 75 TATTTTAAGT TAAATTACAG TCTGGATTG AAAGGACCTT AGAGATGGTT AGGGCTCCCA 1080
 CCTCAGTAGA TAGTCATTGA ACTGGGAGTC CTGGAGAAGA TTGTTCAAAT GCCCATGGGA 1140
 AGTTCATAGC AGAATAGAAA CTCAGGCCAG AGCACTCTCA GTAACACTGC AATTTCCCCC 1200
 TGACAAGATA TTTATAGAAA TTTTAATTGA TTAGATGGAT CTCTACTGAG CATTATTTCC 1260
 ATTTAAGGCA GTATGCTAGG CACTTTGGAC AAATCAATGC CCTAACGTAC TTAATTAAAC 1320
 AACATAAAAC CTAGCAGGAA GGTAAATACAT ATATATAAAT AAATGAAATG CAAAGTAGAT 1380
 80 AGTAATTGGC ATGACGGAGA TGGGCGAGGA AGGGCTGTGC ACTTTTGGGA GACTTGCTCA 1440
 AGGAGACCTC TAGGGTGTCA AGTGATGTGA GCTATGATGG AGGGGTATTT GGACAAGCAG 1500
 AGATGGGAAG AAAAGCATTT GGAAGGGACT GTGTAAGCAC AGACCAGAAG CAAACCCATA 1560
 GAGGCTTAGA TTAATATAAA GCCATCCTAT AAGTCACAGG CTTTCTACAT GGTACTAGGA 1620
 GAGGAAAGTG GTCTGATGCC ATTTTCCAAA AGACCTAATA TGCGGACCTC ATGTCCCTCA 1680
 85 GAAGCCAGCT TAGTAGGGC ATTTTCCAG AACAGATATA AGGTGCCTTG GGTAGGAAGG 1740
 GAGCCAAAGAA GAGAACTCCA ATAAATGGA GCAGAAGAAA TTGCTTTTA GCTCCTCCTC 1800
 TTCAAAGGCG CTGAAATTA TCCAAGCTTA TTTCAATTTT AAATGTAATG GGGGAGCTAA 1860

GGGAGATGAA AGGCTTTCTC TTCTAAAGGG TCCTGAAATA AAATCTGTTT GGCATTGAAT 1920
 TTGTATCCAT CTTTCTTTAA TTGAATCACT GTGTCAGCTT TCTGTCTCTA GAAAAAACA 1980
 CATTTGAAGC ATGAATTTCTC AGCAGCAGAA GCAGCCTTGC ACCCCACCCC CTCAGCCTCA 2040
 GCAGCAGCAG GTGAAACAAC CTTGCCAGCC TCCACCCAG GAACCATGCA TCCCCAAAC 2100
 CAAGGAGCCC TGCCAACCCA AGGTGCCTGA GCCCTGCCAC CCCAAAGTGC CTGAGCCCTG 2160
 CCAGCCCAAG ATTCCAGAGC CCTGCCAGCC CAAGGTGCCT GAGCCCTGCC CTTCAACGGT 2220
 CACTCCAGCA CCAGCCAGC AGAAGACCAA GCAGAAGTAA TGTGGTCCAC AGCCATGCC 2280
 TTGAGGAGCT GGCCACTGGA TACTGAACAC CCTACTCCAT TCTGCTTATG AATCCCATTT 2340
 GCCTATTGAC CCTGCAGTTA GCATGCTGTC ACCCTGAATC ATAATCGCTC CTTTGACCT 2400
 CTAAGAGAT GTCCCTTACC CTCATTCTGG AGGCTCCTGA GCCTCTGCGT AAGGCTGAAC 2460
 GTCTCACTGA CTGAGCTAGT CTTCTGTGTC CTCGGGTGCA TTTGAGGATG GATTGGGGA 2520
 AGGTCAAGTG ACCATCCCTA G

Seq ID NO: 51 Protein sequence:
 Protein Accession #: AAC26838

1 11 21 31 41 51
 | | | | | |
 MNSQQQKQPC TPPPQPOQQQ VKQPCQPPQ EPCIPKTKEP CQPKVPEPCH PKVPEPCQPK 60
 IPEPCQPKVP EPCPSTVTPA PAQQKTKQK

Seq ID NO: 52 DNA sequence
 Nucleic Acid Accession #: NM_002638.1
 Coding sequence: 120-473

1 11 21 31 41 51
 | | | | | |
 CAATACAGCT AAGGAATTAT CCCTTGTAAG TACCACAGAC CCGCCCTGGA GCCAGGCCAA 60
 GCTGGACTGC ATAAAGATTG GTATGGCCTT AGCTCTTAGC CAAACACCTT CCTGACACCA 120
 TGAGGGCCAG CAGCTTCTTG ATCGTGGTGG TGTTCCTCAT CGCTGGGACG CTGGTTCTAG 180
 AGGCAGCTGT CACGGGAGTT CCGTTAAAG GTCAAGACAC TGTCAAAGCG CGTGTTCAT 240
 TCAATGGACA AGATCCCCTT AAAGGACAAG TTTCAGTTAA AGGTCAAGAT AAAGTCAAAG 300
 CGCAAGAGCG ATGCAAGGTT CCACTCTCCA CTAGCCTGG CTCTGCCCTT ATTATCTTGA 360
 TCCGGTGGCG CATGTGTAAG CCCCTAACC GCTGCTTGA AGATACTGAC TGCCCAAGAA 420
 TCAAGAAGTG CTGTGAAGGC TCTTGCGGGA TGGCCTGTTT CGTTCCCCAG TGAAGGGAGC 480
 CGGTCTTTCG TGACCTGTG CCGTCCCAG AGCTACAGGC CCCATCTGGT CCTAAGTCCC 540
 TGCTGCCCTT CCCCTTCCA CACTGTCCAT TCTTCTCCC ATTCAGGATG CCCACGGCTG 600
 GAGCTGCCCTC TCTCATCCAC TTTCAATAA A

Seq ID NO: 53 Protein sequence:
 Protein Accession #: NP_002629.1

1 11 21 31 41 51
 | | | | | |
 MRASSFLIVV VFLIAGTLVL EAAVTGVPVK GQDITVGRVP FNGQDPVKGQ VSVKGQDKVK 60
 AQEPVKGPVS TKPGSCPIIL IRCAMLNPPN RCLKDTDCPG IKKCCGSGSG MACFVPQ

Seq ID NO: 54 DNA sequence
 Nucleic Acid Accession #: NM_019618
 Coding sequence: 75-584

1 11 21 31 41 51
 | | | | | |
 GGCACGAGCC ACGATTCACT CCCCTGGACT GTAGATAAAG ACCCTTCTT GCCAGGTGCT 60
 GAGACAACCA CACTATGAGA GGCACCTCAG GAGACGCTGA TGGTGGAGGA AGGGCGTCT 120
 ATCAATCAAT GTGTAAACCT ATTACTGGGA CTATTAATGA TTTGAATCAG CAAGTGTGGA 180
 CCCTTCAGGG TCAGAACCTT GTGGCAGTTC CACGAAGTGA CAGTGTGACC CCAAGTCACTG 240
 TTGCTGTTAT CACATGCAAG TATCCAGAGG CTCTTGAGCA AGGCAGAGGG GATCCCATTT 300
 ATTTGGGAAT CCAGAATCCA GAAATGTGTT TGTATTGTGA GAAGGTGGA GAACAGCCCA 360
 CATTGCAGCT AAAAGAGCAG AAGATCATGG ATCTGTATGG CCAACCCGAG CCGGTGAAAC 420
 CCTTCTTTT CTACCGTGCC AAGACTGGTA GGACCTCCAC CCTTGAGTCT GTGGCCTTCC 480
 CGGACTGGTT CATTGCCTCC TCCAAGAGAG ACCAGCCCAT CATTCTGACT TCAGAACTTG 540
 GGAAGTCATA CAACACTGCC TTTGAATTAA ATATAAATGA CTGAACCTAG CCTAGAGGTG 600
 GCAGCTTGGT CTTTGTCTTA AAGTTCTGG TTCCCAATGT GTTTTCTGCT ACATTTTCTT 660
 AGTGTCAATT TCAGCTGGT GCTGAGACAG GGGCAAGGCT GCTGTTATCA TCTCATTTTA 720
 TAATGAAGAA GAAGCAATTA CTTATAGCA ACTGAAGAAC AGGATGTGGC CTCAGAAGCA 780
 GGAGAGCTGG GTGGTATAAG GCTGCTCTCT CAAGCTGGTG CTGTGTAGGC CACAAGGCAT 840
 CTGCATGAGT GACTTTAAGA CTCAAGACC AAACACTGAG CTTTCTTCTA GGGGTGGGTA 900
 TGAAGATGCT TCAGAGCTCA TGCGCGTTAC CCACGATGGC ATGACTAGCA CAGAGCTGAT 960
 CTCTGTTTCT TTTTGTCTT ATTCCCTCTT GGGATGATAT CATCCAGTCT TTATATGTTG 1020
 CCAATATACC TCATTGTGTG TAATAGAACC TTCTTAGCAT TAAGACCTTG TAAACAAAAA 1080
 TAATTCTTGT GTTAAGTTAA ATCATTTTGT TCCTAATTGT AATGTGTAAT CTTAAAGTTA 1140
 AATAAACTTT GTGATTTTAT ATAATAAAAA AAAAAAAAAA AAA

Seq ID NO: 55 Protein sequence:
 Protein Accession #: NP_062564

1 11 21 31 41 51
 | | | | | |
 MRGTPGDADG GGRAVYQSMC KPITGTINDL NQQVWTLQGG NLVAVPRSDS VTPVTVAVIT 60
 CKYPEALEQG RGDPYIYLIQ NPENCLYCEK VGEQPTLQLK EQKIMDLYGQ PEPVKPFLFY 120
 RAKTGRSTSL ESVAPFDWFI ASSKRDQPII LTSELGKSYN TAFELMIND

Seq ID NO: 56 DNA sequence
 Nucleic Acid Accession #: NM_003125
 Coding sequence: 65-334

1 11 21 31 41 51
 5 AGCAGTTCTA AGGGACCATA CAGAGTATTC CTCTCTTCAC ACCAGGACCA GCCACTGTGTG 60
 CAGCATGAGT TCCCAGCAGC AGAAGCAGCC CTGCATCCCA CCCCCTCAGC TTCAGCAGCA 120
 GCAGGTGAAA CAGCCTTGCC AGCCTCCACC TCAGGAACCA TGCATCCCCA AAACCAAGGA 180
 GCCCTGCCAC CCCAAGGTGC CTGAGCCCTG CACCCCAAA GTGCCTGAGC CCTGCCAGCC 240
 CAAGCTTCCA GAGCCATGCC ACCCAAGGT GCCTGAGCCC TGCCCTTCAA TAGTCACTCC 300
 10 AGCACCAGCC CAGCAGAAGA CCAAGCAGAA GTAATGTGGT CCACAGCCAT GCCCTTGAGG 360
 AGCCGGCCAC CAGATGCTGA ATCCCCATC CCATTCTGTG TATGAGTCCC ATTTGCGTTG 420
 CAATTAGCAT TCTGTCTCCC CCAAAAAGA ATGTGCTATG AAGCTTTCTT TCCTACACAC 480
 TCTGAGTCTC TGAATGAAGC TGAAGTCTT AGTACCAGAG CTAGTTTCA GCTGCTCAGA 540
 15 ATTCTATCTGA AGAGAGACTT AAGATGAAAG CAAATGATTG AGCTCCCTTA TACCCCCATT 600
 AAATTCACCT TCAATTCCA

Seq ID NO: 57 Protein sequence:
 Protein Accession #: NP_003116

1 11 21 31 41 51
 20 MSSQQKQKPC IPPQLQQQQ VKQPCQPPPP EPCIPKTKEP CHPKVPEPCH PKVPEPCQPK 60
 25 LPEPCHPKVP EPCPSIVTPA PAQKTKQKQ

Seq ID NO: 58 DNA sequence
 Nucleic Acid Accession #: NM_001793.2
 Coding sequence: 71-2560

1 11 21 31 41 51
 30 AAAGGGGCAA GAGCTGAGCG GAACACCGGC CCGCCGTCGC GGCAGCTGCT TCACCCCTCT 60
 CTCTGCAGCC ATGGGGCTCC CTCGTGGACC TCTCGCGTCT CTCCTCCTTC TCCAGGTTTG 120
 35 CTGGCTGCAG TGCGCGCGCT CCGAGCGGTG CCGGGCGGTC TTCAGGGAGG CTGAAGTGAC 180
 CTGGAGGCGG GGAGGCGCGG AGCAGGAGCC CGGCCAGGCG CTGGGGAAGG TATTCAATGG 240
 CTGCCCTGGG CAAGAGCCAG CTCTGTCTAG CACTGATAAT GATGACTTCA CTGTGCGGAA 300
 TGCGGAGACA GTCCAGGAAA GAAGGTCACT GAAGGAAAGG AATCCATTGA AGATCTTCCC 360
 40 ATCCAAACGT ATCTTACGAA GACACAAGAG AGATTGGGTG GTTGCTCCAA TATCTGTCCC 420
 TGAATATGGC AAGGTCCTCT TCCCCAGAG ACTGAATCAG CTCAGTCTA ATAAAGATAG 480
 AGACACCAAG ATTTTCTACA GCATCAGCGG GCCGGGGGCA GACAGCCCCC CTGAGGGTGT 540
 CTTCGCTGTA GAGAGGAGGA CAGGCTGGTT GTTGTGAAT AAGCCACTGG ACCGGGAGGA 600
 GATTGCCAAG TATGAGTCTT TTGGCCACGC TGTGTGAGAG AATGGTGCCT CAGTGGAGGA 660
 CCCCATGAAC ATCTCCATCA TCGTGACCGA CCAGAATGAC CACAAGCCCA AGTTTACCCA 720
 45 GGACACCTTC CGAGGGAGTG TCTTAGAGGG AGTCTTACCA GGTACTTCTG TGATGCAGGT 780
 GACAGCCACG GATGAGGATG ATGCCATCTA CACCTACAAT GGGGTGGTTG CTTACTCCAT 840
 CCATAGCCAA GAACCAAGAG ACCCACACGA CCTCATGTTC ACCATTCAAC GGAGCACAGG 900
 CACCATCAGC GTCATCTCCA GTGGCCTGGA CCGGGAAAAA GTCCCTGAGT ACACACTGAC 960
 CATCCAGGCC ACAGACATGG ATGGGGACGG CTCACCAACC ACGGCAGTGG CAGTAGTGGA 1020
 50 GATCCTTGAT GCCAATGACA ATGCTCCCAT GTTTGACCCC CAGAAGTAGG AGGCCCATGT 1080
 GCCTGAGAAAT GAGTGGGCCC ATGAGGTGCA GAGGCTGACG GTCACTGATC TGGACGCCCC 1140
 CAACTCACCA GCGTGGCGTG CCACCTACCT TATCATGGGC GGTGACGACG GGGACCATTT 1200
 TACCATCACC ACCCAACCTG AGAGCAACCA GGGCATCCTG ACAACCAGGA AGGGTTTGGA 1260
 55 TTTTGAGGCC AAAAACACGC ACACCTGTGA CGTTGAAGTG ACCAACGAGG CCCCTTTTGT 1320
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 ACCTGTGTTT GTCCACCTCT CCAAGTGTGT TGAGGTCCAG GAGGGCATCC CCATGAGGGA 1440
 GCCTGTGTGT GTCTACATG CAGAAGACCC TGACAAGGAG AATCAAAAGA TCAGCTACCG 1500
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 60 GGTCTTGGCC ATGACAAATG GAAGCCCTCC CACCACTGGC ACGGGAACCC TTCTGCTAAC 1680
 ACTGATTGAT GTCAATGACC ATGGCCCATG CCTGAGCCCC CGTCAGATCA CCATCTGCAA 1740
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 65 GGAAGGTGAC ACAGTGGTCT TGTCCCTGAA GAAGTTCTTG AAGCAGGATA CATATGACGT 1920
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 GTGCGACTGC CATGGCCATG TCGAAACCTG CCTGGACCCC TGGAAAGGAG GTTTCATCCT 2040
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 70 CGTCTTCTAC TATGGCGAAG AGGGGGGTGG CGAAGAGGAC CAGGACTATG ACATCACCCA 2220
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 75 CTGTGTGTTT GACTATGAGG GCAGCGGCTC CGACGCGCGT TCCCTGAGCT CCCTCACCTC 2460
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Seq ID NO: 59 Protein sequence:

Protein Accession #: NP_001784.2

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	QEPALFSTDN	DDFTVRNGET	VQERRSLKER	NPLKIFPSKR	ILRRHKRDWV	VAPISVPENG	120
	KGFFPQRLNQ	LKSNKORDTK	IFYSITGPGA	DSPEEGVFAV	EKETGWLLEN	KPLDREEIAK	180
	YELFGHAVSE	NGASVEDPMN	ISIIIVTDQND	HKPKFTQDTF	RGSVLEGVLP	GTSVMQVTAT	240
10	DEDDAIYTYN	GVVAYSIHSQ	EPKDPHDLMP	TIHRSTGTIS	VISSGLDREK	VPEYTLTIQA	300
	TDMGDGSGTT	TAVAVVEILD	ANDNAPMFD	QKYEAVHPEN	AVGHEVQRLT	VTDLDPNSP	360
	AWRATYLMG	GDDGDHFTIT	THPESNQIL	TTRKGLDFEA	KNQHTLYVEV	TNEAPFVLKL	420
	PTSTATIVH	VEDVNEAPVF	VPPSKVVEVQ	EGIPTGEFVC	VYTAEDPDKE	NQKISYRILR	480
	DPAGWLAMP	DSGQVAVGT	LDREDEQFVR	NNIYEVMLA	MDNGSPPTTG	TGTLTLTLID	540
	VNDHGFVPEP	RQITICNQSP	VRQVLNITDK	DLSPHTSPFQ	AQLTDDSDIY	WTAEVNEEGD	600
15	TVVLSLKKFL	KQDPTDVHLS	LSDHGNKEQL	TVIRATVCDC	HGHVETCPGP	WKGGFILPVL	660
	GAVLALLFLL	LVLLLLVRKK	RKIKEPLLLP	EDDTRDNVFI	YGEEGGGEED	QDYDITQLHR	720
	GLEARPEVLL	RNDVAPTIIIP	TPMYRPRPAN	PDEIGNFIIIE	NLKAANTDPT	APPYDTLLVF	780
	DYEGSGSDAA	SLSSLTSSAS	DQDQDYDILN	EWGSRFKKLA	DMYGGGEDD		

Seq ID NO: 60 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 162-428

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	CATACGGACC	GGATTGTPTT	CGCTGGCCCA	GTGTCCCGG	AGCTTGTGTG	CGATACAGAG	120
	AGCACCTCGG	AAGCTGAGGC	AGCTGGTACT	TGACAGAGAG	GATGGCGCTG	TCGACCATAG	180
	TCTCCAGAG	GAGCGAGAG	AAGCGGAAGG	CTCCCCGTGG	CTTTCTAAAG	CGAGTCTTCA	240
30	AGCGAAAGAA	GCCTCAACTT	CGTCTGGAGA	AAAGTGGTGA	CTTATTGGTC	CATCTGAACT	300
	GTTTACTGTT	TGTTTCATCGA	TTAGCAGAAG	AGTCCAGGAC	AAACGCTTGT	GCGAGTAAAT	360
	GTAGAGTCAT	TAACAAGGAG	CATGTACTGG	CCGCAGCAAA	GGTAATCTTA	AAGAAGAGCA	420
	GAGGTTAGAA	GTCAAAGAAC	ATATTCTTGA	AAGTTATGAT	GCATTCTTTT	GGGTGGTAAC	480
	AGATCATAAA	GACATTTTTT	ACACATCAGT	TAATATGGGA	TTATTAATAA	TTGG	

Seq ID NO: 61 Protein sequence:

Protein Accession #: Eos sequence

	1	11	21	31	41	51	
40	MALSTIVSQR	KQIKRKAPRG	FLKRVFKRKK	PQLRLEKSGD	LLVHLNCLLF	VHRLAESRT	60
	NACASKCRVI	NKEHVLAAAK	VILKRSRG				

Seq ID NO: 62 DNA sequence

Nucleic Acid Accession #: NM_000094.2

Coding sequence: 99-8933

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	GAGGCGGGGG	TCCTAGCTGA	CGGCTTTTAC	TGCCTAGGAT	GACGCTGCGG	CTTCTGGTGG	120
	CCGCGCTCTG	CGCCGGGATC	CTGGCAGAGG	CGCCCCGAGT	GCGAGCCGAG	CACAGGGAGA	180
	GAGTGACCTG	CACGCGCCTT	TACGCGGCTG	ACATTGTGTT	CTTACTGGAT	GGCTCCTCAT	240
	CCATTGGCCG	CAGCAATTTT	CGCGAGGTCC	GCAGCTTTCT	CGAAGGGCTG	GTGCTGCCTT	300
55	TCTCTGGAGC	AGCCAGTGCA	CAGGGTGTGC	GCTTTGGCAC	AGTGCACTAC	AGCGATGACC	360
	CACGGACAGA	GTTCCGCGTG	GATGCACCTG	GCTCTGGGGG	TGATGTGATC	CGCGCCATCC	420
	GTGAGCTTAG	CTACAAGGGG	GGCAACACTC	GCACAGGGGC	TGCAATCTCT	CATGTGGCTG	480
	ACCATGTCTT	CCTGCCCCAG	CTGGCCCGAC	CTGGTGTCCC	CAAGGTCTGC	ATCCTGATCA	540
	CAGACGGGAA	GTCCAGGAC	CTGGTGGACA	CAGCTGCCCA	AAGGCTGAAG	GGCGAGGGGG	600
60	TCAAGCTATT	TGCTGTGGGG	ATCAAGAATG	CTGACCTTGA	GGAGCTGAAG	CGAGTTGCCT	660
	CACAGCCAAC	CTCCGACTTC	TTCTTCTTCG	TCAATGACTT	CAGCATCTTG	AGGACACTAC	720
	TGCCCTCGT	TTCGCGGAGA	GTGTGCACGA	CTGCTGGTGG	CGTGCTGTGT	ACCCGACCTC	780
	CGGATGACTC	GACCTCTGCT	CCACGAGACC	TGGTGTGTGC	TGAGCCAAGC	AGCCAATCCT	840
	TGAGAGTACA	GTGGACAGCG	GCCAGTGGCC	CTGTGACTGG	CTACAAGGTC	CAGTACACTC	900
65	CTCTGACGGG	GCTGCGGACG	CCACTGCCGA	GTGAGCGGCA	GGAGGTGAAC	GTCCAGCTG	960
	GTGAGACCAG	TGTGCGGCTG	CGGGGTCTCC	GGCCACTGAC	CGAGTACCAA	GTGACTGTGA	1020
	TTGCCCTCTA	CGCCAACAGC	ATCGGGGAGG	CTGTGAGCGG	GACAGCTCGG	ACCACTGCCC	1080
	TAGAAGGGCC	GGAACTGACC	ATCCAGAATA	CCACAGCCCA	CAGCCTCCTG	GTGGCCTGGC	1140
	GGAGTGTGCC	AGGTGCCACT	GGCTACCGTG	TGACATGGCG	GGTCTCAGT	GGTGGGCCCA	1200
70	CACAGCAGCA	GGAGCTGGGC	CCTGGGCAGG	GTTCAGTGTT	GCTGCGTGAC	TTGGAGCCTG	1260
	GCACGGACTA	TGAGGTGACC	GTGAGCACCC	TATTGGCCG	CAGTGTGGGG	CCCGCACTT	1320
	CCCTGATGGC	TCGCACTGAC	GCTTCTGTTG	AGCAGACCCT	GCGCCCGGTC	ATCCTGGGCC	1380
	CCACATCCAT	CCTCTTTTTC	TGGAACCTTG	TGCCTGAGGC	CCGTGGCTAC	CGGTTGGAAT	1440
	GGCGGCGTGA	GACTGGCTTG	GAGCCACCGC	AGAAGGTGGT	ACTGCCCTCT	GATGTGACCC	1500
75	GCTACCAGTT	GGATGGGCTG	CAGCCGGGCA	CTGAGTACCG	CCTCACACTC	TACACTCTGC	1560
	TGGAGGGCCA	CGAGGTGGCC	ACCCCTGCAA	CCGTGGTTCC	CACTGGACCA	GAGCTGCCTG	1620
	TGAGCCCTGT	AACAGACCTG	CAAGCCACCG	AGCTGCCCGG	GCAGCGGGTG	CGAGTGTCTT	1680
	GGAGCCCACT	CCCTGGTGCC	ACCCAGTACC	GCATCATTTG	GCGCAGCACC	CAGGGGGTTG	1740
	AGCGGACCCT	GGTGCTTCTT	GGGAGTCAGA	CAGCATTCGA	CTTGGATGAC	GTTGAGGCTG	1800
80	GGCTTAGCTA	CAGTGTCCGG	GTGTCTGCTC	GAGTGGGTCC	CCGTGAGGGC	AGTGCCAGTG	1860
	TCCTCACTGT	CGCGCGGGAG	CCGGAAACTC	CACTTGCTGT	TCCAGGGCTG	CGGGTTGTGG	1920
	TGTCAAGTGC	AACGCGAGTG	AGGGTGGCCT	GGGAGCCCGT	CCCTGGAGCC	AGTGGATTTC	1980
	GGATTAGCTG	GAGCACAGGC	AGTGGTCCGG	AGTCCAGCCA	GACACTGCCC	CCAGACTCTA	2040
	CTGCCACAGA	CATCACAGGG	CTGCAGCCTG	GAACCACTA	CCAGGTGGCT	GTGTGGGTAC	2100
85	TGCGAGGCAG	AGAGGAGGGC	CCTGTGTCAG	TCATCGTGGC	TGGAACGGAG	CCACTGGGCC	2160
	CAGTGAGGAC	GGTCCATGTG	ACTCAGGCCA	GCAGCTCATC	TGTACCAATT	ACCTGGAGCA	2220
	GGGTTCTCTG	CGCCACAGGA	TACAGGGTTT	CCTGGCACTC	AGCCACGGC	CCAGAGAAAT	2280

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Seq ID NO: 63 Protein sequence:
 Protein Accession #: NP_000085.1

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 40 AAILHVADHV FLPQLARPGV PKVCILITDG KSQDLVDTA QRLKGQVKL FAVGIKNADP 180
 EELKRVASQP TSDFFFFVND FSIILRLTLLP VSRRVCTTAG GVPVTRPPDD STSAPRDLVL 240
 SEPSQSRLRV QWTAASGPVT GYKVQYTPLT GLGQPLPSER QEVNVPAGET SVRLRGLRPL 300
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 RVLSGGPTTQ QELGPGQSV LRLDLEPGTD YEVTVSTLFG RSVGPATSLM ARTDASVEQT 420
 45 LRPVILGPTS ILLSNLVPE ARGVLEWRR ETGLEPPQKV VLPSTDVTRYQ LDGLQPGTEY 480
 RLTLTYLLEG HEVATPATVV PTGPELPVSP VTDLQATELP GQVRVSWSP VPGATQYRII 540
 VRSTQGVERT LVLPQSQTAF DLDVQAGLS YTVRVSVARV PREGSASVLT VRREPETPLA 600
 VPGLRVVVD ATRRVAVNGP VPGASGFRIS WSTGSGPESS QTLPPDSTAT DITGLQPGTT 660
 YQVAVSVLRG REEGPAIVV ARTDPLGPVR TVHVTQASS SVTITWTRVP GATGYRVSWH 720
 50 SAHGPEKSQL VSGEATVAEL DGLEPDEYTV VHVRAHVAGV DGPASVVRV TAPEPVGRVS 780
 RLQILNASSD VLRITWVGVT GATAYRLAWG RSEGGPMRHO ILPGNTDSAE IRLGEGGSY 840
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 55 ELRVVDTSID VLTWATSVH RASSYILSWR PLRGPQGEVP GSPOTLPGIS SSQRTVGLPE 1020
 GVSYIFSLTP VLDGVRGPEA SVTQTPVCPR GLADVVLPH ATQDNAHRAE ATRRVLERLV 1080
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 85 GLLGPQGPQG AAGIPGDEG PGKDGVPGIR GEKGDVGFMG PRGLKGERGV KGACGLDGEK 2640
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10	TGTCCCACTG	CTCGCCCAAC	TCAGCAGTGC	CAGCAGAAAT	ATCCTCTCTGT	GACACCTTCC	180
	CCACCCCTGCC	AGCCAAGTA	ATCCAGCAAG	AGCAAGTAA			

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PPCPKYPK SK

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	CCGGCGGGCG	GGCGCGGGCG	ACAGGCCCTC	GCTCCGGCGG	TCGTTTGACG	ACCGCGGGCG	240
30	CGGATGTCCG	CCGCGGCCCG	TAGGATGAG	TCTCGGTCG	GGCGAGGAGC	CGCCGCAGCC	300
	GCCGCGCGCC	GAGCGCGGGG	CAGGAGCCTC	GGGAGCCGCG	CGCCCGCCGC	CGCCGCCCGC	360
	GCCGCCCGCC	GACGC CGCCC	GCGCGCCCC	GGGCCCCCGA	CACACGTAG	ATTCCTCAGG	420
	CTCACTTTCA	AGTGCTTCGT	GGACTGCTTC	TGACTGCGCC	GCCCCGCGCC	CGCACCCCGC	480
	CGTCCGCGCG	CCGCCCCGTC	CCCCGGCGCG	GCCGCCCCCG	GGCCCCCGCG	CGCCGCCCGC	540
35	CCTCGGGGCC	CTCCCCGGTG	CCGCGGGTCG	CCCCCGCCTC	ACCGCGCCGC	CCGCTGAGGC	600
	GCCCGACCCC	CGCCCGCGCC	GTGCGCGCCG	CCGGGGCCAT	GGCGAAGAAG	AGCGCCGAGA	660
	ACGCGATCTA	TAGCGTGTCC	GGCGACGAGA	AGAAGGGCCG	CCTCATCGCG	CCCGGGCCCG	720
	ACGGGGCCCC	GGCCAAAGGG	GACGGCCCCG	TGGCGCTGGG	GACACCCGCG	GGCGCCTTGG	780
	CGCTGCGGCC	GCGCGAGACC	TGGACGCGCC	AGATGGACTT	CATCATGTGC	TGCGTGGGCT	840
40	TCGCGGTGGG	CTTGGGCAAC	GTGTGCGCTC	TCCCTACCT	GTGCTACAA	AACGGCGGAG	900
	TGTGTCTCT	TATTCCTCAT	GTCCTGATCG	CCCTGGTTCG	AGGAATCCCC	ATTTCTCTTC	960
	TAGAGATCTC	GCTGGGCGAG	TTTCATGAAG	CCGGACGAT	CAATGTCTGG	AACATCTGTC	1020
	CCCTGTCTCA	AGGCCTGGGC	TACGCTCCCA	TGGTGATCGT	CTTCTACTGC	AACACCTACT	1080
	ACATCATGGT	GCTGGCGCTG	GGCTTCTATT	ACCTGGTCAA	GTCTCTTACC	ACCACGCTGC	1140
45	CCTGGGCGCC	ATGTGGCCAC	ACCTGAACA	CTCCGACTG	CGTGAGATC	TTCGCGCATG	1200
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70	GCCATACGCT	CCCGCTGCTC	AGCCCCACCG	CACCCCTCCA	GGGGCGCTCG	CTTTCCCTGA	2640
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	CAGTGTCTGA	CTCCTCTCTC	CCCTGCCACG	CCACCCCTCT	GCCCACTCTG	CCAGGCTCTG	2880
	CTCTGACGCA	CACCCGTGGG	TGACCCCTCA	CCCCAGAAGC	AGCATGTGCA	GCTTGGGAAA	2940
75	TGTGAGGAAG	GGAAGAGGAG	AGAGACGGGA	GGGAGGAGAG	AGAGAGAGAG	GAGGAGCAGG	3000
	GAGGGGCAGC	AGAACCACAG	CAATATTTCT	AGCTGGGCTA	TACCCCTCTC	CCCATCCCTG	30

CTTCTGTGTA GCAGCTTTAA CCCAGGTTTG TCTGTACGT CCAGTCCCGA GACGGCTGAG 3780
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 Protein Accession #: NP_005620.1

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 GVEGFITGLL DLLPASYYFR FQREISVALC CALCFVIDLS MVTGGMVVF QLFDYYSASG 480
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Protein Accession #: NP_068772.1

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10     LSNIQWLRKM SSDGLGSRSI QEMEEKENC HLEQRQVKVE EPSRPSASWQ NSVSERPPYS 240
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ANGKVSFWTI HPSANRYLTL DQVFKPLDPG SPQLPEHLES QQRPNPELR RNMTIKTELP 360
LGARRKMKPL LPRVSSYLVP IQFPVNQSLV LQPSVKVPLP LAASLMSSEL ARHSKRVRIA 420
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30     CAGTCTGGAG GGTCCACACT TGTGATTCTC AATGGAGAGT GAAACGCGAG ATTCATAATG 180
AAAACTAGCC CCCGTCGGCC ACTGATTCTC AAAAGACGGA GGTGCCCCCT TCCTGTTCAA 240
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AATCAAGCAG AGGCCTCCAA GGAAGTGGCA GAGTCCAAC CTGCAAGTT TCCAGCTGGG 360
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40     CAGAAACGGG AGACCTGTGC AGATGGTGAG GCAGCAGGCT GCACTATCAA CAATAGCCTA 720
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60     TTCCAGCAG ACTCCTCTGA CCCTGCCTCC CAGCTCAGCT ACTCCAGGA AGTGGGAGGA 1920
CCTTTTAAGA CACCCATTAA GGAAACGCTG CCCATCTCCT CCACCCGAG CAAATCTGTC 1980
CTCCCCAGAA CCCCTGAATC CTGGAGGCTC ACGCCCCAG CCAAGTAGG GGGACTGGAT 2040
TTGAGCCAG TACAAACCCC CCAGGGTGCC TCTGACCCCT TGCTGACCC CCTGGGCTG 2100
ATGGATCTCA GCACCACTCC CTTGCAAGT GCTCCCCCCC TTGAATCACC GCAAAGGCTC 2160
65     CTCAGTTCAG AACCTTAGA CCTCATCTCC GTCCCCCTTG GCAACTCTTC TCCTCAGAT 2220
ATAGACGTCC CCAAGCCAGG CTCCCCGAG CCACAGGTTT CTGGCCTTGC AGCCAATCGT 2280
TCTCTGACAG AAGGCCTGGT CCTGGACACA ATGAATGACA GCCTCAGCAA GATCCTGCTG 2340
GACATCAGCT TTCCTGGCCT GGACGAGGAC CCACTGGGCC CTGACAACAT CAACTGGTCC 2400
CAGTTTATTC CTGAGCTACA GTAGAGCCCT GCCCTTGCCC CTGTGCTCAA GCTGTCCACC 2460
70     ATCCCGGGCA CTCCAAGGCT CAGTGCACCC CAAGCCTCTG AGTGAGGACA GCAGGCAGGG 2520
ACTGTCTGTC TCCTCATAGC TCCCTGTGTC CTGATTATGC AAAAGTAGCA GTCACACCCT 2580
AGCCACTGCT GGGACCTTGT GTTCCCCAAG AGTATCTGAT TCCTCTGCTG TCCTGCCAG 2640
GAGCTGAAGG GTGGGAACAA CAAAGGCAAT GGTGAAAAGA GATTAGGAAC CCCCAGCCT 2700
75     GTTTCATTTC TCTGCCAGC AGTCTCTTAC CTTCCCTGAT CTTTGACAGG TGGTCCGTGT 2760
AAATAGTATA AATTCTCCAA ATTATCCTCT AATATATAAT GTAAGCTTAT TTCTTAGAT 2820
CATTATCCAG AGACTGCCAG AAGGTGGGTA GGATGACCTG GGGTTTCAAT TGACTTCTGT 2880
TCCTTGCTTT TAGTTTGTAT AGAAGGGAAG ACCTGCAGTG CACGGTTTCT TCCAGGCTGA 2940
GGTACCTGGA TCTTGGGTTT TTAACCTGAG GGACCCAGAC AAGTGGATCT GCTTGCCAGA 3000
80     GTCTTTTTC CCCCTCCCTG CCACCTCCCC GTGTTTCCAA GTCAGCTTTC CTGCAAGAAG 3060
AAATCCTGGT TAAAAAGTC TTTTGTATTG GGTGAGGAGT TGAATTGGG GTGGGAGGAT 3120
GGATGCAACT GAAGCAGAT GTGGGTGCCC AGATGTGCGC TATTAGATGT TTCTCTGATA 3180
ATGTCCCCAA TCATACCAGG GAGACTGGCA TTGACGAGAA CTCAGGTGGA GGCTTGAGAA 3240
GGCCGAAAGG GCCCTGACC TGCCTGGCTT CCTTAGCTTG CCCCTCAGCT TTGCAAAGAG 3300
85     CCACCTAGG CCCCAGCTGA CCGCATGGGT GTGAGCCAGC TTGAGAACAC TAACTACTCA 3360
ATAAAGCGA AGGTGAAAAA AAAAAAATA AAAAAA

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Seq ID NO: 71 Protein sequence:
Protein Accession #: AAH06529.1

	1	11	21	31	41	51	
	MKTSRRPLI	LKRRRLPLPV	QNAPSETSEE	EPKRSPAQQE	SNQAEASKEV	ABSNSCKFPA	60
5	GIKIINHPTM	PNTQVVAIPN	NANIHSIITA	LTAKGKESGS	SGPNKFILIS	CGGAPTQPPG	120
	LRPQTQTSYD	AKRTEVTLET	LGPKPAARDV	NLPRPPGALC	EQKRETCADG	EAAGCTINNS	180
	LSNIQWLRRM	SSDGLGSRSI	KQEMEEKENC	HLEQRQVKVE	EPSRPSASWQ	NSVSRPPYS	240
	YMAMIQFAIN	STERKRMTLK	DIYTWIEDHF	PYFKHIAPKG	WKNISIRHNS	LHDMFVRETS	300
10	ANGKVSFWTI	HPSANRYLTL	DQVFKQKRP	NPELRRNMTI	KTELPLGARR	KMKPLLPVRS	360
	SYLVPIQFV	NQSLVLPQSV	KVPLPLAASL	MSELARHSK	RVRIAPKVL	AEEGIAPLSS	420
	AGPGKEEKL	FGEGFSPLLP	VQTIKEEIQ	PGEEMPHLAR	PIKVESPPLE	EWSPSPSPFK	480
	ESSHSHWEDS	SQSPTPRPKK	SYSGLRSPTR	CVSEMLVIQH	RERRERSR	RKQHLPLPCV	540
	DEPELLFSEG	PTSTRWAAEL	FFPADSSDPA	SQLSYSQEVG	GPFKTPIKET	LPISSTPSKS	600
15	VLPRTFESWR	LTPPAKVGG	DFSPVQTPQG	ASDPLPDPLG	LMDLSTTPLQ	SAPPLESPQR	660
	LLSSEPLDLI	SVFPNGSSPS	DIDVFKPGSP	EPQVSGLAAN	RSLTEGLVLD	TMNDLSKIL	720
	LDISFPGLDE	DPLGPDNINW	SQFIPELQ				

Seq ID NO: 72 DNA sequence
Nucleic Acid Accession #: U74612.1
Coding sequence: 178-2583

	1	11	21	31	41	51	
25	GGCAGGAGGG	GGACCCGGCC	GGTCCGGCGC	GAGCCCCCGT	CCGGGGCCCT	GGCTCGGCC	60
	CCAGGTTGGA	GGAGCCCGGA	GCCCCTCTTC	GGAGCTACGG	CCTAACGGCG	GCGGCGACTG	120
	CAGTCTGGAG	GGTCCACACT	TGTGATTCTC	AATGGAGAGT	GAAACGCGAG	ATTCTAATG	180
	AAAATAGCC	CCGTCGGGCC	ACTGATTCTC	AAAAGACGGA	GGCTGCCCTT	TCCTGTTCAA	240
30	AATGCCCAAA	GTGAAACATC	AGAGGAGGAA	CCTAAGAGAT	CCCTGCCCCA	ACAGGAGTCT	300
	AATCAAGCAG	AGGCTCCCAA	GGAAGTGGCA	GAGTCCAAC	CTTGCAAGTT	TCCAGCTGGG	360
	ATCAAGATTA	TTAACCACCC	CACCATGCCC	AACACGCAAG	TAGTGGCCAT	CCCCAACAT	420
	GCTAATATTC	ACAGCATCAT	CACAGCACTG	ACTGCCAAGG	GAAAAGAGAG	TGGCAGTAGT	480
	GGGCCCAACA	AATTCATCCT	CATCAGCTGT	GGGGGAGCCC	CAACTCAGCC	TCCAGGACTC	540
35	CGGCTCAAAA	CCCAAAACAG	CTATGATGCC	AAAAGGACAG	AAGTGACCCT	GGAGACCTTG	600
	GGACCAAAAC	CCTCAGCTAG	GGATGTGAAT	CTTCCTAGAC	CACCTGGAGC	CCTTTGCGAG	660
	CAGAAACGGG	AGACCTGTGC	AGATGGTGAG	GCAGCAGGCT	GCACTATCAA	CAATAGCCTA	720
	TCCAACATCC	AGTGGCTTCG	AAAGATGAGT	TCTGATGGAC	TGGGCTCCCG	CAGCATCAAG	780
	CAAGAGATGG	AGAAACAGGA	GAATTTGTAC	CTGGAGCAGC	GACAGGTTAA	GGTTGAGGAG	840
40	CCTTCGAGAC	CATCAGCTGC	CTGGCAGAAC	TCTGTGCTG	AGCGGCCACC	CTACTCTTAC	900
	ATGGCCATGA	TACAATTGCG	CATCAACAGC	ACTGAGAGGA	AGCGCATGAC	TTTGAAAGAC	960
	ATCTATACGT	GGATTGAGGA	CCACTTTCCC	TACTTTAAGC	ACATTGCCAA	GCCAGGCTGG	1020
	AAGAACTCCA	TCCGCCACAA	CCTTTCCCTG	CACGACATGT	TTGTCCGGGA	GACGCTGCTC	1080
	AATGGCAAGG	TCTCCTTCTG	GACCATTAC	CCCAGTGCCA	ACCGCTACTT	GACATTGGAC	1140
45	CAGGTGTTTA	GCACTCTGGA	CCCAGGTGCT	CCACAATTGC	CCGAGCACTT	GGAATCACAG	1200
	CAGAAACGAC	CGAATCCAGA	GCTCCGCCGG	AACATGACCA	TCAAAACCGA	ACTCCCCCTG	1260
	GGCGCACGGC	GGAAGATGAA	GCCACTGCTA	CCACGGGTCA	GCTCATACCT	GGTACCTATC	1320
	CAGTTCCCGG	TGAACCAAGT	ACTGGTGTG	CAGCCCTCGG	TGAAGGTGCC	ATTGCCCTGT	1380
	GCGGCTTCCC	TCATGAGCTC	AGAGCTTGCC	CGCCATAGCA	AGCGAGTCCG	CATTGCCCTC	1440
50	AAGGTTTTTG	GGGAACAGGT	GGTGTGTTGT	TACATGAGTA	AGTTCTTTAG	TGGCGATCTG	1500
	CGAGATTTTG	GATACCCCAT	CACAGCTGTG	TTTAAATTTA	TCTTCTTTTG	TTTATCAGTG	1560
	CTGCTAGCTG	AGGAGGGGAT	AGCTCCTCTT	TCTTCTGCAG	GACCAGGGAA	AGAGGAGAAA	1620
	CTCCTGTTTG	GAGAAGGGTT	TTCTCCTTTG	CTTCCAGTTC	AGACTATCAA	GGAGGAAGAA	1680
	ATCCAGCCTG	GGGAGGAAAT	GCCACACTTA	GCGAGACCCA	TCAAAGTGGA	GAGCCCTCCC	1740
55	TTGGAAGAGT	GGCCCTCCCC	GGCCCCATCT	TTCAAAGAGG	AATCATCTCA	CTCCTGGGAG	1800
	GATTCTGCTC	AATCTCCAC	CCCAGAGCCC	AAGAAGTCCT	ACAGTGGGCT	TAGGTCCCCA	1860
	ACCCGGTGTG	TCTCGGAAT	GCTTGTGATT	CAACACAGGG	AGAGGAGGGA	GAGGAGCCGG	1920
	TCTCGGAGGA	AACAGCATCT	ACTGCCTCCC	TGTGTGGATG	AGCCGGAGCT	GCTCTTCTCA	1980
	GAGGGGCCCA	GTACTTCCCG	CTGGGCCGCA	GAGCTCCCGT	TCCCAGCAGA	CTCCTCTGAC	2040
60	CCTGCTCCCC	AGCTCAGTCA	CTCCCAGGAA	GTGGGAGGAC	CTTTAAGAC	ACCCATTAAG	2100
	GAAACGCTGC	CCATCTCCTC	CACCCGAGC	AAATCTGTCC	TCCCCAGAAC	CCCTGAATCC	2160
	TGGAGGCTCA	CGCCCCAGC	CAAAGTAGGG	GGACTGGATT	TCAGCCAGT	ACAAACCTCC	2220
	CAGGGTGCTC	CTGACCTCCT	GCCTGACCCC	CTGGGGCTGA	TGGATCTCAG	CACCACTCCC	2280
	TTGCAAAATG	CTCCCCCCTC	TGAATCACCG	CAAAGGTCC	TCAGTTCAGA	ACCCTTAGAC	2340
65	CTCATCTCCG	TCCCTTTTGG	CAACTCTTCT	CCCTCAGATA	TAGACGTCCC	CAAGCCAGGC	2400
	TCCCGGAGC	CACAGGTTTC	TGGCCTTGCA	GCCAATCGTT	CTCTGACAGA	AGGCCTGGTC	2460
	CTGGACACAA	TGAATGACAG	CCTCAGCAAG	ATCCTGTCTG	ACATCAGCTT	TCCTGGCCTG	2520
	GACGAGGACC	CAGTGGGCCC	TGACAAATC	AACTGGTCCC	AGTTTATTCC	TGAGCTACAG	2580
	TAGAGCCCTG	CCCTTGCCCC	TGTGCTCAAG	CTGTCCACCA	TCCCGGGCAC	TCCAAGGCTC	2640
70	AGTGACCCCC	AAGCCTCTGA	GTGAGGACAG	CAGGCAGGGA	CTGTTCTGCT	CCTCATAGCT	2700
	CCCTGCTGCC	TGATTATGCA	AAAGTAGCAG	TCACACCTTA	GCCACTGTCT	GGACCTTGTC	2760
	TTCCCCAAGA	GTATCTGATT	CCTCTGCTGT	CCCTGCCAGG	AGCTGAAGGG	TGGGAACAAC	2820
	AAAGGCAATG	GTGAAAAGAG	ATTAGGAACC	CCCCAGCCTG	TTTCCATTCT	CTGCCAGCA	2880
	GTCTCTTACC	TTCCCTGATC	TTTGACGGGT	GGTCCGTGTA	AATAGTATAA	ATTCTCCAAA	2940
75	TTATCCTCTA	ATTATAAATG	TAAAGCTTAT	TCCTTAGATC	ATTATCCAGA	GACTCCAGGA	3000
	AGGTGGGTAG	GATGACCTGG	GGTTTCAATT	GACTTCTGTT	CCTTGCTTTT	AGTTTGTATA	3060
	GAAGGGAAGA	CCTGCAGTGC	ACGGTTTCTT	CCAGGCTGAG	GTACCTGGAT	CTTGGGTTCT	3120
	TCAGTCCAGG	GACCCAGACA	AGTGGATCTG	CTTGCCAGAG	TCCTTTTTCG	CCCTCCCTGC	3180
	CACCTCCCCG	TGTTTCCAAG	TCAGCTTTCC	TGCAAGAAGA	AATCCTGGTT	AAAAAAGTCT	3240
	TTTGATTGCG	GTCAGGAGTT	GAATTTGGGG	TGGGAGGATG	GATGCAACTG	AAGCAGAGTG	3300
80	TGGGTGCCCA	GTCAGTCCCT	ATTAGATGTT	TCTCTGATAA	TGTCCTCAAT	CATACCAGGG	3360
	AGACTGGCAT	TGACGAGAAC	TCAGGTGGAG	GCTTGAGAAG	GCCGAAAGGG	CCCCTGACCT	3420
	GCCTGGCTTC	CTTAGCTTGC	CCCTCAGCTT	TGCAAGAGAG	CACCTTAGGC	CCCAGCTGAC	3480
	CGCATGGGTG	TGAGCCAGCT	TGAGAACACT	AACTACTCAA	TAAAGCGGAA	GGTGGACAAA	3540
85	AAAAAAAAAA	AAAAA					

Seq ID NO: 73 Protein sequence:
Protein Accession #: AAC51128.1

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1      11      21      31      41      51
|      |      |      |      |      |
5  MKTSPRRPLI LKRRRLPLPV QNAPSETSEE EPKRSPAQQE SNQAEASKEV AESNSCKPFA 60
   GIKIINHPTM PNTQVVAIPN NANIHSIITA LTAKGKESGS SGPKNKFILIS CGGAPTQPPG 120
   LRPTQTSTSD AKRTEVTLET LGPKPAARDV NLPRPPGALC EQKRETCADG EAAGCTINNS 180
   LSNIQWLRKM SSDGLGSRSI KQEMEEKENC HLEQRQVKVE EPSRPSASWQ NSVSRPPYS 240
   YMAMIQFAIN STERKMTLK DIYTWIEDHF PYFKHIAKPG WKNSIRHNL S LHDMPVRETS 300
10  ANGKVSFWTI HPSANRYLTL DOVFKPLDPG SPQLPEHLES QQKRPNPPELR RNMTIKTELP 360
   LGARRKMKPL LPRVSSYLVP IQFPVNQSLV LQPSVKVPLP LAASLMSEL ARHSKRVRIA 420
   PKVFGQVVP GYMSKFFSGD LRDFGTPITS LFNFIPLCLS VLLAEEGIAP LSSAGPGKEE 480
   KLLFGEFGFP LFPVGTIKEE EIQGEEMPH LARPIKVESP PLEEWPSAP SFKEESSHSW 540
   EDSSQSPTPR PKKSYSLGRS PTRCVSEMLV IQHRERRERS RSRKQHLPL PCVDEPELFL 600
15  SEGPSTSRWA AELPPADSS DPASQLSYSQ EVGGPFKTP I KETLPISSTP SKSVLPRTPE 660
   SWRLTPPARV GGLDFSPVQT SQGASDPLPD PLGLMDLSTT PLQSAPPLES PQRLLSSEPL 720
   DLISVFFGNS SPSDIDVFKP GSPEPQVSGL AANRSLTEGL VLDTMNDSL S KILLDISPPG 780
   LDEDPLGPDN INWSQFIPEL Q

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20 Seq ID NO: 74 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 111-416

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1      11      21      31      41      51
|      |      |      |      |      |
25  GGAAGAGACC AGGCTGAGCC TTATAAAGGA CTGCTCTTTG TCCAAACACA CACATCTCAC 60
   TCATCCTTCT ACTCGTGACG CTTCAGAGCT CTGGCTTTT GAAAGCAAAG ATGAGCAAACA 120
   CTCAAGCTGA GAGGTCCATA ATAGGCATGA TCGACATGTT TCACAAATAC ACCAGACGTG 180
   ATGACAAGAT TGAGAAGCCA AGCCTGTGTA CGATGATGAA GGAGAACTTC CCCAACTTCC 240
   TTAGTGCCCTG TGACAAAAG GGCACAAATT ACCTCGCCGA TGTCTTTGAG AAAAAGGACA 300
30  AGAATGAGGA TAAGAAGATT GATTTTCTG AGTTTCTGTC CTGCTGGGA GACATAGCCA 360
   CAGACTACCA CAAGCAGAGC CATGGAGCAG CGCCTGTTC CGGGGCGAGC CAGTGACCCA 420
   GCCCCACCAA TGGGCTCCA GAGACCCAG GAACAATAA ATGTCTTCTC CCACCAGA

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35 Seq ID NO: 75 Protein sequence:
Protein Accession #: Eos sequence

```

1      11      21      31      41      51
|      |      |      |      |      |
40  MSNTQAERSI IGMIDMFHKY TRDDKIEKP SLLTMMKENF PNFLSACDKK GTNYLADVFE 60
   KKDKNEDKKI DFSEFLSLLG DIATDYHKQS HGAAPCSGGS Q

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45 Seq ID NO: 76 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 111-416

```

1      11      21      31      41      51
|      |      |      |      |      |
50  GGAAGAGACC AGGCTGAGCC TTATAAAGGA CTGCTCTTTG TCCAAACACA CACATCTCAC 60
   TCATCCTTCT ACTCGTGACA CTTCAGAGCT CTGGCTTTT GAAAGCAAAG ATGAGCAAACA 120
   CTCAAGCTGA GAGGTCCATA ATAGGCATGA TCGACATGTT TCACAAATAC ACCGACGTG 180
   ATGGCAAGAT TGAGAAGCCA AGCCTGTGTA CGATGATGAA GGAGAACTTC CCCAACTTCC 240
   TCAGTGCCCTG TGACAAAAG GGCATACATT ACCTCGCCGA TGTCTTTGAG AAAAAGGACA 300
55  AGAATGAGGA TAAGAAGATT GATTTTCTG AGTTTCTGTC CTGCTGGGA GACATAGCCG 360
   CAGACTACCA CAAGCAGAGC CATGGAGCGG CGCCTGTTC TGGGGGAGC CAGTGATCCA 420
   GCCCCACCAA GGGGCTCCA GAGACCCAG GAACAATAA TGTCTCTCTC CACCAGA

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60 Seq ID NO: 77 Protein sequence:
Protein Accession #: XP_048124.1

```

1      11      21      31      41      51
|      |      |      |      |      |
65  MSNTQAERSI IGMIDMFHKY TGRDGKIEKP SLLTMMKENF PNFLSACDKK GIHYLATVFE 60
   KKDKNEDKKI DFSEFLSLLG DIAADYHKQS HGAAPCSGGS Q

```

70 Seq ID NO: 78 DNA sequence
Nucleic Acid Accession #: Z73678.1
Coding sequence: 253-2433

```

1      11      21      31      41      51
|      |      |      |      |      |
75  GGGGTGGTGC AGGGCAGGGG TGGTATATCC TGTCTGACGG AGGGCGGGCC TCGCCAGTGC 60
   CAGAGAGGGA CGAACCAGGG TGGAGCGGCC AGGAGCAGCT GCAGGGAGCC CTCACGCGGA 120
   CCTCGCACTC TATGGCCGTA GGGAGCCGCT GAGAGCGAGA AGAGCACGCT CCTGCCCGCC 180
   CGCTGCACCG CACCTCGCCT CGCCTCTCTG CTCTCCTAGG CCCCAGCGCG GCGCCACCCG 240
   CCTCCGCGCA CCATGAACCA CTCGCCGCTC AAGACCGCCT TGGCGTACGA ATGCTTCCAG 300
   GACCAGGACA ACTCCACGTT GGCTTTGCCG TCGGACCAAA AGATGAAAAC AGGCACGTCT 360
   GGCAAGGAGC GCGTGACGAG GCAGGTGATG ATGACCGTCA AGCGGCAGAA GTCCAAAGTCT 420
80  TCCAGTCTGT CCACCTGAG CCACTCCAAT CGAGGTCCA TGTATGATGG CTGGCTGAC 480
   AATTACAAC ATGGGACCAC CAGCAGGAGC AGCTACTACT CCAAGTCCA GGCAGGGAAT 540
   GGCTCATGGG GATATCCGAT CTACAATGGA ACCCTCAAGC GGGAGCCTGA CAACAGGCGC 600
   TTCAGCTCTT ACAGCCAGAT GGAGAACTGG AGCCGGCACT ACCCCGCGGG CAGCTGTAAC 660
85  ACCACCGGCG CAGGCAGCGA CATCTGCTTC ATGCAGAAAA TCAAGGCGAG CCGCAGTGAG 720
   CCGCACTCT ACTGTGACCC ACGGGGCACC CTGCGCAAGG GCACGCTGGG CAGCAAGGGC 780
   CAGAGAGCCA CCCAGAACCG CTACAGCTTT TACAGCACCT GCAGTGGTCA GAAGGCCATA 840
   AAGAAGTGCC CTGTGCGCCC GCCCTCTTGT GCCTCCAAGC AGGACCCTGT GTATATCCCG 900

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	CCCATCTCCT	GCAACAAGGA	CCTGTCTCTT	GGCCACTCTA	GGGCCAGCTC	CAAGATCTGC	960
	AGTGAGGACA	TCGAGTGACG	TGGGCTGACC	ATCCCCAAGG	CTGTGACGTA	CCTGAGCTCC	1020
	CAGGATGAGA	AGTACCAGGC	CATTGGGGCC	TATTACATCC	AGCATACCTG	CTTCCAGGAT	1080
5	GAATCTGCCA	AGCAACAGGT	CTATCAGCTG	GGAGGCATCT	GCAAGCTGGT	GGACCTCCTC	1140
	CGCAGCCCCA	ACCAGAACGT	CCAGCAGGCC	GCGGCAGGGG	CCCTGCGCAA	CCTGGTGTTC	1200
	AGGAGCACC	CCAACAAGCT	GGAGACCCGG	AGGCAGAAATG	GGATCCGCGA	GGCAGTCAGC	1260
	CTCCTGAGGA	GAACCGGGAA	CGCCGAGATC	CAGAAGCAGC	TGACTGGGCT	GCTCTGGAAC	1320
	CTGTCTTCCA	ATGATGAGCT	GAAGGAGGAA	CTCATTGCGG	ACGCCCTGCC	TGTTCTGGCC	1380
10	GACCGGCTCA	TCATTCCCTT	CTCTGGCTGG	TGCGATGGCA	ATAGCAACAT	GTCCCGGGAA	1440
	GTGGTGGACC	CTGAGGTCTT	CTTCAATGCC	ACAGGCTGCT	TGAGGAACCT	GAGCTCGGCC	1500
	GATGACGGCC	GCCAGAGCTC	GCGTAACTAC	TCAGGGCTCA	TTGATTCCCT	CATGGCCTAT	1560
	GTCCAGAACT	GTGTAGCGGC	CAGCCGCTGT	GACGACAACT	CTGTGGAAAA	CTGCATGTGT	1620
	GTTCTGCACA	ACCTCTCCTA	CCGCCTGGAC	GCCGAGGTGC	CCACCCGCTA	CCGCCAGCTG	1680
15	GAGTATAACG	CCCGCAACGC	CTACACCGAG	AAGTCTCTCA	CTGGCTGCTT	CAGCAACAAG	1740
	AGCGACAAGA	TGATGAACAA	CACTATGAC	TGCCCCCTGC	CTGAGGAAGA	GACCAACCCC	1800
	AAGGGCAGCG	GCTGGTTGTA	CCATTGAGAT	GCCATCCGCA	CCTACCTGAA	CCTCATGGGC	1860
	AAGAGCAAGA	AAGATGCTAT	CCTGGAGGCC	TGTGCTGGTG	CCCTGCAGAA	CCTGACAGCC	1920
	AGCAAGGGGC	TGATGTCCAG	TGGCATGAGC	CAGTTGATTG	GGCTGAAGGA	AAAGGGCCTG	1980
20	CCACAAATTC	CCCGCTCTCT	GCAATCTGGC	AACTCTGATG	TGGTGGGGTC	CGGAGCCTCC	2040
	CTCCTGAGCA	ACCATGTCGG	CCACCCTCTG	CTGCACAGAG	TGATGGGGAA	CCAGGTGTTC	2100
	CCGGAGGTGA	CCAGGCTCCT	CACCAGCCAC	ACTGGCAATA	CCAGCAACTC	CGAAGACATC	2160
	TTGTCTCTCG	CTGTCTACAC	TGTGAGGAAC	CTGATGGCCT	CGCAGCCACA	ACTGGCCAAG	2220
	CAGTACTTCT	CAGCAGCAT	GCTCAACAAC	ATCATCAACC	TGTGCCGAAG	CAGTGCCTCA	2280
25	CCCAAGGCCG	CAGAAGCTGC	CCGGCTTCTC	CTGTCTGACA	TGTGGTCCAG	CAAGGAACTG	2340
	CAGGGTGTCC	TCAGACAGCA	AGGTTTCGAT	AGGAACATGC	TGGGAACCTT	AGCTGGGGCC	2400
	AACAGCCTCA	GGAACTTCAC	CTCCGATTTC	TAAGAAGAGA	CTGTCCAAGC	AAGTTAGGCT	2460
	TGCAGGAAGA	TATGACCCAG	CTGAGAAGCC	CTCAGGCCTC	GCTGGATGGG	GTTTTCTGTC	2520
	CATCTCTGTC	AGTATTTGGG	AAAGTTTACA	AGAAACTGAG	AAGAAACCTA	AAAACCTGTG	2580
30	ATAGTGGAAA	CTTTTTTAGA	TTTTTTTTTT	CCTTGGGGAA	ACTGGCAGGC	AATGGGGGTT	2640
	AGGGAGGTTG	GGGCGGGGGG	GGCTTTCTTG	AGTTAAAGGG	GCTTATATGT	GATGTCAATA	2700
	TTTCTCTCTC	TGAGAAATGG	TATATATATG	TGTCTAATGT	AAGTGTGTGC	ATGCATGTGC	2760
	GGGTGATGTG	TGTGTGTGTG	GAGTGTCTTA	AAGCATAACC	ACAAACTGCA	AAAAGCTAGG	2820
	TAAGCTATTT	TGTTGCAGCT	CATAAGGTGG	TGAAAAGGAC	TCTCTGTGTG	TTCTTACTCA	2880
35	TAGGCAAGGA	CAACATGTGC	TTTTTGGTGA	GCTGCTCATA	ATTCTGAAA	TGTGTGGTGC	2940
	CAGGCAAGG	GGCCATCAC	TGCAGTCAGG	CCCTCAGAGG	AGTCTGCGAC	GCTTCTTACC	3000
	AGTGGTCTCC	AAGGGTGCAG	GAGTAACTGG	GGCTGGGCCA	GCCTCCCCCC	TTACAAGGCT	3060
	GCCTTCCACG	AAGGGAGGTC	TGGTGTATCT	CATGGGAGAA	TCTGGGGTGT	CTGTAGTGTG	3120
	ACCCCTCCAG	CAGCCGCCAC	AGGACTGAGG	TGGGTAGGT	GTGAGGTTCC	AGAGGACAGC	3180
40	AGGACACTCT	CGCATACTTT	GCCAAATGAG	GCCTGCTCAG	AGGAGTAGGA	GCTGAAAGAT	3240
	GGTGCCTTCC	ACCCCTCTGG	GCTGTGTGCC	CATCAGAGCA	GGCTCAGCCT	GCAAGGGCCC	3300
	TGCAITCAGA	GGTCTTGTAA	TCTACTTGT	GCAGGAGAAA	GAAGGTAAAA	AATGATTTTT	3360
	TTAAGAAAAG	CTATTTTATT	GCAGCTCTTT	CCCAAGAGCT	GTCTGGGAA	TGGCTGGTCT	3420
	TCATATTTCC	AGTGAGAGG	GGAAACAATG	GGGCTGGGCA	TATACCTATT	CCGGCTTCTA	3480
45	GTGGGATGGA	TTGGGGTCT	AGAAATTAAC	CAGGAAGATG	TTTCCACCAA	GCCTGCTGTG	3540
	AGTCAATTGA	GGGAGTGT	GGGTCCCAGG	AGACTTGGAC	GGGGGGAGTT	TGGGTAGACT	3600
	AGGAAAGGAA	AGTGCCATAT	CAGGGTACCG	GTACCGGCAA	GCTCACATCT	CAGCCAGGGG	3660
	CCATGCCCCA	CTTCCCTGA	CCCCAGCTGT	CTTGTCTCCA	CTCTGTGAAA	CCCAAGGGG	3720
	ATGTGATAAA	CAGGGCTATT	AGGGGTATCA	GCCACGTCGA	GCCCCCAGAC	TCGTGTCACT	3780
50	TCAGACCCAG	AGCAGCAGGA	GGGCTCCCGA	GGGCTTATG	AGAAAACTG	TGTGGACATC	3840
	CCTTGGTGTA	CACCTAAGCA	GAGCAGAGCC	CAGCGCTCCC	AAGCCTTCTC	CCTTCCAGCT	3900
	TCTACCTCCA	TGCTAGCATT	GCTGGTGT	GAGAGGAATT	AACCTCTCTG	TCTGTGCCCT	3960
	TCCTTAGAAG	AATATAAGAT	GCTCTCTCTC	CTACCCCTT	CTCAGCCTCC	TCCCAAGTCT	4020
	TCTCTTCTG	CACCACCCCC	GAGTCCAAAC	CCACCTCTTG	CCCCAGCATT	CAGGCTGGAA	4080
55	AACTACTGAT	TGGACTCAGT	ATGACAACCTG	AGATGGGGGA	AGCCAGACAT	GTGAGGACGC	4140
	TGTCTCCGA	GAGGTGTCTC	CGGCTGTAG	CCAGCTGTGC	TGTGGTGTG	TGGGTCTGTC	4200
	ATACCTCTCC	TGCTTCTCT	TCACACTGGG	AGGCCCACTC	CTGGCTCACC	TCTCCCTCTC	4260
	AGGGACCCAC	GTGGGAGCCT	GGATCCCTGG	ACTGTCTCTG	GCATAGGTTT	CAGGGGCCTC	4320
	CTTGTGTGTC	ATCAGAACCC	AGAGGAATTC	TTCTCTTAAA	AAATACGTAT	GGCATACCAA	4380
60	TCGTGCGGG	CGAGTGTCT	AAGCACTTAG	ACTACATCAG	GGAAGAACAC	AGACCAATC	4440
	CCCGTCTCTA	TGCGGCTTAT	GTTTTCTGGA	GGAAAGTGG	GACACAAGTC	CTTGGCTTTA	4500
	GGGCTCCCCC	GGCTGGGGG	TGTGAGTCC	GGTCAGGGCG	GGAGGGGAAA	TGCACCGCTG	4560
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	GCATCCCTCT	GCCTCATGTT	CCTCCACCT	TCAAAGAATG	AAGAGCCCCA	TGGGCCAGC	4680
65	CCCTGCCCTC	GGAAACAGGC	AGCCTTCCAG	ACCTCAGGGG	CTGAGGCAGA	CTATTAGGGC	4740
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	CTGACCCAGG	CCTGTCACTT	TGAGAGGGGC	AAAACCTGAGA	GGGGCTTTTC	CTAGAGAAAG	4860
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	ATTGGCCTCA	CACCTAGCCTA	GGCCAATGCC	CAAAATAAGG	AGTTCCAATT	TGGGGCCAAA	4980
70	TGAGGAAGGA	CACAGACTCT	GCCCTGGGAT	CTCCTGTGCT	AGCGGCCAAT	GACAAATCCA	5040
	GTCATTGGCC	ACCAGCCACC	TCTGCAGTGG	GGACCACACT	AGCAGCCCTG	ACTCCACACT	5100
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	ACTGGCTGGG	AGGACCAAGA	CTGCGGCTGG	GGTGGGCAGG	GAAGGGAAGC	CGGGGGCTGC	5220
	TGTGAGGGAT	CTTGGAGCTT	CCCTGTAGCC	CACCTTCCCC	TTGCTTCATG	TTTGTAGAGG	5280
75	AACTTGTGTC	CGGCCAGGCC	CAGTTTCTCT	GTGTGATACA	CTAATGTATT	TGCTTTTTTT	5340
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Seq ID NO: 79 Protein sequence:
Protein Accession #: CAA98022.1

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	SQMNWSRHY	PRGSCNTTGA	GSDICFMQKI	KASRSEPDLY	CDPRGTLRKG	TLGSKGQKTT	180
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	ECSGLTIPKA	VQYLTIQDEK	YQAIQAYYIQ	HTCFQDESAK	QQVQLGGIC	KLVDLLRSPN	300
	QNVQAAAGA	LRNLVFRSTT	NKLETRRQNG	IREAVSLRR	TGNAEIQKQL	TGLLWNLST	360

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 RNAYTEKSST GCFPSNKSDBM MNMNYDCPLP EBETNPKGSG WLYHSDAIR YLNLGMKSKF 540
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Seq ID NO: 80 DNA sequence
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Seq ID NO: 81 Protein sequence:
 Protein Accession #: NP_006507.1

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 GNKDLWPLLL SIIFIPALLQ CIVLPFCPE PRFLINRNE ENRAKSVLKK LRGTADVTHD 240
 75 LQEMKEESRQ MMREKKVTIL ELFRSPAYRQ PILIAVVLQL SQQLSGINAV FYYSTSIPEK 300
 AGVQPPVYAT IGSIVNTAP TVVSLFVVER AGRRTLHLIG LAGMAGCAIL MTIALALLEQ 360
 LPWMSYLSIV AIFGFVAFPE VGGPIPWFI VAELEFSQGR PAIAVAFGS NWTNPFIVGM 420
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Seq ID NO: 82 DNA sequence
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Protein Accession #: AAH01291

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Seq ID NO: 85 Protein sequence:
Protein Accession #: NP_075044.1

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60	SAWFLQHAQ	NTHGLRIYLE	SEHGSPLTPR	VGIPSGLGA	CPSQPPLHGI	HIADNNPFNL	240
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65	ENGDEEEED	DEEEEEEED	EEBELTESER	VDYGFGLSLE	AARHHENSSR	GAVVGVGDES	540
	RALPDVMQGM	VLSSMQHFSE	AFHQVLGEKH	KRGLHAEAG	HRDTCDEDSV	AGESDRIDDG	600
	TVNNGRCSPG	ESASGGLSKK	LLLGSPPSL	PFSKRIKLEK	EFDLPPATMF	NTENVYSQWL	660
	AGYAASRLQK	DPFLSFGDSR	QSPFASSEH	SENGSLRFS	TPPGELDGGI	SGRSGTSGGG	720
70	STPHISGPGT	GRPSSKEGRR	SDTCEYCGKV	FKNCSNLTVH	RRSHTGERPY	KCELCNYACA	780
	QSSKLTRHMK	THGQVGKDVY	KCEICKMPFS	VYSTLEKHMK	KWHSRDLNN	DIKTE	

Seq ID NO: 86 DNA sequence
Nucleic Acid Accession #: XM_035292.2
Coding sequence: 53-1576

80	1	11	21	31	41	51	
	GCTCGCTGGG	CCGCGCTCC	CGGGTGTCCC	AGGCCCGGCC	GGTGCGCAGA	GCATGGCGGG	60
	TGCGGGCCCG	AAGCGCGCG	CGCTAGCGGC	GCCGGCGGCC	GAGGAGAAGG	AAGAGCGCGG	120
	GGAGAAGATG	CTGGCGGCCA	AGAGCGCGGA	CGGCTCGCGG	CCGGCAGGCG	AGGGCGAGGG	180
	CGTGACCTGT	CAGCGGAACA	TCACGCTGCT	CAACGGCGTG	GCCATCATCG	TGGGGACCAT	240
	TATCGGCTCG	GGCATCTTCG	TGACGCCAC	GGCGTGCTC	AAGGAGGCG	GCTCGCGGG	300
	GCTGGCGCTG	GTGGTGTGGG	CCGCGTGGG	CGTCTTCTCC	ATCGTGGGCG	CGCTCTGCTA	360
85	CGCGGAGCTC	GGCACCACCA	TCTCCAAATC	GGCGGGCGAC	TACGCTTACA	TGCTGGAGGT	420
	CTACGGCTCG	CTGCCCGCT	TCTCAAGCT	CTGGATCGAG	CTGCTCATCA	TCCGGCTTC	480
	ATCGCAGTAC	ATCGTGGCCC	TGGTCTTCG	CACCTACCTG	CTCAAGCCGC	TCTTCCCCAC	540

CTGCCCGGTG CCGGAGGAGG CAGCCAAGCT CGTGGCCTGC CTCTGCGTGC TGCTGCTCAC 600
 GGCCGTGAAC TGCTACAGCG TGAAGGCCGC CACCCGGGTC CAGGATGCCT TTGCCGCGC 660
 CAAGCTCCTG GCCTCGGCCG TGATCATCCT GCTGGGCTTC GTCCAGATCG GGAAGGGTGA 720
 TGTGTCCAAT CTAGATCCCA ACTTCTCATT TGAAGGCACC AAATCGGATG TGGGGAACAT 780
 TGTGCTGGCA TTATACAGCG GCCTCTTTGC CTATGGAGGA TGGAAATTACT TGAATTTCTG 840
 CACAGAGGAA ATGATCAACC CCTACAGAAA CCTGCCCTCG GCCATCATCA TCTCCTCGCC 900
 CATCGTGACG CTGGGTGACG TGCTGACCAA CCTGGCCTAC TTCACCACCC TGTCCACCGA 960
 GCAGATGCTG TCGTCCGAGG CCGTGGCCGT GGACTTCGGG AACTATCACC TGGGCGTCAT 1020
 GTCCTGGATC ATCCCGTCT TCGTGGGCCT GTCCTGCTTC GGCTCCGTC ATGGGTCCCT 1080
 GTTCACATCC TCCAGGCTCT TCTTCGTGGG GTCCCGGAA GGCCACCTGC CCTCCATCCT 1140
 CTCATGATC CACCCACAGC TCCTCACCCC CGTGCCGTCC CTCGTGTTCA CGTGTGTGAT 1200
 GACGCTGCTC TACGCTTCT CCAAGGACAT CTCTCCGTC ATCAACTTCT TCAGCTTCTT 1260
 CAACTGGCTG TCGGTGGCCC TGGCCATCAT CGGCATGATC TGGCTGCGCC ACAGAAAGCC 1320
 TGAGCTTGAG CGGCCATCA AGGTGAACCT GGCCCTGCCT GTGTTCTTCA TCCTGGCCTG 1380
 CCTCTTCTG ATGCGGTCT CTCTCTGGAA GACACCCGTG GAGTGTGGCA TCGGCTTAC 1440
 CATCATCTC AGCGGGCTGC CCGTCTACTT CTTCGGGGTC TGGTGGAAAA ACAAGCCCAA 1500
 GTGGCTCTC CAGGGCATCT TCTCCACGAC CGTCTGTGT CAGAAGCTCA TGCAGGTGGT 1560
 CCCCAGGAG ACATAGCCAG GAGCCGAGT GGCTGCCGGA GGAGCATGC

Seq ID NO: 87 Protein sequence:
 Protein Accession #: XP_035292.2

1 11 21 31 41 51
 | | | | |
 MAGAGPKRRA LAAPAAEKE EAREKMLAAK SADGSAPAGE GEGVTLQRNI TLINGVAIIV 60
 GTIIGSGIFV TPTGVLKEAG SPGLALVWVA ACGVFSIVGA LCYAEGLTTI SKSGGDYAYM 120
 LEVYGSPLPAF LKLWIELLII RPSSQYIVAL VFATYLLKPL PFTCPVPEEA AKLVAACLVL 180
 LLTAVNCYSV CAATRVQDAF AAKLLALAL IILLGFVQIG KGDVSNLDPN FSFEGTKLDV 240
 GNIVLALYSG LFAYGGWNYL NFTEEMINP YRNLPALIII SLPIVTLVYV LTNLAYFTTL 300
 STEQMLSSEA VAVDFGNHYL GVMSWIIPVF VGLSCFGSVN GSLFTSSRLF FVGSREGHLP 360
 SILSMIHQPL LTPVPSLVFT CVMTLLYAFS KDIFSVINFF SFFNWLCLVAL AIGMIWLRLH 420
 RKPELERIK VNLALPVFFI LACLFLIAVS FWKTPVECGI GPTIILSLGP VYFPGVWVK 480
 KPKWLLQGIF STTVLCQKLM QVVPQET

Seq ID NO: 88 DNA sequence
 Nucleic Acid Accession #: NM_005268.1
 Coding sequence: 168-989

1 11 21 31 41 51
 | | | | |
 TAAAAAGCAA AAGAATTGCG GGCCGCGTCG ACACGGGCTT CCCCAGAAAC CTTCCCCGCT 60
 TCTGGATATG AATTCAAGC TGCTTGCTGA GTCCATATGC CGGCTGCTGG GAGCCAGGAG 120
 AGCCCTGAGG AGTAGTCACT CAGTAGCAGC TGACGCGTGG GTCCACCATG AACTGGAGTA 180
 TCTTTGAGGG ACTCCTGAGT GGGGTCAACA AGTACTCCAC AGCCTTTGGG CGCATCTGGC 240
 TGTCTCTGGT CTTTCATCTC CGCGTGCTGG TGTACCTGGT GACGGCCGAG CGTGTGTGGA 300
 GTGATGACCA CAAGGCTTC GACTGCAATA CTCGCCAGCC CGGCTGTCC AACGCTGCT 360
 TTGATGAGTT CTTCCCTGTG TCCCATGTGC GCCTCTGGGC CCTGCAGCTT ATCCTGGTGA 420
 CATGCCCTC ACTGCTCGTG GTCATGCAAG TGGCCTACCG GGAGGTTTCA GAGAAGAGGC 480
 ACCGAGAAAG CCAATGGGGAG AACAGTGGGC GCCTCTACCT GAACCCCGGC AAGAAGCGGG 540
 GTGGGCTCTG GTGGACATAT GTCTGCAGCC TAGTGTTCAA GGCAGCGTG GACATCGCCT 600
 TTCTCTATGT GTTCCACTCA TTCTACCCCA AATATATCCT CCTCCTGTG GTCAAGTGCC 660
 ACGCAGATCC ATATCCCAAT ATAGTGGACT GCTTCATCTC CAAGCCCTCA GAGAAGAACA 720
 TTTTCAACCT CTTTCATGGT GCCACAGCTG CCATCTGCAT CCTGCTCAAC CTCGTGGAGC 780
 TCATCTACCT GGTGAGCAAG AGATGCCACG AGTGCCTGGC AGCAAGGAAA GCTCAAGCCA 840
 TGTGCACAGG TCAATACCCC CACGGTACCA CCTCTTCTG CAAACAAGAC GACCTCCTTT 900
 CGGGTGACCT CATCTTCTG GGTCTCAGCA GTTCATCTCC TCTCTTACCA GACCGCCCCC 960
 GAGACCATGT GAAGAAAAC ATCTTGTGAG GGGCTGCTCG GACTGTGCTG GCAGGTGGG 1020
 CCTGGATGGG GAGGCTCTAG CATCTCTCAT AGGTGCAACC TGAGAGTGGG GGAGCTAAGC 1080
 CATGAGGTAG GGGCAGGCAA GAGAGAGGAT TCAGACGCTC TGGGAGCCAG TTCCTAGTCC 1140
 TCAACTCCAG CCACCTGCCC CAGCTCGACG GCACTGGGCC AGTTCCCCCT CTGCTCTGCA 1200
 GCTCGGTTTC CTTTCTAGA ATGGAATAG TGAGGGCCAA TGC

Seq ID NO: 89 Protein sequence:
 Protein Accession #: NP_005259.1

1 11 21 31 41 51
 | | | | |
 MNWSIFEGLL SGVKNYSTAF GRINLSLVFI FRVLVYLVT A ERVWSDDHKD PDCNTRQPGC 60
 SNVCFDEFPF VSHVRLWALQ LILVTCPSLL VVMHVAYREV QEKHREAHG ENSGRLYLNP 120
 GKRRGLNWT YVCSLVFKAS VDIAFLYVFH SFYPKYILPP VVKCHADPCP NIVDCFISKP 180
 SEKNIFTLFM VATAAICILL NLVELIYLV S KRCHECLAAR KAQAMCTGHH PHGTTSSCKQ 240
 DDLLSGDLIF LGSDSHPLL PDRPRDHVKK TIL

Seq ID NO: 90 DNA sequence
 Nucleic Acid Accession #: NM_002391.1
 Coding sequence: 26-457

1 11 21 31 41 51
 | | | | |
 CGGGCGAAGC AGCGCGGCA GCGAGATGCA GCACCGAGGC TTCCTCCTCC TCACCTCCT 60
 CGCCCTGCTG GCGCTCACT CCGCGTCCG CAAAAGAAA GATAAGGTGA AGAAGGGCGG 120
 CCGGGGAGC GAGTGCCTG AGTGGGCTG GGGGCCCTG ACCCCAGCA GCAAGGATTG 180
 CGGCGTGGT TTCCGCGAGG GCACCTGCGG GGGCCAGACC CAGCGCATCC GGTGCGAGGT 240
 GCCCTGCAAC TGGAGAAGG AGTTTGGAGC CGACTGCAAG TACAAGTTTG AGAACTGGGG 300
 TCGTGTGAT GGGGCGACAG GCACCAAGT CCGCCAAGGC ACCCTGAAGA AGGCGCGCTA 360

CAATGCTCAG TGCCAGGAGA CCATCCGCGT CACCAAGCCC TGCACCCCA AGACCAAAGC 420
 AAAGGCCAAA GCCAAGAAAG GGAAGGGAAA GGACTAGACG CCAAGCCTGG ATGCCAAGGA 480
 GCCCTGGTGG TCACATGGGG CCTGGCCACG CCCTCCCTCT CCCAGGCCCG AGATGTGACC 540
 CACCAAGTGC TTCTGTCTGC TCGTTAGCTT TAATCAATCA TGCCCTGCCT TGTCCCTCTC 600
 ACTCCCAAGC CCAACCCCTA AGTGCCCAAA GTGGGGAGGG ACAAGGGATT CTGGGAAGCT 660
 TGAGCCTCCC CCAAGGAAT GTGAGTCCCA GAGCCCGCTT TTGTTCTTCC CCACAATTCC 720
 ATTACTAAGA AACACATCAA ATAAACTGAC TTTTCCCCC CAATAAAAGC TCTTCTTTT 780
 TAATAT

Seq ID NO: 91 Protein sequence:
 Protein Accession #: NP_002382.1

1 11 21 31 41 51
 | | | | |
 MQHRGFLLLT LLALLALTSA VAKKKDKVKK GGPSECAEW AWGPCTPSSK DGVGVFREGT 60
 CGAQTRIRRC RVPNCNWKKEF GADCKYKFEN WGACDGGTGT KVRQGLTKKA RYNAQCQSTI 120
 RVTKPCTPKT KAKAKAKKKG GKD

Seq ID NO: 92 DNA sequence
 Nucleic Acid Accession #: NM_005130.1
 Coding sequence: 98-802

1 11 21 31 41 51
 | | | | |
 CTCTACCTGA CACAGCTGCA GCCTGCAATT CACTCCCACT GCCTGGGATT GCACTGGATC 60
 CGTGTGCTCA GAACAAGGTG AACGCCACGC TGCAGCCATG AAGATCTGTA GCCTCACCTC 120
 GCTCTCCTTC CTCTACTTGG CTGCTCAGGT GCTCCTGGTG GAGGGGAAAA AAAAAAGTGAA 180
 GAATGACTTC CACAGCAAAAG TGGTCTCAGA ACAAAAGGAC ACTCTGGGCA ACACCCAGAT 240
 TAAGCAGAAA AGCAGGCCCG GGAACAAAGG CAAGTTTGTC ACCAAAGACC AAGCCAACCTG 300
 CAGATGGGCT GCTACTGAGC AGGAGGAGGG CATCTCTCTC AAGGTTGAGT GCACTCAATT 360
 GGACCATGAA TTTTCCCTGT TCTTTGCTGG CAATCCAACC TCATGCCTAA AGCTCAAGGA 420
 TGAGAGAGTC TATTGGAAC AAGTTGCCCG GAATCTGCGC TCACAGAAAG ACATCTGTAG 480
 ATATTCCAAG ACAGCTGTGA AAACCAGAGT GTGCAGAAAG GATTTTCCAG AATCCAGTCT 540
 TAAGCTAGTC AGCTCCATC TATTGGGAA CACAAAGCCC AGGAAGGAGA AAACAGAGAT 600
 GTCCCCCAGG GAGCACATCA AGGGCAAAGA GACCACCCCT TCTAGCCTAG CAGTGACCCA 660
 GACCATGGCC ACCAAAGCTC CCGAGTGTGT GGAGGACCCA GATATGGCAA ACCAGAGGAA 720
 GACTGCCCTG GAGTTCTGTG GAGAGACTTG GAGCTCTCTC TGCACATTCT TCCTCAGCAT 780
 AGTGCAGGAC ACGTCATGCT AATGAGGTCA AAAGAGAAGC GGTTCCTTTA AGAGATGTCA 840
 TGTGTAAGT CCCTCTGTAT ACTTTAAAGC TCTCTACAGT CCCCCAAAAA TATGAACCTT 900
 TGTGCTTAGT GAGTTCAGACG AAATATTAA ACAAGTTTGT TATTTTGTG TTTTGTGTTT 960
 TGGAAATTTG CTTATTTTTC TTGGATGCGA TGTTCAGAGG CTGTTTCTCT CAGCATGTAT 1020
 TTCCATGGCC CACACAGCTA TGTGTTTGTG CAGCGAAGAG TCTTTGAGCT GAATGAGCCA 1080
 GAGTGATAAT TTCAGTGCAA CGAACTTTCT GCTGAATTAA TGTAATAAA ACTCTGGGTG 1140
 TTTTCAAAA AAAAAAAA AAA

Seq ID NO: 93 Protein sequence:
 Protein Accession #: NP_005121.1

1 11 21 31 41 51
 | | | | |
 MKICSLTLLS FLLLAQVLL VEGKKVKNG LHSKVVSEK DTLGNTQIKQ KSRPGNKGKP 60
 VTKDQANCRW ALLQEEGIS LKVBCTQLDH EFSCVFAGNP TSCLKLKDER VYWKQVARNL 120
 RSQKDICRYS KTAVKTRVCR KDFPSSLKL VSSTLFGNTK PRKEKTEMSP REHIKGETT 180
 PSSLAVTQTM ATKAPCEVED PDMANQRKTA LEPCGETWSS LCTFFLSIVQ DTSC

Seq ID NO: 94 DNA sequence
 Nucleic Acid Accession #: NM_012101
 Coding sequence: 125-1891

1 11 21 31 41 51
 | | | | |
 CTCCTCACAG GTGTGTCTCT AGTCCTCGTG GTTGCCTGCC CCACTCCCTG CCGAGACGCC 60
 TGCCAGAAAG GTACCTATC CTGAACCCCA GCAAGCCTGA AACAGCTCAG CCAAGCACCC 120
 TGCATGGAA GCTGCAGATG CCTCCAGGAG CAACGGGTGG AGCCAGAAAG CCAGGGATGC 180
 CCGGAGCCCG TCGGGCCCA GTGGCAGCCT GGAGAATGGC ACCAAGGCTG ACGGCAAGGA 240
 TGCCAAGACC ACCAACGGGC ACGGCGGGGA GGCAGCTGAG GGCAAGAGCC TGGGACGCGC 300
 CCTGAAGCCA GGGGAAGSTA GGAGCGCCCT GTTCGCGGGC AATGAGTGGC GGCAGCCCAT 360
 CATCCAGTTT GTCGAGTCCG GGGACGACAA GAACTCCAAC TACTTCAGCA TGGACTCTAT 420
 GGAAGGCAAG AGGTGCGCGT ACGCAGGGCT CCAGCTGGGG GCTGCCAAGA AGCCACCCCT 480
 TACCTTTGCC GAAAAGGGCG ACGTGCACAA GTCCATTTTC TCGGAGTCCC GGAAGCCAC 540
 GGTGTCCATC ATGGAGCCCG GGGAGACCCG GCGGAACAGC TACCCCGGG CCGACACGGG 600
 CCTTTTTC CAAGTCCAAGT CCGGCTCCGA GGAGGTGCTG TGCGACTCCT GCATCGGCAA 660
 CAAGCAGAA GCGTCAAGT CCTGCCTGGT GTGCCAGGCC TCCTTCTGCG AGCTGCATCT 720
 CAAGCCCCAC CTGGAGGGCG CCGCCTTCCG AGACCACAG CTGCTCGAGC CCATCCGGGA 780
 CTTTGAGGCC CGCAAGTGT CCGTGCATGG CAAGACGATG GAGCTCTTCT GCCAGACCGA 840
 CAGACCTGC ATCTGCTACC TTTGCATGTT CCAGGAGCAC AAGAATCATA GCACCGTGAC 900
 AGTGGAGGAG GCCAAGGCCG AGAAGGAGAC GGAGCTGTCA CTGCAAAAGG AGCAGCTGCA 960
 GCTCAAGATC ATTGAGATTG AGGATGAAGC TGAGAAGTGG CAGAAGGAGA AGGACCGCAT 1020
 CAAGAGCTTC ACCACCAATG AGAAGGCCAT CCTGGAGCAG AACTTCCGGG ACCTGGTGCG 1080
 GGACCTGGAG AAGCAAAAGG AGGAAGTGAG GGCTGCGCTG GAGCAGCGGG AGCAGGATGC 1140
 TGTGAGCAA GTGAAGGTGA TCATGGATGC TCTGGATGAG AGAGCCAAAG TGCTGCATGA 1200
 GGACAAGCAG ACCCGGAGC AGCTGCATAG CATCAGGAC TCTGTGTTGT TTCTGCAGGA 1260
 ATTTGGTGCA TTGATGAGCA ATTACTCTCT CCCCCACCC CTGCCCACCT ATCATGTCTT 1320
 GCTGAGGGGG GAGGCGCTGG GACAGTCACT AGGCAACTTC AAGGACGACC TGCTCAATGT 1380
 ATGCATGCGC CACGTTGAGA AGATGTGCAA GGCGGACCTG AGCCGTAAC TCAATTGAGAG 1440
 GAACACATG GAGAACGGTG GTGACCATCG CTATGTGAAC AACTACACGA ACAGCTTCGG 1500

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GGGTGAGTGG AGTGACCCGG ACACCATGAA GAGATACTCC ATGTACCTGA CACCCAAAGG 1560
TGGGGTCCGG ACATCATACC AGCCCTCGTC TCCTGGCCGC TTCACCAAGG AGACCACCCA 1620
GAAGAATTTC AACAACTCTCT ATGGCACCAG AGGTAACCTAC ACCTCCCGGG TCTGGGAGTA 1680
CTCCTCCAGC ATTCAGAACT CTGACAATGA CCTGCCCGTC GTCCAAGGCA GCTCCTCCTT 1740
CTCCCTGAAA GGCTCTCCCT CCTCATGCG GAGCCAAAGC CCCAAGGCC AGCCCCAGAC 1800
TTGGAATCT GGCAAGCAGA CTATGCTGTC TCACTACCGG CCATTCTACG TCAACAAAGG 1860
CAACGGGATT GGGTCCAACG AAGCCCCATG AGCTCCTGGC GGAAGGAACG AGGCGCCACA 1920
CCCTGCTCT TCCTCTGAC CTGCTGCTC TTGCCTTCTA AGCTACTGTG CTTGTCTGGG 1980
TGGGAGGGAG CCTGGTCTG CACCTGCCCT CTGAGCCCT CTGCCAGCT CTTGGGGGCA 2040
GTTCCGGCCT CTCGACTTC CCCACTGGCC ACACCTCCATT CAGACTCCTT TCCTGCCCTG 2100
TGACCTCAGA TGGTCAACAT CATTCCTGTG CTCAGAGGCC AACCCATCAC AGGGGTGAGA 2160
TAGGTTGGGG CTGCCCTTAA CCCGCCAGCC TCCTCCTCTC GGGCTGGATC TGGGGGCTAG 2220
CAGTGAGTAC CCGCATGGTA TCAGCCTGCC TCTCCCGCCC ACGCCCTGCT GTCTCCAGGC 2280
CTATAGACGT TTCTCTCCAA GGCCCTATCC CCCAATGTTG TCAGCAGATG CCTGGACAGC 2340
ACAGCCACCC ATCTCCCAAT CACATGGCCC ACCTCCTGCT TCCCAGAGGA CTGGCCCTAC 2400
GTGCTCTCTC TCGTCTTACC TATCAATGCC CAGCATGGCA GAACCTGCAG TGGCCAAGGG 2460
CTGCAGATGG AAACCTCTCA GTGTCTTGAC ATCACCCTAC CCAGGCGGTG GGTCTCCACC 2520
ACAGCCACTT TGAGTCTGTG GTCCCTGGAG GGTGGCTTCT CTGACTGGC AGGATGACCT 2580
TAGCCAAGAT ATTCTCTGT TCCTCTGCT GAGATAAAGA ATTCCTCTAA CATGATATAA 2640
TCCACCCATG CAAATAGTCA CTGGCCAGC TACCATTAC CATTTGCCA CAGAATTTCA 2700
TTCAGTCTAC ACTTTGGCAT TCTCTCTGGC GATGGAGTGT GGCTGGGCTG ACCGCAAAAG 2760
GTGCCTTACA CACTGCCCCC ACCTCAGCC GTTGGCCCAT CAGAGGCTGC CTCTCCTTC 2820
TGATTACCCC CCATGTTGCA TATCAGGGT CTCAAGGATT GGAGAGGAGA CAAAACCAAG 2880
AGCAGCACAG TGGGGACATC TCCCGTCTCA ACAGCCCCAG GCCTATGGGG GCTCTGGAAG 2940
GATGGGCCAG CTGACAGGGG TTGGGGAGGG AGACATCCAG CTTGGGCTTT CCCCTTGGGA 3000
ATAAACCAAT GGTCTGTC

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Seq ID NO: 95 Protein sequence:
Protein Accession #: NP_036233.1

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35
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1 11 21 31 41 51
| | | | |
MEAADASRSN GSSPEARDAR SPSGPSGSLE NGTKADGKDA KTTNGHGGEA AEGKSLGSAL 60
KPEGGRSALF AGNEWRRPII QFVESGDDKN SNYFSMDSME GKRSPYAGLQ LGAARKPPVT 120
FAEKGDVRKS IFSESRRPTV SIMEPGETRR NSYPRADTGL FSRSKSGSEE VLCDSCIGNK 180
QKAVKSCILVC QASFCELHLK PHLEGAAFRD HQLLEPIRDF EARKCPVHVK TMLFQCQTDQ 240
TCICYLCMFQ EHKNHSTVTV EEAKAEKETE LSLQKEQLQL KIIIEIDEAE KWQKEKDRIK 300
SFTTNEKAIL EQNFRDLVRD LEKQKEEVRA ALBQREQDAV DQVKVIMDAL DERAKVLHED 360
KQTRQLHSI SDSVLFLQEF GALMSNYSLP PPLPTYHVLL EGEGLQSLG NFKDDLNLNV 420
MRHVEKMCKA DLSRNFIERN HMENGSDHRY VNNTNSFSGG EWSAPDTMKR YSMYLTTPKGG 480
VRTSYQPSPP GRFTKETTKQ NFNNLVGTKG NYTSRVWEYS SSIQNSDNDL PVVQSSSFS 540
LKGYPPLMRS QSPKAQPQTW KSGKQTMLSH YRPFYVKNKN GIGSNEAP

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Seq ID NO: 96 DNA sequence
Nucleic Acid Accession #: NM_080668.1
Coding sequence: 83-841

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65
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75
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1 11 21 31 41 51
| | | | |
GGCACGAGGG CAGCGAGTGG CCTTCCCGGT TGGCGCGCGC CCGGGGCGGC GGCCTGGAG 60
GAGCTCGAGA CGGAGCCTAG TTATGCTCTG GAGGCGAACG CGGTCCGGAG GAGCCGCTCA 120
GCGCTCCGGG CCAAGGGCCC CATCTCCTAC TAAGCCTCTG CGGAGGTCCC AGCGGAAATC 180
AGGCTCTGAA CTCCCGAGCA TCCTCCCTGA AATCTGGCCG AAGACACCCA GTGCGGCTGC 240
AGTCAGAAAG CCCATCGTCT TAAAGAGGAT CGTGGCCCAT GCTGTAGAGG TCCAGCTGT 300
CCAATCACCT CGCAGGAGCC CTAGGATTTT CTTTCTCTTG GAGAAAGAAA ACGAGCCCCC 360
TGGCAGGGAG CTTACTAAGG AGGACCTTTT CAAGACACAC AGCGTCCCTG CCACCCCCAC 420
CAGCACTCCT GTGCCGAACC CTGAGGCCGA GTCCAGCTCC AAGGAAGGAG AGCTGGACGC 480
CAGAGACTTG GAAATGTCTA AGAAAGTCAG GCGTCTCTAC AGCCGCTGG AGACCTGGG 540
CTCTGCCTCT ACCTCCACCC CAGGCCGCGG GTCTGCTTT GGCTTCGAGG GGCTGCTGGG 600
GGCAGAGAC TTGTCGGGAG TCTCGCCAGT GGTGTGCTCC AAACCTCACG AGGTCCCCAG 660
GGTTTGTGCA AAGCCCTGGG CCCCAGACAT GACTCTCCTT GGAATCTCCC CACCACCCGA 720
GAAACAGAAA CGTAAGAAGA AGAAAATGCC AGAGATCTTG AAAACGGAGC TGGATGAGT 780
GGCTGCGGCC ATGAATGCCG AGTTTGAAGC TGCTGAGCAG TTTGATCTCC TGGTTGAATG 840
AGATGCACTG GGGGGTGCAC CTGGCCAGAC TCTCCCTCCT GTCCTGTACA TAGCCACCTC 900
CCTGTGGAGA GGACACTTAG GGTCCCCTCC CCTGGTCTTG TTACCTGTGT GTGTGCTGGT 960
GCTGCGCATG AGGACTGTCT GCCTTTGAGG GCTTGGGCAG CAGCGGCAGC CATCTTGGTT 1020
TTAGGAAATG GGGCCGCTG GCCAGCCAC TCACTGGTGT CCTGTCTCTT GTCGTCCTGT 1080
CCTTCTATC TCCCAAAGT ACCATAGCCA GTTTCAGAT GGGCCACAGA CTGGGGAGGA 1140
GAATCAGTGG CCCAGCCAGA AGTTAAAGGG CTGAGGGTTG AGGTGAGAGG CACCTCTGCT 1200
CTTGTGGGA GGGGTGGCTG CTTGGAATA GGCCAGGGG CTCTGCCAGC CTCGGCCTCT 1260
CCCTCCTGAG TTGCTTCTG TTGGTGGCTT TCTTCTTGAA CCCACCTGTG TAAAGAGGTT 1320
TTCAGTTCGG TGGTTTCCC CTTTGATTCT GTAAATAGTC CCAGAGAGAA TTCGTGGGCT 1380
GAGGGCAATT CTGCTTGGA GGAAGAAGCT GGACATTGAG CCTGTGGAGT CTGAGTTTG 1440
AAGGATGTAG GGAGCCTTAG TTGGGTCTCA GACCATAAGT GTGTACTACA CAGAAGCTGT 1500
GTTTTCTAGT TCTGGTCTGC TGTGAGATG TTGTGTAAT GCCAGGTGTA TAGGGCGCTG 1560
GCTGCTTGA GCAAAGGGTG CATTTCAGG TGTGGCCACC AGGTGCTGTG AGTTTCTGTG 1620
GCTCATGGCC TCTGGGCTGG TCCCTTGCAC AGGGCCACG CTGGAGTCTT ACCACTCTGC 1680
TGCAAGGGTG GAAGTGGGCC CCTCTGTGCA CCCATACCCA TTTCTTACAA AATAAGTTAC 1740
ACCGAGTCTA CTGGCCCTA GAAGAGAAAG TTGAAGAGTC CCAGACCTAC TAGCATTTG 1800
CAACTATGCT TGTAAAGTTC TCGGAAAGTT TCCTCGCGTA CCAGACAGCG GCGGGGCTG 1860
ATAGCAATTT TAGTTTTTGG CCTCCCTATC CTCTCACATG AGAACACTGC CTGGATGCAT 1920
CTCATGATCT CTGGAGAATT TCCCCATCTT TCTCTTCTTT CCATCGTGTG GATTCAATAG 1980
TTTGGATTG AAGGCTGCCC TGCCCCGAC TCTCTGCGG CACCCCTGGC CATTGTACCT 2040
TTTGATGTTT AGAAGTTCGT GGAAGTAGAC GCTGAGGTGT GCAGAGGAGC TGGTGATTA 2100
CAGAGAAATG CAGGGAAGT GAGTGTCTGG TCAGGGTACT TGGATGAAAC GGTGCAGGCC 2160
AGGCGGGCCC TAATAAAACC CTTGCCAGG TCTGGAGTCT CCAGGCCATC TGCTCAACGC 2220

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TCTGTGGTTT GTGAGACCTG CAAGCAAGCC CCCTGCTGGG GAAGCCTAGG TGTCTCTGAG 2280
 CTGAACCGCA CTGAAGAAGT CTTGTCTCTA CTGGCTGATG CAGCAGAAGT CTTGGGAAAT 2340
 GTCTTAGTCC TGCAGAAATCA GGAGTCACCA GATGATGCAG AGTTGAGATC ATCATTGCAA 2400
 AGTTCTCTGT TCTGAGGAA CTAAATTTAA GGAAAAATG GATTTTGT TTAGAGTTGG 2460
 AAAAAAAGCC TGATTAAAGA GTTTCTGCCT GTTAAAAAAA AAAAAA AAAA

Seq ID NO: 97 Protein sequence:
 Protein Accession #: NP_542399.1

1 11 21 31 41 51
 MSGRRTRSGG AAQRSGPRAP SPTKPLRRSQ RKSSELPESI LPEIWPKTPS AAIVRKPVL 60
 KRIVAHAVEV PAVQSPRRSP RISPFLEKEN EPPGRELTKE DLFKTHSVPA TPTSTPVPNP 120
 ERESSSKEGE LDARDLEMSK KVRYSYRLE TLGSASTSTP GRRSCFGFEG LLGAEDLSGV 180
 SPVVCCKLTE VPRVCAKPWA PDMTLPGISP PPEKQKRKKK KMPEILKTEL DEWAAAMNAE 240
 FEAAEQFDLL VE

Seq ID NO: 98 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 58-12444

1 11 21 31 41 51
 GGGGCATTTC CGGTCGCGG CCGAGCGGGC GCACGCGCGG GAGCGGGACT CGGCGGCATG 60
 GCGGGCTCCG GAGCCGGTGT GCGTGTCTCC CTGCTGCGGC TGCAGGAGAC CTTGTCCGCT 120
 GCGGACCGCT GCGGTGCTGC CCGGCGGT CATCACTGA TCCGCGGCT GGGCAGGAA 180
 TCGTCTCTGA GCAGCAGCCC CGCGGTGCTG GCATTACAGA CATCTTAGT TTTTCCAGA 240
 GATTTCCGTT TGCTTGTATT TGTCGGGAA TCACTCAACA GTATTGAAT TCGTGAATGT 300
 AGAGAAGAAA TCCTAAAGTT TTTATGTATT TTCTTAGAAA AAATGGGCCA GAAGATCGCA 360
 CCTTACTCTG TTGAATTTAA GAACACTTGT ACCAGTGTAT ATACAAAAGA TAGAGCTGCT 420
 AAATGTAAAA TTCCAGCCCT GGACCTTCTT ATTAAGTTAC TTCAGACTTT TAGAAGTTCT 480
 AGACTCATGG ATGAATTTAA AATTGGAGAA TTATTTAGTA AATTCTATGG AGAAGTTGCA 540
 TTGAAAAAAA AAATACCAGA TACAGTTTAA GAAAAAGTAT ATGAGCTCCT AGGATTATTG 600
 GGTGAAGTTC ATCTAGTGA GATGATAAAT AATGCAGAAA ACCTGTTCG CGCTTTCTG 660
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75	TTTGGAGGCT	CTTCTGTGAT	TTTGAGAAGT	ATACTCTTGA	GTGTTTAATA	AAGTTTTTTT	13500
	CCAAAAGTA						

Seq ID NO: 99 Protein sequence:
Protein Accession #: NP_008835.5

80	1	11	21	31	41	51	
	MAGSGAGVRC	SLLRLQETLS	AADRCGAALA	GHQLIRGLGQ	ECVLSSSPAV	LALQTSLVPS	60
	RDFGLLVFVR	KSLNSIEPRE	CREILKFLC	IFLEKMGQKI	APYSVEIKNT	CTSUYTKDRA	120
85	AKCKIPALDL	LIKLLQTPRS	SRLMDEPKIG	ELFSKPYGEL	ALKKKIPDTV	LEKVYELLGL	180
	LGEVHPSEMI	NNAENLPRAF	LGEIKTQMTS	AVREPKLPLV	AGCLKGLSSL	LCNFTKSMEE	240
	DPQTSREIFN	DLKKAIRPQI	DLKRYAVPSA	GLRLFALHAS	QFSTCLLDNY	VSLFEVLLKW	300
	CAHTNVELKK	AALSALSF	KQVSNMVAKN	AEMHKNKLOQ	FMDQFYGIIR	NVDSNNKELS	360

	IAIRGYGLFA	GPCKVINAKD	VDFMYVELIQ	RCKQMFLTQT	DTGDDRVYQM	PSFLQSVASV	420
	LLYLDTPPEV	YTPVLEHLVV	MQIDSPFPQYS	PKMQLVCCRA	IVKVFALALAA	KGPVLRNCIS	480
	TVVHQGLIRI	CSKPVVLPKG	PESESEDHRA	SGEVRTGKWK	VPTYKYDYVDL	FRHLLSSDQM	540
5	MDSILADEAF	FSVNSSSESL	NHLLYDEFVK	SVLKIVEKLD	LTLEIQTVGE	QENGDEAPGV	600
	WM1PTSDPAA	NLHPAKPKDF	SAPINLVEFC	REILPEKQAE	FFPEWVYSFS	YELILQSTRL	660
	PLISGFYKLL	SITVRNAKKI	KYFEGVSPKS	LKHSPEDEPK	YSCFALFVKF	GKEVAVKMKQ	720
	YKDELLASCL	TFLLSLPHNI	IELDVRAIVP	ALQMAFKLGL	SYTPLAEVGL	NALEWSIYI	780
	DRHVMQPYK	DILPCLDGYL	KTSALSDETK	NNEVSALSRL	AAQKGFNKVV	LKHLKTKKNL	840
10	SSNEAISLEE	IRIRVQMLG	SLGGQINKNL	LTVTSSDEMM	KSYVAVDREK	RLSFAVPPRE	900
	MKPVIFLDVF	LPRVTEALAT	ASDRQTKVAA	CELLHSMVMF	MLGKATQMP	GGQGAFFMYQ	960
	LYKRTFPVLL	RLACDQDVPT	RQLYEPLVMQ	LJHWFTNNKK	FESQDVTALL	EAILDGVDP	1020
	VDSTLRDFCG	RCIREFLKWS	IKQITPQQQE	KSPVNTKSLF	KRLYSALHP	NAFKRLGASL	1080
	AFNNIYREFR	EEESLVEQFV	FEALVIYMES	LALAHADEKS	LGTIQCCDA	IDHLCRIIEK	1140
15	KHVSINKAKK	RRLPRGFPFS	ASLCLDLVK	WLLAHCGRQP	TECRHKSIEL	FYKFPVLLPG	1200
	NRSPLNLWKD	VLKEGVSFPL	INTFEGGGCG	QPSGILAQPT	LLYLGRPFSL	QATLCWLDLL	1260
	LAALCEYNTF	IGERTVGAQV	VLGTEAQSSL	LKAVAFFLES	IAMHDIIAAE	KCFGTGAAGN	1320
	RTSPQEGERY	NYSKCTVVVR	IMEFTTLLN	TSPEGWLLK	KDLCNTHLMR	VLVQTLCEPA	1380
	SIGFNTGVDQ	VMAHLPDVCV	NLMKALKMSP	YKDILETHLR	EKITAQSIIE	LCAVNLYGPD	1440
20	AQVDRSRLAA	VVSACKQLHR	AGLLHNILPS	QSTDLLHHSV	TELLSLVYKG	IAPGDERQCL	1500
	PSLDLSCQKL	ASGLLELAPA	FGGLCERLVS	LLLNPAVLST	ASLGSSQGSV	IHFSHGEFFY	1560
	SLFSETINTE	LLKNLDLAVL	ELMQSSVDNT	KMVSAILNGM	LDQSFREAN	QKHQGLKLAT	1620
	TILQHWKKCD	SWWAKDSPL	TKMAVALALLA	KILQIDSSVS	FNTSHGSFPE	VFTTYISLLA	1680
	DKTKLDLHLG	QAVTLLPFFT	SLTGGSELEL	RRVLEQLIVA	HFPMQSREFF	PGTFRFNYYV	1740
25	DCMKKFLDAL	ELSQSPMLLE	LMTEVLCREQ	QHVMEELFQS	SFRRIARRGS	CVTQVGLLES	1800
	VYEMFRKDDP	RLSFTFRQSV	DRSLTLTLWH	CSLDALREFF	STIVVDAIDV	LKSRTFKLNE	1860
	STFDTQITKK	MGYYKILDMV	YSRLPKDDVH	AKESKINQVF	HGSCITEGNE	LTKTILKLCY	1920
	DAFTENMAGE	NQLLERRRLY	HCAAYNCAIS	VICCVFNEKL	FYQGFLESEK	PEKNLLIFEN	1980
	LIDLKRRYNF	PVEVEVPMER	KKKYIEIRKE	AREAANGSDS	GPSYMSLSLY	LADSTLSEEM	2040
30	SQDFSTGTVQ	SYSYSSQDPR	PATGRFRRRR	QRDPTVHDDV	LELEMDLNR	HECMAPLTAL	2100
	VKMHRSLSGP	PQGEEDSVPR	DLPSWMKFLH	GKLGNPVPL	NIRLFLAKLV	INTEEVFRPY	2160
	AKHWLSPLQL	LAASENNGGE	GIHYMVVEIV	ATILSWTGLA	TPTGVPKDEV	LANRLNLFML	2220
	KHVFHPKRAV	FRHNLEIKT	LVECWKDCLS	IPYRLIFEKF	SGKDPNSKDN	SVGIQLLGIV	2280
	MANDLPPYDP	QCGIQSSEYF	QALVNMMSFV	RYKEVYAAAA	EVGLGLILRYV	MERKNILEES	2340
35	LCELVAQKQL	QHNTMEDKF	IVCLNKVTKS	FPPPLADRFM	AVFLLPKFH	GVKTLCLLEV	2400
	VLCRVEGME	LYFQKSKDF	VQVMRHRDDE	RQKVCLEIY	KMPKPKPVE	LRELLNPFVE	2460
	FVSHPTTCCR	EQMYNLMWI	HDNYRDPSE	TDNDSQSBIF	LAKDVLQGL	IDENPGLQLI	2520
	IRNFWSHETR	LPSNTLDRL	ALNSLYSPKI	EVHFLSLATN	FLEEMTSMSP	DYPNPMFEHP	2580
	LGSECFQEYT	IDSDFRFRST	VLTMPFVETQ	ASQGTLOTRT	ASQGTLOTRT	VAGQIRAGTQ	2640
40	QHDFTLTQTA	DGRSSFDWLT	GSSTDPLVDH	TSPSSDSLLF	AHKRSERLQR	APLKSVCQDF	2700
	GKRLGLPGD	EVDNKVKGAA	GRDOLLRLRR	RFMRDQEKLS	LMYARKGVAE	QKREKEIKSE	2760
	LKMKQDAQV	LYRSYRHKDI	PDIIQKSSSL	ITPLQAVAR	DPPIAKQLFS	SLFSGILKEM	2820
	DKFKTLSEKN	NITQKLLQDF	NRFLNTPFSF	PPPVSQIQD	ISQQAALLS	LDPAAVSAGC	2880
	LASLQQPVG	RLLEAALLRL	LPAELPAKRV	RGKARLPD	LRWVELAKLY	RSIGEYDVL	2940
45	GIFTSEIGTK	QITQSALLAE	ARSQYSEAAK	QYDEALNKQD	WVDGEPTAE	KDFWELASLD	3000
	CYNHLAEWKS	LEYCSTASID	SENPPDLNKI	WSEPPYQETY	LPYMIRSKLK	LLLQGEADQS	3060
	LLTFIDKAMH	GELQKAILLE	HYSQELSLLY	LLQDDVDRAK	YYIQNGIQSF	MQNYSSIDVL	3120
	LHQSLTLKQL	QITQSALLAE	FISFISKQGN	LSSQVPLKRL	LNTWTNRYPD	AKMDPMNIWD	3180
	DIITNRCFFL	SKIEEKLTP	PEDNSMNVQ	DGDPSDRMEV	QEQEEDISSL	IRSCKFSMKM	3240
50	KMIDSARKQN	NFLSAMKLLK	ELHESKSTRD	DWLVSQVQSY	CRLSHCRSRS	QGCSEQVLTV	3300
	LKTVSLLDEN	SVSYSLKNDI	LAFRDQNIL	GTTYRIIANA	LSSEPACLAE	IIEEDKARRIL	3360
	ELSGSSSEDS	EKVIAGLYQR	AFQHLSEAVQ	AAEBEAQPPS	WSCGPAAGVI	DAYMTLADFC	3420
	DQDLRKEEEN	ASVIDSAELQ	AYPALVVEKM	LKALKLNSNE	ARLKFPRLQ	IERYPEETL	3480
	SLMTKEISSV	PCWQCTISWI	HMVALLDKDQ	AVAVQHSVEE	ITDNYQPAIV	YPFIISSSESY	3540
55	SFKDSTGCHK	NKEFVARIKS	KLDQGGVIQD	FINALDQLSN	PELLFKDWSN	DVRAELAKTP	3600
	VNKNIEKMY	ERMYAALGDP	KAPGLGAPRR	KFIQTFGKEF	DKHFGKGGSK	LLRMKLSDFN	3660
	DTNMLLLKM	KEDSKPNNL	KVEFLRNELE	IPGQYDGRGK	PLPEYHVRIA	3720	
	GFDERVTVMA	SLRRPKRIII	RGHDEREHPF	LVKGGEDLRQ	DQVEQLFQV	MNGILAQDSA	3780
	CSQALQLRT	YSVVPMTSRL	GLIEWLENTV	TLKDLLLNTM	SQEEKAAYLS	DPRAPPCEYK	3840
60	DWLTMSGKHX	DVGAMLMYK	GANRTEVTS	FRKRRESKVA	DLKRAFVRM	STSPAEFLAL	3900
	RSHFASSHAL	ICISHWILGI	GDRHLNFMV	AMETGGVIGI	DFGHAFGSAT	QFLFVPELMP	3960
	FRLTRQFINL	MLPMKETGLM	YSIMVHALRA	FRSDPGLLTN	TMDVPVKEPS	FDWKNFEQKM	4020
	LKKGGSWQIE	INVAEKNWYP	RQKICYAKRK	LAGANPAVIT	CEDELLLGHEK	APAFRDYVAV	4080
	ARGSKDHNIR	AQEPESGLSE	ETQVKCLMDQ	ATDPNILGRT	WEGWEPWM		

Seq ID NO: 100 DNA sequence
Nucleic Acid Accession #: NM_000673
Coding sequence: 101-1225

	1	11	21	31	41	51	
70	ATGTGAAGGC	ACAAGCTGCT	GTTATATACA	ACAGAGTGAA	CTGAGCATCA	GTCAGAAAAA	60
	GTCTATGTTT	GCAGAAATAC	AGATCCAAGA	CAAAGACAGG	ATGGGCACTG	CTGGAAAAAGT	120
	TATTAAATGC	AAAGCAGCTG	TGCTTTGGGA	GCAGAAAGCA	CCCTTCTCCA	TTGAGGAAAT	180
	AGAAGTTGCC	CCACCAAGAG	CTAAGAAGT	TCGCATTAAAG	ATTTTGGCCA	CAGGAATCTG	240
75	TCGCACAGAT	GACCATGTGA	TAAAAGGAAC	AATGGTGTCC	AAGTTTCCAG	TGATTGTGGG	300
	ACATAGAGCA	ACTGGGATCT	TAGAGAGCAT	TGGAGAAGGA	GTGACTACAG	TGAAACACAGG	360
	TGACAAAGTC	ATCCCTCTCT	TTCTGCCACA	ATGTAGAGAA	TGCAATGCTT	CTCGCAACCC	420
	AGATGGCAAC	CTTTGCATTA	GGAGCGATAT	TACTGGTCTG	GGAGTACTGG	CTGATGGCAC	480
	CACCAAGATT	ACATGCAAGG	GCAACACAGT	ACACCACTTC	ATGAACACCA	GTACATTTCAC	540
80	CGAGTACACA	GTGGTGGAGT	AATCTTCTGT	TGCTAAGATT	GATGATGCAG	GTCTCTCTAG	600
	GAAAGTCTGT	TTAATTGGCT	GTGGGTTTTC	CACTGGATAT	GGCGCTGCTG	TTAAACTTGG	660
	CAAGGTCAAA	CTGGTTTCCA	CTTGGCTCGT	CTTTGGCCTG	GGAGGAGTTG	GCCTGTTCAGT	720
	CATCATGGGC	TGTAAGTCAG	CTGGTGACAT	TAGGATCATT	GGGATTGACC	TCAACAAAGA	780
	CAAAATTGAG	AAGGCCATGG	CTGTAGGTGC	CACTGAGTGT	ATCAGTCCCA	AGGACTCTAC	840
85	CAAAACCATC	AGTAGGTTGC	TGTCAGAAAT	GACAGGCAAC	AACGTGGGAT	ACACCTTTGA	900
	AGTTATTGGG	CATCTTGAAA	CCATGATTGA	TGCCCTGGCA	TCTGTCCACA	TGAACACTAG	960
	GACCAGCGTG	GTTGTAGGAG	TTCCTCCATC	AGCCAAGATG	CTCACCTATG	ACCCGATGTT	1020

GCTCTTCACT GGACGCACAT GGAAGGGATG TGTCTTTGGA GGTTTGAAAA GCAGAGATGA 1080
 TGTCCCAAAA CTAGTGACTG AGTTCTCTGGC AAAGAAATTT GACCTGGACC AGTTGATAAC 1140
 TCATGTTTFA CCATTTAAAA AAATCAGTGA AGGATTTGAG CTGCTCAATT CAGGACAAAG 1200
 CATTGGAACG GTCCTGACGT TTTGAGATCC AAAGTGGCAG GAGGTCTGTG TTGTCATGGT 1260
 GAACCTGGAGT TTCTCTTGTG AGAGTTCCCT CATCTGAAAT CATGTATCTG TCTCACAAT 1320
 ACAGCATAA GTAGAAGATT TGTGAAGAC ATAGAACCCT TATAAGAAT TATTAACCTT 1380
 TATAACATT TAAAGTCTTG TGAGCACCTG GGAATTAGTA TAATAACAAT GTTAATATTT 1440
 TTGATTTACA TTTTGAAGG CTATAATTGT ATCTTTTAAG AAAACATACA CTGGGATTTT 1500
 TATGTTGAAA TGGAGATTTT TAAGAGTTT AACCAGCTGC TGCAGATATA TAACTCAAAA 1560
 CAGATATAGC GTATAAAGAT ATAGTAAATG CATCTCCAG AGTAATATTC ACTTAACACA 1620
 TTGAACTAT TATTTTATAG ATTTGAATAT AAATGTATTT TTTAAACACT TGTATGAGT 1680
 TAACTTGGAT TACATTTTGA AATCAGTTCA TTCCATGATG CATATTACTG GATTAGATTA 1740
 AGAAAGACAG AAAAGATTAA GGGACGGGCA CATTTTTCAA CGATTAAAGAA TCATCATTAC 1800
 ATAACCTGGT GAAACTGAAA AAGTATATCA TATGGGTACA CAAGGCTATT TGCCAGCATA 1860
 TATTAATATT TTAGAAAATA TTCCTTTTGT AATACTGAAT ATAAACATAG AGCTAGAGTC 1920
 ATATTATCAT ACTTATCATA ATGTTCAATT TGATACAGTA GAATTGCAAG TCCTTAAGTC 1980
 CCTATTCACT GTGCTTAGTA GTGACTCCAT TTAATAAAAA GTGTTTITAG TTTTAAACAA 2040
 CTAACCG

Seq ID NO: 101 Protein sequence:
 Protein Accession #: NP_000664

1 11 21 31 41 51
 | | | | |
 25 MGTAGKVIK KAALVWEQKQ PFSIEIEVA PPKTEVRIK ILATGICRTD DHVIKGTMS 60
 KFPVIVGHEA TGIVESIGEG VTTVKPGDKV IPLFLPQCRE CNACRNPDPN LCIRSDITGR 120
 GVLADGTTTF TCKGKPVHVF MNTSTFTTEYT VVDESSVAKI DDAAPPEKVC LIGCGFSTGY 180
 GAAVKTGKVK PGSTCVVFLG GGVGLSVIMG CKSAGASRII GIDLNKDKFE KAMAVGATEC 240
 ISPKDSTKPI SEVLSMENTN NVGYTFEVIH HLETMIDALA SCHMNYGTSV VVGVPSSAKM 300
 30 LTYDPMMLPT GRTWKGCVEF GLKSRDDVPK LVTEFLAKKF DLDQLITHVL PFKKISEGFE 360
 LLNSGQSIRT VLTF

Seq ID NO: 102 DNA sequence
 Nucleic Acid Accession #: NM_006783.1
 Coding sequence: 1..786

1 11 21 31 41 51
 | | | | |
 40 ATGGATTGGG GGACGCTGCA CACTTTCATC GGGGGTGTCA ACAACACTC CACCAGCATC 60
 GGGAAAGTGT GGATCACAGT CATCTTTATT TTCGAGTCA TGATCCTAGT GGTGGCTGCC 120
 CAGGAAGTGT GGGGTGACGA GCAAGAGGAC TTCGTCTGCA ACACACTGCA ACCGGGATGC 180
 AAAAAATGTT GCTATGACCA CTTTTTCCCG GTGTCCACA TCCGGCTGTG GGCCTCCAG 240
 CTGATCTTCG TCTCACCCCG AGCGCTGCTG GTGGCCATGC ATGTGGCCTA CTACAGGCAC 300
 45 GAAACCACTC GCAAGTTCAG GCGACGAGAG AAGAGGAATG ATTTCAAAGA CATAGAGGAC 360
 ATTAAAAAGC ACAAGGTTCC GATAGAGGGG TCGCTGTGGT GGACGTACAC CAGCAGCATC 420
 TTTTTCGAA TCATCTTTGA AGCAGCCCTT ATGTATGTGT TTTACTTCCT TTACAATGGG 480
 TACCACCTGC CCTGGGTGTT GAAATGTGGG ATTGACCCCT GCCCAACCT TGTGACTGC 540
 TTTATTTCTA GGCCAAACAGA GAAGACCGTG TTTACCATT TTTATGTTTC TGCGTCTGTG 600
 50 ATTTGATGTC TGCTTAACCT GGCAGAGTGT TGCTACCTGC TGCTGAAAGT GTGTTTATAG 660
 AGATCAAGAA GAGCAGACAG GCAAAAAAAT CACCCCAATC ATGCCCTAAA GGAGAGTAAG 720
 CAGAATGAAA TGAATGAGCT GATTTCAGAT AGTGGTCAAA ATGCAATCAC AGGTTTCCCA 780
 AGCTAA

Seq ID NO: 103 Protein sequence:
 Protein Accession #: NP_006774.1

1 11 21 31 41 51
 | | | | |
 60 MDWGLHTFI GGVNKHSTSI GKVVITVIFI FRVMILVVAA QEVWGDEQED FVCNTLQPGC 60
 KNVCYDHFPP VSHIRLWALQ LIPVSTPALL VAMHVAYYRH ETTRKFRERGE KRNDPKDIED 120
 IKKKVRIEG SLWWTYTSSI PFRIIFEAAF MYVFYFLYNG YHLPWVLKCG IDPCPNLVDC 180
 FISRPTEKTV FTIFMISASV ICMLLNVAEL CYLLKVCFR RSKRAQTQKN HPNHALKESK 240
 QNEMNELISD SQNNAITGFP S

Seq ID NO: 104 DNA sequence
 Nucleic Acid Accession #: NM_020411
 Coding sequence: 86-526

1 11 21 31 41 51
 | | | | |
 70 GGACCTGGGA AGGAGCATAG GACAGGGCAA GCGGGGATAA GGAGGGGCAC CACAGCCCTT 60
 AAGGCACGAG GGAACCTCAC TGCGCATGCT CCTTTGGTGC CCACCTCAGT GCGCATGTTT 120
 ACTGGGCGTC TTCCCATCGG CCCCTTCGCC AGTGTGGGGA ACGCGGCGGA GCTGTGAGCC 180
 75 GCGGACTCGG TGCCCTGAGG TCTGGATTCT TTCTCGCTA CTGAGACACG GCGGACACAC 240
 ACAACACAG AACACACAG CAGTCCAG GAGCCAGTA ATGGAGAGCC CAAAAAGAA 300
 GAACACGACG CTGAAAGTCG GGATCTTACA CCTGGGCAGC AGACAGAAGA AGATCAGGAT 360
 ACAGCTGAGA TCCAGTGC CGACATGGAA GGTGATCTGC AAGAGCTGCA TCAGTCAAAC 420
 ACCGGGGATA AATCTGGATT TGGGTTCGG CGTCAAGGTG AAGATAATAC CTAAGAGGA 480
 80 AACTGTAAA ATGCCAGAAG CAGGTGAAGA GCAACACAA GTTTAAATGA AGACAAGCTG 540
 AAACAAACGA AGCTGGTTTT ATATTAGATA TTTGACTTAA ACTATCTCAA TAAAGTTTGT 600
 CAGCTTTCAC CAAAAA AAAA

Seq ID NO: 105 Protein sequence:
 Protein Accession #: NP_065144.1

1 11 21 31 41 51

MLLWCPQCA CSLGVFPSP SPVWGTRRSC EPATRVPEVW ILSPLLRHGG HTQTQNHAS 60
 PRSPVMESPK KKNQQLKVG LHLGSRQKKI RIQLRSQCAT WKVICKSCIS QTPGINLDLG 120
 SGVKVKIIPK EEHCKMPEAG EEQPPQV

Seq ID NO: 106 DNA sequence
 Nucleic Acid Accession #: J04129
 Coding sequence: 99-587

1 11 21 31 41 51
 CATCCCTCTG GCTCCAGAGC TCAGAGCCAC CCACAGCCGC AGCCATGCTG TGCCTCCTGC 60
 TCACCCTGGG CGTGGCCCTG GTCTGTGGTG TCCCGGCCAT GGACATCCCC CAGACCAAGC 120
 AGGACCTGGA GCTCCCAAGG TTGGCAGGGA CCTGGCACTC CATGGCCATG GCGACCAACA 180
 ACATCTCCCT CATGGCGACA CTGAAGGCC CTCTGAGGGT CCACATCACC TCACTGTGTG 240
 CCACCCCGGA GGACAACCTG GAGATCGTTC TGCACAGATG GGAGAACAAC AGCTGTGTG 300
 AGAAGAAGGT CCTTGGAGAG AAGACTGGGA ATCCAAAGAA GTTCAAGATC AACTATACGG 360
 TGGCGAAGCA GGCCACGCTG CTGATACTG ACTACGACAA TTCTCTGTTT CTCTGCCTAC 420
 AGGACACCAC CACCCCATC CAGAGCATGA TGTGCCAGTA CCTGGCCAGA GTCCTGGTGG 480
 AGGACGATGA GATCATGCAG GGATTCATCA GGGCTTTCAG GCCCTGCCCC AGGCACCTAT 540
 GGTACTTGCT GGAATTGAAA CAGATGGAAG AGCGTGCCG TTTCTAGCTC ACCTCGCCT 600
 CCAGGAAGAC CAGACTCCCA CCCTCCACA CCTCCAGAGC AGTGGGACTT CCTCCTGCCC 660
 TTTCAAAGAA TAACCAACAG TCAGAAGACG ATGACGTGGT CATCTGTGTC GCCATCCCT 720
 TCCTGCTGCA CACCTGCACC ATTGCCATGG GGAGGCTGCT CCCTGGGGGC AGAGTCTCTG 780
 GCAGAGGITA TTAATAAACC CTTGAGCAT G

Seq ID NO: 107 Protein sequence:
 Protein Accession #: AAA60147

1 11 21 31 41 51
 MDIPQTKQDL ELPKLAGTWH SMAMATNNIS LMATLKAPLR VHITSLLP T EDNLEIVLHR 60
 WENNSCVEKK VLGEKTNPK KFKINYTVAN EATLLD TDYD NFLFLCLQDT TPIQSMCCQ 120
 YLARVLVEDD EIMQGFIRAF RPLRHLWYL LDLQMEEPC RF

Seq ID NO: 108 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 48-794

1 11 21 31 41 51
 TCCAGGCAG CAGTTAGCCC GCCGCCGCC TGTGTGTCCC CAGAGCCATG GAGAGAGCCA 60
 GTCTGATCCA GAAGGCCAAG CTGGCAGAGC AGGCCGAACG CTATGAGGAC ATGGCAGCCT 120
 TCATGAAAGG CGCCGTGGAG AAGGGCGAGG AGCTCTCCTG CGAAGAGCGA AACCTGCTCT 180
 CAGTAGCCTA TAAGAACGTG GTGGCGGCC AGAGGGCTGC CTGGAGGGTG CTGTCCAGTA 240
 TTGACAGAAA AAGCAACGAG GAGGGCTCGG AGGAGAAGGG GCCCGAGGTG CGTGAGTACC 300
 GGGAGAAGGT GGAGACTGAG CTCCAGGGCG TGTGCGACAC CGTGCTGGGC CTGCTGGACA 360
 GCCACCTCAT CAAGGAGGCC GGGGACGCC AGAGCCGGGT CTTCTACCTG AAGATGAAGG 420
 GTGACTACTA CCGCTACCTG GCCGAGGTGG CCACCGGTGA CGACAAGAAG CGCATCATTG 480
 ACTCAGCCCG GTCAGCCTAC CAGGAGGCCA TGGACATCAG CAAGAAGGAG ATGCCGCCCA 540
 CCAACCCCAT CCGCCTGGGC CTGGCCCTGA ACTTTCCGT CTTCCACTAC GAGATCGCCA 600
 ACAGCCCGCA GGAGGCTGTC TCTCTGGCCA AGACCACTTT CGACGAGGCC ATGGCTGATC 660
 TGCACACCCT CAGCGAGGAC TCCTACAAAG ACAGCACCCT CATCATGCAG CTGCTGCGAG 720
 ACAACCTGAC ACTGTGAGC GCGCAACAG CCGGGGAAGA GGGGGCGAG GCTCCCCAGG 780
 AGCCCGAGAG CTGAGTGTG CCGGCCACCG CCGGCCCTG CCCCCTCCAG TCCCCACCC 840
 TGCCGAGAGG ACTAGTATGG GGTGGGAGGC CCCACCCTTC TCCCCTAGGC GCTGTTCTTG 900
 CTCCAAAGGG CTCCTGGAG AGGACTGGC AGAGCTGAGG CCACCTGGGG CTGGGGATCC 960
 CACTCTTCTT GCAGCTGTTG AGCGCACCTA ACCACTGGTC ATGCCCCAC CCCTGCTCTC 1020
 CGCACCCGCT TCCTCCCGAC CCCAGGACCA GGCTACTTCT CCCCTCCTCT TGCCTCCCTC 1080
 CTGCCCCGTC TGCTCTGAT CGTAGGAATT GAGGAGTGTG CCGCCTGTG GCTGAGAACT 1140
 GGACAGTGGC AGGGCTGGG GATGGGTGTG TGTGTGTGTG TGTGTGTGTG TGTGTGTGTG 1200
 CGCGCGCGCC AGTGCAAGAC CGAGATTGAG GGAAAGCATG TCTGCTGGGT GTGACCATGT 1260
 TTCCTCTCAA TAAAGTTCCT CTGTGACACT C

Seq ID NO: 109 Protein sequence:
 Protein Accession #: NP_006133.1

1 11 21 31 41 51
 MERASLIQKA KLAQAERYE DMAAFMKGAV EKGEELSCEE RNLLSVAYKN VVGQRAAWR 60
 VLSSIEQKSN EEGSEKGP VREYREKVT ELQGVCDTVL GLLDShLIKE AGDAESRVFY 120
 LKMKGDYYRY LAEVATGDDK KRIIDSARSA YQEA MDISK EMPPTNPRL GLALNFSVFH 180
 YEIANSPPEA ISLAKTTFDE AMADLHTLSE DSYKDSLIM QLLRDNLTW TADNAGEEGG 240
 EAPQSPQS

Seq ID NO: 110 DNA sequence
 Nucleic Acid Accession #: NM_000695
 Coding sequence: 407-1564

1 11 21 31 41 51
 CACGAGTTGG TTTGGGAGCT GCCAGTCTCC TGGGAGGATC GCAGTCAGCA GAGCAGGGCT 60
 GAGGCCTGGG GGTAGGAGCA GAGCCTGCGC ATCTGGAGGC AGCATGTCCA AGAAAGGGAG 120
 TGGAGGTGCA GCGAAGGACC CAGGGGCGA GCCACGCTG GGGATGGACC CCTTCGAGGA 180
 CACACTGGCG CGGCTGGTGG AGGCCTTCAA CTGAGGGCGC ACGCGGCGG CCGAGTTCCG 240
 GGCTGCGCAG CTCCAGGGCC TGGGCCACTT CCTTCAAGAA AACAAGCAGC TTCTGCGCGA 300

	CGTGCTGGCC	CAGGACCTGC	ATAAGCCAGC	TTTCGAGGCA	GACATATCTG	AGCTCATCCT	360
	TTGCCAGAAC	GAGGTGTGACT	AGCSTCTCAA	GAACCTTCAG	GCCCTGGATGA	AGGATGAACC	420
	ACCGTCCACG	AACCTGTTCA	TGAAGCTTGA	CTCGGTCTCG	ATCTCGAAGG	AACCTTTTGG	480
5	CCTGGTCTCT	ATCATCGCAC	CCTGGAACTA	CCCATTTGAAC	CTGACCCCTGG	TGCTCTCTGGT	540
	GGGCAACCTC	CCCGCAGGGG	ATTGCTGTGT	GCTGAAGCCG	CGACAAATCA	GCCAGGGGCA	600
	AGAGAAGGTC	TGCTGCTGAG	TGCTGCCCCA	GTACCTGAGC	CAGAGCTGCT	TTCCGCTGGT	660
	GCTGGGCGGA	CCCCAGGAGA	CAGGGCAGCT	GCTAGAGCAC	AAGTTGGACT	ACATCTTCTT	720
	CACAGGGAGC	CCTCTGTGTG	GCAAGATTGT	CATGACTGCT	GCCACCAAGC	ACTGACGCCC	780
10	TGTCACCTCT	GAGCTGTGGG	GCAAGAACCT	TGCTCTACGT	GACGACAACT	GCGACCCCCA	840
	GACCGTGGCC	AACCGCGTGG	CCTGGTTCCT	CTACTTCAAT	GCCGGCCAGA	CCTGCGTGGC	900
	CCCTGTACTAC	GTCTCTGTGCA	GCCCCAGAT	CAGGAGGAGC	CTGCTGTCCG	CCCTGTCAGAG	960
	CACCATCACC	CGTTTCTATG	GCGACGACCC	CCAGAGCTCC	CCAAACCTTG	GCCGCATCAT	1020
	CAACCAGAAA	CAGTTCACAG	GGCTGCGGGC	ATTGCTGGGC	TGCGGCCCGG	TGGCCATTGG	1080
	GGGCGCAGAG	AACGAGAGCG	ATCGCTACAT	CGCCCCCACG	GTGTCGTGGG	AGCTGTCAGAA	1140
15	GAGCGTGAGC	GTGATGTCAG	AGGAGATCTT	CGGGCCCCAT	TGCCCCATCG	TGAAGCTGCA	1200
	CTTCTCCAAC	AGGACAGCAG	TTGTGAACCA	GATGCTGGAG	CGGACCCAGA	CGGCGAGCTT	1320
	TGGAGGCAAT	GAGGGCTTCA	CTCATCATAT	TTCTGCTGCC	TGTGCATTCT	GGGAGCTGCG	1380
	CCACAGTGGT	ATGGGCGCGT	ACCACGGCAA	GTTCACTTTC	GACACCTTCT	CCCACCACCG	1440
20	CACCTGCGCT	CTCGCCCCCT	CGGGCTGGGA	GAATTTAAAG	GAGATTCGCT	ACCCACCTTA	1500
	TACCGACTGC	AACACAGCAG	TGTTACGCTG	GGGCATGGGC	TCCGAGAGCT	GCACCTCCTT	1560
	GTGAGCGTCC	CACCCGCGCT	CAACGGGTCA	CACAGAGAAA	CCTGAGTCTA	GCCATGAGGG	1620
	GCTTATGCTC	CCAACTCACA	TTGTTCTCTC	AGAGCCGACG	CTCCCCACGT	CTCAGGTTTC	1680
	TGGAGCTGTC	ACATGACTGC	ATCTGCTGCT	CCAGGGCTGC	AAAGCAAGGT	TCTGCTTCTA	1740
25	TCTGGGGGAC	GCTGCTCGAG	AGAGGCCGAG	AGGCCGCGA	ACATGCCAGG	TGTCCTCACT	1800
	CACCCCCACG	TCCCCAAATT	CAGCCCTTTG	CCCTCTCGGT	CAGGGTTGGC	CAGGCCCACT	1860
	CACAGGGGCA	GTGTCAACCT	GGAATAATCA	GTCGCTGGC	TCTTTAGGGG	CATCAGCCCT	1920
	GAACGGTTGA	GAGCGTGGAG	CCCTCCAGGC	CTTGTCTCTC	CCCTCTAGGC	ACACGCGCAC	1980
	TTCCACCTCT	GTCCTGATCC	AACCTGCACCA	GCACCTGCTC	CCCCAGGATG	CCTCTTCACAT	2040
30	CCCACTATGG	TCTCTGCACC	ACCCCTCTGG	CTCAACCCG	ACCTCTGACT	CACCCACAGC	2100
	AGCTCCATCC	ACTGGGAAAA	CTGGGGTTTG	CATCACTCCA	CTGCACAGTG	TTAGTGGGAC	2160
	CTGGGGGCAA	GTCCCTTTGAC	TTCTCTGAGC	CTCAGTTTCC	TTATGTGAAA	GTGTCTGGAA	2220
	CCAAATATGA	GTCACCTTAG	CCAAACTCTA	ATAAAAATGA	FTCGGGGGGG	CACATGAGAAG	2280
	CCCTCACACA	CACATGCCCG	TAACAGGATT	TATACCAAG	ACAACGCTGC	ATGTAAGACC	2340
	AGACACAGGG	CTCATGTGAAA	AGGACGCTCT	CAAAAGACTG	AGTATTTCCAG	ATGAGCTGCA	2400
	GATGCTTATC	TACCAAGGCC	GTCTCCACCA	GA AAAACCAT	GCCAACTCCT	GCGATCAGCT	2460
35	TGTGACTTAC	AAACCTTGTT	TAAAGACTGC	TTACATCATG	TTCTGTCTCT	TAAACAGTTC	2520
	CCCTTGGCTG	TGGCCCTCTG	TGATGCTGCT	GGATCCTTCC	AAGCACTCAT	AGCCCCAGATA	2580
	GGAACTCCTCT	GCTCTTCCCCA	AATAAATTC	TCGTGTC			

Seq ID NO: 111 Protein sequence:
Protein Accession #: NP_000686

45	1	11	21	31	41	51	
	MKDEPRSTNL	FMKLDVSFVIF	KEPFGVLVII	APWNYPNLNT	LVLVLGTLPA	GNCVVLPKPE	60
	ISQGTGKVL	EVLPQYLDQS	CFAVVLGGPQ	ETGQLLEHLK	DYIFPTGSPR	VGKIVMTAAT	120
50	KHLPTVLTLE	GKNKPCYVDD	NCDPQTVANR	VAWFCYFNAG	QTCVAPDYYL	CSPMEQERLL	180
	PALQSTITFR	YGGDPQSSPN	LGRIINQKFP	QLRLALLGCC	RVAIGGQSNR	SDRYIAPTVL	240
	VDVQETEFVM	QEEIFGPILP	IVNVQSVDEA	IKFINRQKEP	LALYAFSNSR	QVVNQMLERT	300
	SSGSFGNGNG	FTYISLLSPV	FVGCVGHSMG	RYHGKFTFDT	FSHHRCTCLA	PSGLEKLEKI	360
	RYPPYTDWNO	OLLRWGMGSO	SCTLT				

Seq ID NO: 112 DNA sequence
Nucleic Acid Accession #: NM_004456
Coding sequence: 58-2298

60	1	11	21	31	41	51	
	GAATTCGGGG	CGACGCGCGG	GAACAACGCG	AGTCGGCGCG	CGGGACGAAG	AATAATCATG	60
	GGCCAGACTG	GGAGAAATC	TGAGAAGGGA	CCAGTTTGT	GGCGGAAGCG	TGTAAAATCA	120
	GAGTACATCG	GCTGAGACGA	GCTCAAGGAG	TTCAGACGAG	CTGATGAAGT	AAAGAGTATG	180
	TTTAGTTTCCA	ATGCTGCAGAA	AAATTTGGAA	AGAAACGGAAA	TTCTAAACCA	AGAAATGGAAA	240
65	CAGCGAAGGA	TACAGCCTGT	GCACATCCTG	ACTTCTGTGA	GCTCATTGCG	CGGGACTAGG	300
	GAGTGTTCGG	TACCCAGTCA	CTTGGATTTT	CCAACACAAG	TCATCCCCAT	AAAGACTCTG	360
	AATGCAGTTG	GTTCAAGTACC	CATAATGTAT	TC TTGGTCTC	CCCTACAGCA	GAAATTTATG	420
	GTGGAAGATG	AAACTGTTTT	ACATAACATT	CCTTATATGG	GAGATGAAGT	TTTAGATCAG	480
	GATGGTACTT	TCATTGGAAG	ACTTAATAAA	AATTTATGAT	GGAAAGATAC	CGGGGATAGA	540
70	GAATTTGGGT	TTATAAATGA	TGAAATTTTT	GTGGAGTTGG	TGAATGCCCT	TGGTCAATAT	600
	AATGATGATG	ACGATGATGA	TGATGGAGAC	GATCCTGAAG	AAAGAGAAGA	AAAGCAGAAA	660
	GATCTGGAGG	ATCACCAGGA	TGATAAAGAA	AGCCGCCAC	CTCCGAAATT	TCCTTCTGAT	720
	AAAATTTTGG	ATGCCCAATT	CTCAATGTTT	CCAGATAAAG	GCACAGCAGA	AGAACTAAAG	780
	GAAAAATATA	AAGAATCCAC	CGAACGACG	CTCCCAGCG	CACCTTCTCC	TGAATGCTAT	840
75	CCCAACATAG	ATGGACCAA	TGCTAAATCT	GTTCCAGAG	AGCAAAGCTT	ACACTCTCTT	900
	CATACGCTTT	TCTGTAGCGG	ATGTTTTAAA	TATGACTGCT	TCTCATACCT	TTTTTCATGA	960
	ACACCCAACA	CTTTAAGCG	GAAAGAACCA	GAAACAGCTC	TAGACAACA	ACCTTTGTGA	1020
	CCACAGTGT	ACCAGCAATT	GGAGGAGCA	AAGGAGTTTG	CTGTGCTCT	ACCGCTGAG	1080
80	CGGATAAAGA	CCCCACCAA	ACGTCACGGA	GGCGCGAGAA	GAGGACGGCT	TCCCAATAAC	1140
	AGTAGCAGCG	CCGACACCCC	CACCAATTAAT	GTGCTGGAAT	CAAGAGGATC	AGACAGTGAAT	1200
	AGGGAAGCAG	GGACTGAAAC	GGGGGGAAG	AACAAATGATA	AAGAAGAAGA	AGAGAAGAAA	1260
	GATGAAACTT	CGAGCTCCTC	TGAAGCAAAT	TCTCGGTGTC	AAACACCAAT	AAAGATGAAG	1320
	CCAAATTTTG	AAACCTCTGA	GAAATGTGGG	TGGAGTGGTG	CTGAAGCCCT	AATGTTTAAA	1380
	GTCCTCATTG	GCACCTTACTA	TGACAAATTC	TGTGCCATT	CTAGGTAAAT	TGGGACCAA	1440
85	ACATGTAGAC	AGGTGATATGA	GTTTAGAGTC	AAAGAATCTA	GCATCATAGC	TCCAGCTCCC	1500
	CTCGGAGGTG	TGGATATCTC	TCCAAGGAAA	AAGAAGAGGA	ARACCCGGTT	TGGGCTCGCA	1560
	GACTGACGAA	AGATACAGCT	GAAAAGGACG	GGCTCCTCTA	ACCATGTTTA	CAACTATCAA	1620

5 CCCTGTGATC ATCCACGGCA GCCTGTGTAC AGTTCTGTGCC CTTGTGTGAT AGCACAAAAT 1680
 TTTTGTGAAA AGTTTGTGCA ATGTAGTTCA GAGTGTCAAA ACCGCTTTCC GGGATGCCGC 1740
 TGCAAGCAC AGTGTCAACAC CAAGCAGTGC CCGTGTCTACC TGGCTGTCCG AGAGTGTGAC 1800
 CCTGACCTCT GTCTTACTTG TGGAGCCGCT GACCATTGGG ACAGTAAAAA TGTGTCTCTG 1860
 AAGAAGTGCAT GTATTACGCG GGGCTCCAAA AAGCATCTAT TGCTGGCACC ATCTGACGTG 1920
 GCAGGCTGGG GGATTTTTAT CAAAGATCCT GTGCAGAAAA ATGAATTCAT CTCAGAATAC 1980
 TGTGGAGAGA TATTTTCTCA AGATGAAGCT GACAGAAGAG GGAAAGTGTG TGATAAATAC 2040
 ATGTGCAGCT TTCTGTTCAT CTTGAACAAT GATTTTGTGG TGGATGCAAC CGCAAGGGT 2100
 AACAAAATTC GTTTTGTGAAA TCATTTCGTA AATCCAAACT GCTATGCAAA AGTTATGATG 2160
 10 GTTAAACGGTG ATCAGAGAT AGGTATTTTT GCCAAGAGAG CCATCCAGAC TGGCGAAGAG 2220
 CTGTTTGTGG ATTACAGATA GAGCCAGGCT GATGCCCTGA AGTATGTCTG CATCGAAAGA 2280
 GAAATGGAAG TCCCTTGACA TCTGCTACCT CCTCCCCCTC CTCTGAAACA GCTGCTTAG 2340
 CTTGAGAAC CTCGAGTACT GTGGGCAATT TAGAAAAAGA ACATGCAGTT TGAAATCTG 2400
 AATTGTGAAA GTACTGTAAAG AATAATTAT AGTAATGAGT TTAATAATCA ACTTTTATT 2460
 15 GCCTTCTCAC CAGCTGCAAA GTGTTTGTGA CCAGTGAATT TTTGCAATAA TGCAGTATGG 2520
 TACATTTTTC AACTTTGAAT AAAGAATACT TGAACCTGAA AAAAAA AAAAAA

20 Seq ID NO: 113 Protein sequence:
 Protein Accession #: NP_004447

1 11 21 31 41 51
 25 MGQTGKKSEK GPVCRWRKVK SEYMRLRQLK RFRRADEVKS MFSSNRQKIL ERTEILNQEW 60
 KQRIQPVHI LTSVSSLRGT RECVTSDDL FPTQVPLKT LNAVASVPIM YSWSPLOQNF 120
 MVEDETVLHN IPYMGDEVLD QDGTPIELI KNYDGKVHGD RECGFINDEI FVELVNALGQ 180
 YNDDDDDDG DPEEREKQ KDLBDHRDDK ESRPRKFPSS DKILEAISM FPDKGTAEEL 240
 KEKYKELTEQ QLPALPPEC TPNIDGPNK SVQREQSLHS FHTLFCRRCP KYDCFHHPFH 300
 30 ATPTNYKRNK TETALDNKPC GPQCYQHLEG AKFPAALTA ERIKTPPKRP GRRRRRLPN 360
 NSSRPSTPTI NVLESKDTDS DREAGTETGG ENNDKEEEK KDRTSSSSEA NSRCQTPIM 420
 KPNIEPPENV EWSGAESMF RVLIGTYIDN FCAIARLIGT KTCRQVYEF VKESSIIAPA 480
 PAEDVDTPPR KKKRKHRLWA AHCRKIQLKK DGSSNHVNY QPCDHPRQPC DSSCPCVIAQ 540
 NFCEKFCQCS SECQNRFPGC RCKAQCNKQ CPCYLAVREC DPDLCLTCGA ADHWDSKNVS 600
 35 KCNCSIQRGS KKHLLAPSD VAGNGIFIKD PVQKNEFISE YCGEIIISQDE ADRRGKVYDK 660
 YMCSEFLNINL NDFVVDATRK GNKIRFANHS VNPNCYAKVM MVNGDHRIGI FAKRAIQTGE 720
 ELFVDYRYSQ ADALKYVGIE REMEIP

40 Seq ID NO: 114 DNA sequence
 Nucleic Acid Accession #: NM_001827
 Coding sequence: 96-335

1 11 21 31 41 51
 45 AGTCTCCGCG GAGTTGTTGC CTGGGCTGGA CGTGGTTTGG TCTGCTGCGC CCGCTCTTCG 60
 CGCTCTCGTT TCATTTTCTG CAGCGCGCCA CGAGGATGGC CCACAAGCAG ATCTACTACT 120
 CGGACAAGTA CTTGACGAA CACTACGAGT ACCGGCATGT TATGTTACCC AGAGAACTTT 180
 CCAACAAGT ACCTAAAAT CATCTGATGT CTGAAGAGGA GTGGAGGAGA CTTGGTGTCC 240
 AACAGAGTCT AGGCTGGGTT CATPACATGA TTCATGAGCC AGAACCAT ATCTCTCTCT 300
 50 TTAGACGACC TCTTCCAAA GATCAACAAA AATGAAGTTT ATCTGGGGAT CGTCAAATCT 360
 TTTTCAAAAT TAATGTATAT GTGTATATAA GGTAGTATTC AGTGAATACT TGAGAAATGT 420
 ACAAACTTTT CATCCATACC TGTGCATGAG CTGTATTCTT CACAGCAACA GAGCTCAGTT 480
 AAATGCAACT GCAAGTAGGT TACTGTAAGA TGTTTAAGAT AAAAGTTCTT CCAGTCAGTT 540
 55 TTTCTCTTAA GTGCTGTGTT GAGTTACTG AAACAGTTTA CTTTGTGTCA ATAAAGTTTG 600
 TATGTTGCAT TTAACAAAAA AAAAAA

60 Seq ID NO: 115 Protein sequence:
 Protein Accession #: NP_001818

1 11 21 31 41 51
 60 MAHKIYYSD KYFDEHYEYR HVMLPRELSK QVPKTHLMSE EEWRLGLVQQ SLGWVHYMIH 60
 EPEPHILLFR RPLPKDQK

65 Seq ID NO: 116 DNA sequence
 Nucleic Acid Accession #: CAT cluster

1 11 21 31 41 51
 70 TCAGACCTCA TGAGTCACTT GGACTCTTGA GCCACCTCTG GGGGTGGAGT CTCTCTCTG 60
 GCATCTGGAC CCTTGGTGCT ATCAGCAAGG CTTGGGTGGG GCTCTTAGCT GCTATGTGCA 120
 AGAGGTGTGT TCCAGGAAA GCCCTATCT CTCTGCAGAG GTCAAGTGAA AGCGACGGCC 180
 GCAGCCAACA GAGTTCAAAA TGCAGGCTTG GAAAGTACAG GGGCTCTGT GGAGGATGGG 240
 AAGGACTGAT CCACATTCCT ACCAGGAAGT TTAGCAGAAC CCCCCTGCTG CAATGGACC 300
 75 CCTTGAAGG ACCTGGCTCA GGCTGGACCA CCTCTTGAGA GGGAGGAGCT CTGGATTGTA 360
 TCAAGAAATC TTGCTGAGC ATGCTGCCTC ATGCTATAA TACCAACACT TTGGGAGGCC 420
 AGTGTGGGAG GATCTCTTGA GCCCAGGAGT TCAAGACTAG CCTGGGCAAC ACAGAGAGAA 480
 CCATCTCTTA AATAATAATA AATAATAATA TAAAAAATA GCAGGGCATG GTGGCATGTG 540
 CCTGTAGTTC CAGCTACCCA GGAGGCTGAG GCAAGAGGAT GGCTGGAGCC TGGGATGTTG 600
 80 AGGCTGCAAT GAACTGTGAT TACCCACTG CACTCCAGCC TGGGCAAAAG AGCGAGAGAA 660
 CTGTCTCTAA ATAATAATAA TAATAATAAT CTTATTTTGG AGAATAAGA GACCTCTGGA 720
 TTTGAGGTGC CATTTGGGTA GAAAGAAAAG ACGTTTACAC CGAGAAATAG TCTGTGTTGC 780
 CCTGAAGGAG CAGAGGGATG CATCGCTGGA GGTGACCTAC AGTTGAAGAA GACTCATTAT 840
 85 GACAGACCTT GTCTTCTTTC CTTGTGGAAA GTGTTCTCTC TGCTGCTACT GCTCATGAGA 900
 CTCTTCCCCC TCCCTGTCCC AGGGAACCAA AGGGCTTTCT ACCACACCTT TCTTGTCCCC 960
 CCGCCTCCCA TGTCTGCTGT GCCTTTGTAC TCAGCAATTC TTGTTTGTCT CATTATCTTC 1020
 CAGCCGGATA CAGAGTGAAT AGTTAACAC ACTTAGGTCA AATAGGATCT AATTTTGTG 1080
 TCCTGCTCCG TGTAAAGAGG CCAGTGTTTG TGTGTTGCAA GCAGCCTTGG AATAGTAAT 1140

CTTCTCATTT GTTTGGGATC TGGCCACCAA GTTCCAGAAT GATACACGGA TCAGTGCAGA 1200
 AGTTTCATCAG GCTCTCGGAC CTTAGGGCTG TTGGAGAAGG CTTGAGCAGC AGAACTGATG 1260
 GTGAAGGCTC GTGTTCTCCA TCCTCAACTT TCTTTGCTTC GATCATACAC AAGAATACAT 1320
 TTGGAAGGCG AAAAAATGAA CACTGTGCTT CATTGACGCC GTGTTTTGTG ACACAGATGC 1380
 ACAGTCTGCT GTGAAGACCT TCTCTCAAGT GGCATTTGGG AGTCCATGCC AGATCATGGT 1440
 GCTTCATGAG AGACTGACAG CTATCAGGGG TTGTGGCACT TAGTGAGGAC TCTCTCCCCC 1500
 CAGTGTGTGC TGATGACACA TACACACCTG ACAATAGCTT GAGTCTTCTC TGTTCCTTTT 1560
 ACTCTGTAGC CAACATACAC ATGATTTAAA ACCCTTTCTA AATATCTATC ATGGTTTCATC 1620
 CTTGTCCAAA TGCAGAGTCA GAGCTATTGT TACTTCATTA TTATTTCCAA GCGGAATAGT 1680
 TGGCTTTCTT TTGTCAAAAA TAAATTAAGT TTTTGTATGT TGCAAAAAAA AAAAAAAA 1740
 AAACAAAAAA

Seq ID NO: 117 DNA sequence
 Nucleic Acid Accession #: BC012178.1
 Coding sequence: 204-2285

1 11 21 31 41 51
 CTTCTCTCCC GCGCGCTGG GCGCCGCGCT CCGCTGCTGT TGCTCCATTC GCGCTTTTC 60
 TGGCGGCTGG CTCTCTCCG CTGCGGCTGG CTCTCGACC AGGCCTCCTT CTCAACCTCA 120
 GCCCGCGGCG CGACCCCTTC CGGCACCCCTC CCGCCCCGTC TCGTACTGTC GCGCTCACC 180
 CCGCGGCTCC GCGCCTGGCC CCGATGGCTC TGTGCAACGG AGACTCCAAG CTGGAGAATG 240
 CTGGAGGAGA CCTTAAGGAT GGCCACCACC ACTATGAAGG AGCTGTTGTC ATTCTGGATG 300
 CTGGTGCTCA GTACGGGAAA GTCATAGACC GAAGAGTGAG GGAAGTGTTC GTGCAGTCTG 360
 AAATTTTCCC CTTGGAACCA CCAGCATTTG CTATAAAGGA ACAAGGATTC CGTGCTATTA 420
 TCATCTCTGG AGGACCTAAT TCTGTGTATG CTGAAGATGC TCCCTGGTTT GATCCAGCAA 480
 TATTTCACTAT TGGCAAGCTT GTTCTTGGA TTTGCTATGG TATGCAGATG ATGAATAAGG 540
 TATTTGGAGG TACTGTGCAC AAAAAAAGTG TCAGAGAAGA TGGAGTTTTC AACATTAGTG 600
 TGGATAATAC ATGTTTCATTA TTCAGGGGCC TTCAGAAGGA AGAAGTTGTT TTGCTTACAC 660
 ATGGAGATAG TGTAGACAAA GTAGCTGATG GATTCAAGGT TGTGGCACGT TCTGGAAAAC 720
 TAGTAGCAGG CATAGCAAAAT GAATCTAAAA AGTTATATGG AGCACAGTTC CACCCGTAAG 780
 TTGGCCTTAC AGAAAATGGA AAAGTAATAC TGAAGAATTT CCTTTATGAT ATAGCTGGAT 840
 GCAGTGGAAC CTTACCCGTG CAGAACAGAG AACTTGAGTG TATTCGAGAG ATCAAAGAGA 900
 GAGTAGGCAC GTCAAAAGTT TTGTTTTTAC TCAGTGGTGG AGTAGACTCA ACAGTTTGTA 960
 CAGCTTTGCT AAATCGTGCT TTGAACCAAG AACAGTCAT TGCTGTGCAC ATTGATAATG 1020
 GCTTTATGAG AAAACGAGAA AGCCAGTCTG TTGAAGAGGC CCTCAAAAAG CTGGGAATTC 1080
 AGGTCAAAGT GATAAATGCT GCTCATCTT TCTACAATGG AACACAACCC CTACCAATAT 1140
 CAGATGAAGA TAGAACCCTA CGGAAAAGAA TTAGCAAAAC GTTAAATATG ACCACAAGTC 1200
 CTGAAGAGAA AAGAAAAATC ATTGGGGATA CTTTGTGTAA GATTGCCAAT GAAGTAATG 1260
 GAGAAATGAA CTTGAAAACA GAGGAGGTTT TCCCTGCCCA AGGTACTTTA CCGCCTGATC 1320
 TAATTGAAAG TGCATCCCTT GTTGCAAGTG GCAAAGCTGA ACTCATCAAA ACCCATCACA 1380
 ATGACACAGA GCTCATCAGA AAGTTGAGAG AGGAGGGAAA AGTAATAGAA CCTCTGAAAG 1440
 ATTTTCATAA AGATGAAGTG AGAATTTGG GCACAGAACT TGGACTTCCA GAAGAGTTAG 1500
 TTTCCAGGCA TCCATTTCCT GGCTCTGGCC TGGCAATCAG AGTAATATGT GCTGAAGAAC 1560
 CTTATATTGG TAAGGACTTT CCTGAAACCA ACAATATTTT GAAAATAGTA GCTGATTTT 1620
 CTGCAAGTGT TAAAAAGCCA CATACCCCTAT TACAGAGAGT CAAAGCCTGC ACAACAGAAG 1680
 AGGATCAGGA GAAGCTGATG CAAATTACCA GTCTGCATTC ACTGAATGCC TTCTTGCTGC 1740
 CRAATTAAC TGTAGGTGTG CAGGGTGACT GTCGTTCTTA CAGTTACGTG TGTGGAATCT 1800
 CCAGTAAAGA TGAACCTGAC TGGGAATCAC TTATTTTCTT GGCTAGGCTT ATACCTCGCA 1860
 TGTGTACAAA CGTTAACAGA GTTGTATTATA TATTTGGCCC ACCAGTTAAA GAACCTCCTA 1920
 CAGATGTTAC TCCACTTTC TTGACAACAG GGGTGCTCAG TACTTTACGC CAAGCTGATT 1980
 TTGAGGCCCA TAACATCTC AGGAGTCTG GGTATGCTGG GAAATCAGC CAGATGCCGG 2040
 TGATTTTGAC ACCATTACAT TTTGATCGGG ACCCACTTCA AAAGCAGCCT TCATGCCAGA 2100
 GATCTGTGGT TATTGCAACC TTTATTACTA GTGACTTCAT GACTGGTATA CTGCAACAC 2160
 CTGGCAATGA GATCCCTGTA GAGGTGGTAT TAAAGATGGT CACTGAGATT AAGAAGATTC 2220
 CTGGTATTTT TCGAATTATG TATGACTTAA CATCAAAGCC CCCAGGAAC ACTGAGTGGG 2280
 AGTAATAAAC TTCTGTGTTT ATTAATA

Seq ID NO: 118 Protein sequence:
 Protein Accession #: AAH12178.1

1 11 21 31 41 51
 MALCNGSKL ENAGGDLKDG HHYEGAVVI LDAGAQYQKV IDRRVRELFV QSEIFPLETP 60
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 KSVREDFVFN ISVDNTCSLF RGLQKEEVLV LTHGDSVDKV ADGFKVVARV GNIVAGIANE 180
 SKKLYGAQFH PEVGLTENK VILKNFLYDI AGCSGTFVQ NRELECIREI KERVGTSKVL 240
 VLLSGGVDS VCTALLNRL NQEQVIAVHI DNGFMRKRES QSVEEALKKL GIQVKVINAA 300
 HSFYNGTTT LISDEDRTPR KRISKTLNMT TSPEEKRII GDTFVKIANE VIGEMNLKPE 360
 EVFLAQGTLR PDLIESASLV ASGKAELIKT HHNDTELIRK LREEGKVIEP LKDFHKDEV 420
 ILGRELGLPE ELVSRHPPFG PGLAIRVICA EEPYICKDFP ETNNILKIVA DPSASVKKPH 480
 TLLQRVKACT TEEDQEKLMQ ITSLSHSLNAP LLPIKTVGVQ GDCRSYSYVC GISSKDEPDW 540
 ESLIFLARLI PRMCHNVNRV VYIFGPPVKE PPTDVTPTFL TGTGLSTLRQ ADFEAHNILR 600
 ESGYAGKISQ MPVILTPLHF DRDPLQKQPS QRSVVIPTF ITSDFMGTIP ATPGNEIPVE 660
 VVLKMWTEIK KIPGISRIMY DLTSKPPGTT EWE

Seq ID NO: 119 DNA sequence
 Nucleic Acid Accession #: NM_006500.1
 Coding sequence: 27..1967

1 11 21 31 41 51
 ACTTGCTCTC GCGCCTCCGG CCAAGCATGG GGCTTCCAG GCTGGTCTGC GCCTTCTTGC 60
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 CGCTGAGCT GTGGAGGTG GAAGTGGGCA GCACAGCCCT TCTGAAGTGC GGCCTCTCCC 180
 AGTCCCAAGG CAACCTCAGC CATGTCGACT GGTTTTCTGT CCACAAGGAG AAGCGGACGC 240

	TCATCTTCCG	TGTGCGCCAG	GGCCAGGGCC	AGAGCGAACC	TGGGGAGTAC	GAGCAGCGGC	300
	TCAGCCTCCA	GGACAGAGGG	GCTACTCTGG	CCCTGACTCA	AGTCACCCCC	CAAGACGAGC	360
	GCATCTTCTT	GTGCCAGGGC	AAGCGCCCTC	GGTCCCAGGA	GTACCGCATC	CAGTCCGCG	420
5	TCTACAAAGC	TCCGAGGAG	CCAAACATCC	AGGTCAACCC	CCTGGGCATC	CCTGTGAACA	480
	GTAAGGAGCC	TGAGGAGGTC	GCTACCTGTG	TAGGGAGGAA	CGGGTACCCC	ATTCTCAAG	540
	TCATCTGGTA	CAAGAAATGG	CGGCCTCTGA	AGGAGGAGAA	GAACCGGGTC	CACATTCAGT	600
	CGTCCAGAC	TGTGGAGTCG	AGTGGTTTGT	ACACCTTGCA	GAGTATTCTG	AAGGCACAGC	660
	TGGTTAAAGA	AGACAAAGAT	GCCCAAGTTT	ACTGTGAGCT	CAACTACCCG	CTGCCCCAGT	720
10	GGAACCAT	GAAGGAGTCC	AGGGAAGTCA	CCGTCCCTGT	TTTCTACCCG	ACAGAAAAAG	780
	TGTGGCTGGA	AGTGGAGCCC	GTGGGAATGC	TGAAGGAAGG	GGACCGCGTG	GAAATCAGGT	840
	GTTTGGCTGA	TGGCAACCTC	CCACCACACT	TCAGCATCAG	CAAGCAGAAC	CCCAGCACC	900
	GGGAGGCAGA	GGAAGAGACA	ACCAACGACA	ACGGGGTCCT	GGTGTGGAG	CCTGCCCGGA	960
	AGGAACACAG	TGGGCGCTAT	GAAATGTGAG	CCTGGAACCT	GGACACCATG	ATATCGCTGC	1020
	TGAGTGAAAC	ACAGGAACCT	CTGGTGAAGT	ATGTGTCTGA	CGTCCGAGTG	AGTCCCGCAG	1080
15	CCCCTGAGAG	ACAGGAAGGC	AGCAGCCTCA	CCCTGACCTG	TGAGGCAGAG	AGTAGCCAGG	1140
	ACCTCGAGTT	CAAGTGGCTG	AGAGAAGAGA	CAGACCAAGT	GCTGGAAAGG	GGGCGTGTGC	1200
	TTCAAGTTGCA	TGACCTGAAA	CGGAGGCGAG	GAGGCGGCTA	TGCTCGCTG	CGCTCTGTGC	1260
	CCAGCATACC	CGGCCTGAAC	CGCACACAGC	TGGTCAAGCT	GGCCATTTT	GGCCCCCTTT	1320
20	GGATGGCATT	CAAGGAGAGG	AAGGTGTGGG	TGAAAGAGAA	TATGGTGTG	AATCTGTCTT	1380
	GTGAAGCGTC	AGGGCACCCC	CGGCCACCA	TCTCTGGAA	CGTCAACGGC	ACGGCAAGTG	1440
	AACAAGACCA	AGATCCACAG	CGAGTCTCTG	GCACCTTGAA	TGTCCTCGTG	ACCCCGGAGC	1500
	TGTTGGAGAC	AGGTGTTGAA	TGCACGGCCT	CCAACGACCT	GGGCAAAAAC	ACCAGCATCC	1560
	TCTTCTCTGA	GCTGGTCAAT	TTAACCAACC	TCACACAGAG	CTCCAACACA	ACCCTGGGCC	1620
	TCAGCACTTC	CAGTCCAGGT	CCTCATACCA	GAGCCAACAG	CACCTCCACA	GAGAGAAAGC	1680
25	TGCCGGAGCG	GGAGAGCCGT	GGCGTGGTCA	TGCTGGCTGT	GATTGTGTGC	ATCCTGGTCC	1740
	TGGCGGTGCT	GGGCGCTGTC	CTCTATTTCC	TCTATAAGAA	GGGCAAGCTG	CCGTGCAGGC	1800
	GCTCAGGGAA	GCAGGAGATC	ACGCTGCCCC	CGTCTCGTAA	GACCGAATTT	GTAGTTGAAG	1860
	TTAAGTCAGA	TAAGTCCCA	GAAGAGATGG	GCCTCTGCA	GGGCAGCAGC	GGTGACAAGA	1920
	GGGCTCCGGG	AGACCAGGGA	GAGAAATACA	TCGATCTGAG	GCATTAGCCC	CGAATCACTT	1980
30	CAGCTCCCTT	CGCTCCCTGG	ACCATTTCCA	GCTCCCTGCT	CACCTCTTCT	TCAGCCAAAG	2040
	CCTCCAAAGG	GACTAGAGTT	AAGCCTCCTG	CTCCCTCCAC	CTGCACACCC	CCTTTCAGAG	2100
	GGCCACTGGG	TTAGGACCTG	AGGACCTCAC	TTGGCCCTGC	AAGCCGCTTT	TCAGGGACCA	2160
	GTCCACCACC	ATCTCTCTCA	CGTTGAGTGA	AGCTCATCCC	AAGCAAGGAG	CCCCAGTCTC	2220
35	CCGAGCGGGT	AGGAAGGTTT	CTTGACAGAAC	GTGTTTTTTC	TTTACACACA	TTATGGCTGT	2280
	AAATACCTGG	CTCCTGCCAG	CAGCTGAGCT	GGGTAGCCTC	TCTGAGCTGG	TTTCTGCCCC	2340
	CAAGAGCTGG	CTTCCACCAT	CCAGGTGCAC	CACTGAAGTG	AGGACACACC	GGAGCCAGGC	2400
	GCCTGCTCAT	TTTGAAGTGC	GCTGTTTACA	CCCGCTCCGG	AGAGCACCCC	AGCGGCATCC	2460
	AGAAGCAGCT	GCAGTGTGTC	TGCCACCACC	CTCCTGCTCG	CCTCTTCAAA	GTCTCTGTGT	2520
40	ACATTTTTTC	TTTGGTCAGA	AGCCAGGAAC	TGGTGTCAAT	CCTTAAAGA	TACGTGCCGG	2580
	GGCCAGGTGT	GGTGGCTCAC	GCCTGTAATC	CCAGCACTTT	GGGAGGCCGA	GGCGGGCGGA	2640
	TCACAAAGTC	AGGACGAGAC	CATCCTGGCT	AACACGGTGA	AACCTGTCT	CTACTAAAAA	2700
	TACAAAAAAA	AATTAGCTAG	CGGTAGTGGT	TGGCACCTAT	AGTCCCAGCT	ACTCGGAAGG	2760
	CTGAAGCAGG	AGAAATGGAT	GAAATCCAGG	GGTGGAGCTT	GCAGTGAGCC	GAGACCGTGC	2820
45	CAGTGCACCT	CAGCCTGGGC	AACACAGCGA	GACTCCGCTC	CGAGGAAAAA	AAAAGAAAAA	2880
	ACCGTACCT	GGGCTGAGGA	AGCTGGGCGC	TGTTTTCCAG	TTCAAGGTGA	TTAGCCTCAA	2940
	TCCCGTGT	CAGTGTCTCC	CATAGCCCTC	TTGATGGATC	ACGTAAAACT	GAAAGGCAGC	3000
	GGGAGCAGA	CAAAGATGAG	GTCTACACTG	TCCTTCATGG	GGATTAAAGC	TATGGTTATA	3060
	TTAGACCAA	ACTTCTACAA	ACCAAGCTCA	GGGCCCCAAC	CCTAGAAGGG	CCCAATAGAG	3120
50	AGAAATGGTAC	TTAGGATGAG	AAAACGGGGC	CTGGCTAGAG	CTTCGGGTGT	GTGTGTCTGT	3180
	CTGTGTGTAT	GCATACATAT	GTGTGTATAT	ATGGTTTTGT	CAGGTGTGTA	AATTTGCAAA	3240
	TTGTTTCTT	TATATATGTA	TGTATATATA	TATATGAAAA	TATATATATA	TATGAAAAAT	3300
	AAAGCTTAAT	TGTCACAGAA	AATCATACAT	TGCTTTTTTA	TTCTACATGG	GTACCACAGG	3360
	AACCTGGGGG	CCTGTGAAAC	TACAACCAAA	AGGCACACAA	AACCGTTTCC	AGTTGGCAGC	3420
55	AGAGATCAGG	GGTTACCTCT	GCTTCTGAGC	AAATGGCTCA	AGCTCTACCA	GAGCAGACAG	3480
	CTACCTACT	TTTCAGCAGC	AAAACGTCCC	GTATGACGCA	GCACGAAGGG	CCTGGCAGGC	3540
	TGTTAGCAGG	AGCTATGTCC	CTTCTATCG	TTTCCGTCCA	CTT		

Seq ID NO: 120 Protein sequence:
Protein Accession #: NP_006491.1

65	1	11	21	31	41	51	
	MGLPRLVCAF	LLAACCCCPR	VAGVPGEAEQ	PAPELVEVEV	GSTALLKCGL	SQSQGNLSHV	60
	DWFSVHKR	TLIFVRVQSQ	GQSEPEGEYQ	RLSLQDRGAT	LALTQVTPQD	ERIFLQCKR	120
	PRSQEYRIQL	RUYKAPPEFN	IQVNLPIPV	NSKEPEEVAT	CVGRNGYPIPI	QVIWYKNGRP	180
	LKEEKNRVHI	QSSQTVESSG	LYTLQSLKA	QLVKEDKDAQ	FYCELNRYLP	SGNHMKESRE	240
70	VTVPVPYPT	KVWLEVEPVG	MLKEGDRVEI	RCLADGNPPP	HFSISKQNP	TREAEETTN	300
	DNGVLVLEPA	RKEHSGRYEC	QAWNLDTMIS	LLSEPEQLLV	NYVSDVRVSP	AAPERQEGSS	360
	LTLTCEAESS	QDLFQWLRE	ETDQVLERGP	VLQLHDLKRE	AGGGYRCVAS	VPSIPGLNRT	420
	QLVKLAIFGP	PWMAFKERKV	WVKENMVLNL	SCEASGHPRP	TISWNVNGTA	SEQDQDPQRV	480
	LSTLNLVFTP	ELLETVGECT	ASNDLGKNTS	ILFLELVNLT	TLTPDSNTTT	GLSTSTASPH	540
75	TRANSTSTER	KLPEPESRGV	VIVAVIVCIL	VLAVLGAVLY	FLYKKGKLP	RRSGKQEITL	600
	PPSRKTELTV	EVKSKDLPEE	MGLLQSSGD	KRAPGDQGEK	YIDLRLH		

Seq ID NO: 121 DNA sequence
Nucleic Acid Accession #: NM_018306
Coding sequence: 60-671

80	1	11	21	31	41	51	
	ATAGTCTACA	CAGAGCTCCC	CTTGCTGCCC	AGACAAGCTG	AAGGACCACA	GGAAAAAGCCA	60
	TGGAGACTTC	AGCATCTCTC	TCCCAGCCTC	AGGACAACAG	TCAAGTCCAC	AGAGAAACAG	120
85	AAGATGTAGA	CTATGGAGAG	ACAGATTTC	ACAAGCAAGA	CGGGAAGGCT	GGACTCTTTT	180
	CCCAAGAACA	ATATGAGAGA	AACAAGTCTT	CTTCTCTCTC	CTTCTCTTCC	TCCTCATCCT	240
	CCTCATCTTC	TTCATCTCTC	TCCTCTCTCAG	GTCCTGGGCA	TGGGGAGCCT	GACGTTTTGA	300

5
10
15
20

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AGGATGAGCT TCAACTCTAT GGAGATGCTC CTGGAGAGGT GGTACCCTCT GGGGAATCAG 360
GACTCCGAAG GAGAGGCTCT GACCCAGCAA GTGGAGAAAGT GGAGGCCTCT CAGTTAAGAA 420
GACTGAATAT AAAGAAAGAT GATGAGTTTT TCATTTCGT CCTCCTGTGC TTTGCCATCG 480
GGGCTTGTCT GGTGTGTTAT CACTATTACG CAGACTGGTT CATGTCTCTT GGGGTGCGCC 540
TGCTCACCTT CGCCTCCCTG GAAACCGTTG GCATCTACTT CGGACTAGTG TACCGTATCC 600
ACAGCGTCTT CCAAGGCTTC ATCCCCTCTT TCCAGAAGTT TAGGCTGACA GGGTTCAGGA 660
AGACTGACTG AGGCCACTTC CAGGTGGGCA GCAGAGGCAG GCCCAGTGT GACCACCACT 720
GCGACCCCTG AGCCCAACAG GGCAGAGCAG CATTCTGAGA GACGCACAGG AGACCAAGCC 780
AGACCAATAA ACAGAACACT TTTCTTCCA TGTGCTCTGA ATGTTGGCAC CAGCCCGGGC 840
AGGGGCATCT CATTTGGGCA GTACTGCTGT GCAACCCAGC TGCAAGGATG GAAGGCAGAG 900
GGTGGGTGTG GGGCTGAGG CTTCACAGTA CCTGGACCAG CAGGAAGATT CTGGGAGGTC 960
ACTGCTCTCA GAGGACAGCA AGGGACCTCT AGCTCTGCAA GCTGTGATCT GTCTGGGTTT 1020
ATGGTTTTTC TCAATCCCA GGTATCTGCT ATGCGCTCTC AGGTGCTACC GAGCCATCCT 1080
GGGAGAGATG GATGTTCCAC TGCTTTGAGG CAGGGAGCCA TCGGCTGGG GCCCTTGGT 1140
GAACCTGATG CAGTAAGAT GCTGAGGACT AAAACCATTT TTTTTCAGCC CAAAAAATAA 1200
GGCAGGAAAA TGATCATCAG AAATAAATG GCAGCCAGGC ATGGGGGCTC ACGACTGTAA 1260
TCCTCGCACT TTGGGAGGCT CAGGCTAAGG GTCGCTTGAA GCTGAGAGTT CAAGACCAAC 1320
CTGGGCAACA TAGTGAGACC CCCATCTCTA CAATTTTTTT TTAATGACCA AATGTGGCGG 1380
TACATACCTG TACATACCTG CGGTTCAGC TACTCAAGAG GCTGAGGCAG GAGGACTGCT 1440
TGAGCCACAG AGTTTCAGGC TGCAGTGAGG TACGATCAAG CCACCTGCACT CCAGCCTGGG 1500
CGACAGAGCA AGATCGTTTC TCTAAAATT

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25 Seq ID NO: 122 Protein sequence:
Protein Accession #: NP_060776

30

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1 11 21 31 41 51
| | | | |
METSASSSQP QDNSQVHRET EDVDYGETDF HKQDGKAGLF SQEQYERNKS SSSSFSSSSS 60
SSSSSSSSSS GPFGHEPDLV KDELQLYGDA PGEVVPSEGS GLRRRGSDDPA SGEVEASQLR 120
RLNIKKDDEF FHFVLLCFAI GALLVCYHYW ADWFMSLGVG LLTFASLETV GIYFGLVYRI 180
HSVLQGFPL FQKRLTGFR KTD

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35 Seq ID NO: 123 DNA sequence
Nucleic Acid Accession #: BC022542
Coding sequence: 243..896

40
45
50
55
60
65
70

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1 11 21 31 41 51
| | | | |
ACTTGGTCCC AGCCGATAAA TCTGGGGCAG CGCGCGGTAG GAGCTGCGGG CGGCCAGGCC 60
CCTTCTCTCG TCCGCACCTG GCCCCGCGCG CCCCTCTCGG GCGTCCGGCT TCCGGCGTCC 120
TGGCGGCTCG GGTGGCGCGG GTTCGGGCGG CCGCCTGGCT GCTCCTCGGG GCGGCGACGG 180
GGCTCAGCGG CGGGCCCGCG ACGCCCTTCA CCGCGCGCGG CTCTGACGCC GGCATAAGGG 240
CCATGTGTTT TGAAATTATT TTGAGGCAAG AAGTTTGTAA AGATGGTTTC CACAGAGACC 300
TTTAAATCAA AGTGAAGTTT GGGGAAAGCA TTGAGGACTT GCACACGTGC CGTCTCTTAA 360
TTAAACAGGA CATTCTGCA GGACTTTATG TGGATCCGTA TGAGTTGGCT TCATTACGAG 420
AGAGAAACAT AACAGAGGCA GTGATGGTTT CAGAAAATTT TGATATAGAG GCCCTAACT 480
ATTTGTCCAA GGAGTCTGAA GTTCTCATTT ATGCCAGAGC AGATTACAG TGCATTGACT 540
GTTTTCAAGC TTTTTGCCT GTGCACTGCC GCTATCATCG GCCGCACAGT GAAAGTGGAG 600
AAGCCTCGAT TTGGTCAAT AACCCAGATT TGTGTATGTT TTGTGACCAA GAGTTCCTGA 660
TTTGAATG CTGGGCTCAC TCAGAAAGTG CAGCCCTTGG TGGCTTGGAT AATGAGGATA 720
TATGCCAATG GAACAAGATG AAGTATAAAT CAGTATATAA GAATGTGATT CTACAAGTTC 780
CAGTGGGACT GACTGTACAT ACCTCTCTAG TATGTTCTGT GACTCTGTCT ATTACAATCC 840
TGTGCTCTAC ATTGATCCTT GTAGCAGTTT TCAATATGCG CCAATTTTCC CTATAAGTTT 900
TATGTAGTTA AATGCTTCTT AGAAACCTAA ATAAGATCTA TTAATTTCTG ACGAGAGGTG 960
TTCTTCTAGA ATTAATTACT TTTATCTTTT GTCTTCATTT GTGGCCAAAA TTATGTTTAC 1020
TAGAGGAAT TTGGGATCAT TCTCAGCTAA TTCCAAAATG TAGTGCTCTA TTGCATGGAT 1080
CCTTGGTAAT CCTCAAGCAT CAGATGCCAT AAGGGGAAAC TTAATTTCTG TAAATTAATG 1140
TTTATTTTGT GAGAAGTGAC TTTATCTTCA TTTGGGGTAG AAAAATTATT TCTTTATGTA 1200
GTAGAGACAA ATTATTCTCA TTTTGCAAGT ACTTTCAATT TAAGTACAAA ATTGAGAAAA 1260
CCGTTATAAA TAAGAATAAA ATAGGCCAGG CACAGTGGCT CACACCTGTA ATCCAGCAC 1320
TTTGGGAGCG CGAGGTGGCG GGAATCACCAG AGGTCAAGAG TTTGAGACCA GCTTGGTGAA 1380
ACCTGTCTCT TACTAAAAAT ACAAAAGTTA GCTGGGGCTG GTGGTGGGCA TCTGTAGTCC 1440
CAGCTAATTG GAAGGGTGAG GCGGGAGGAT CGCTTGAACC TGGGAGGCGG AGGTTCCAGA 1500
GAGCCAGAT CGCACCACTG CACTACAGCC TGGGCGACAG AACGAGACCC TGCTCCAAA 1560
GGAAAAACAA AAAAGAAGAA TAAATAAATT TGGATGAAAA TCATGTTTAT TTAATAGTA 1620
ATGTCATGAG ACTATTAAAG ATGTGCCAGA GTTCAATGA AAATCATTAA AGTAGGACAG 1680
CTAAGAAATT AATATTAATA TAAAAATTAT TGATAATCTT AAATTATTGA TTATTCCTTA 1740
ACGCACTCCA TTCTCTTTT ACATTTTATC ATGTTTCTTT TGAATATATG AATTGGCAAA 1800
GGACTTGATG AAAGTGAAGT CTAAGATTG GTACAGAGTA TGTGAGGAAG ACAACTCAGA 1860
TTGCCATTTT AATAAAGTT GTACATGAAC AAAAAAATAA AAAAAA

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75 Seq ID NO: 124 Protein sequence:
Protein Accession #: AAH22542

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1 11 21 31 41 51
| | | | |
MCSEILRQE VLKDGPHRDL LIKVKFGESI EDLHTCRLLI KQDIPAGLYV DPYELASLRE 60
RNITEAVMVS ENFDIEAPNY LSKSEVLIY ARRDSQCIDC FQAFIPVHCR YHRPHSEEDGE 120
ASIVVNNPDL LMFCDQAGSR RMIRFRFDSF DKTIEFPILK CWAHSEVAAP CALENEDICQ 180
WNKMKYKSVY KNVILQVPVG LTVHTSLVCS VTLLITILCS KKKKK

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85 Seq ID NO: 125 DNA sequence
Nucleic Acid Accession #: NM_004994.1
Coding sequence: 20..2143

	1	11	21	31	41	51	
	AGACACCTCT	GCCCTCACCA	TGAGCCTCTG	GCAGCCCTG	GTCCTGGTGC	TCCTGGTGTCT	60
	GGGCTGCTGC	TTTGCTGCCC	CCAGACAGCG	CCAGTCCACC	CTTGTGCTCT	TCCCTGGAGA	120
5	CCTGAGAAC	AATCTCACCG	ACAGGCAGCT	GGCAGAGGAA	TACCTGTACC	GCTATGGTTA	180
	CACTCGGGTG	GCAGAGATGC	GTGGAGAGTC	GAATCTCTG	GGGCTGCGC	TGCTGCTTCT	240
	CCAGAAGCAA	CTGTCCCTGC	CCGAGACCGG	TGAGCTGGAT	AGCGCCACGC	TGAAGGCCAT	300
	GCGAACCCCA	CGGTGCGGGG	TCCCAGACCT	GGGAGATTTC	CAAACCTTTG	AGGGCGACCT	360
	CAAGTGGCAC	CACCACAACA	TCACCTATTG	GATCCAAAAC	TACTCGGAAG	ACTTGCCGCG	420
10	GGCGGTGATT	GACGACGCGT	TTGCCGCGCG	CTTCGCACTG	TGGAGCGCGG	TGACGCGCGT	480
	CACCTTCACT	CGCGTGTACA	GCCGGGACGC	AGACATCGTC	ATCCAGTTTG	GTGTGCGGGA	540
	GCACGGAGAC	GGGTATTCCTT	TCCAGCGGAA	GGACGGGCTC	CTGGCACACG	CCTTTCCTCC	600
	TGGCCCCGGC	ATTGAGGGAG	ACGCCCATTT	CGACGATGAC	GAGTTGTGGT	CCCTGGGCAA	660
	GGGCGTCGTG	GTTCCAATCT	GGTTTGAAA	CGCAGATGGC	GCGGCTGCGC	ACTTCCCTCT	720
15	CATCTTCGAG	GGCGCTCCT	ACTCTGCTG	CACCACCGAC	GGTCGCTCGG	ACGGCTTGCC	780
	CTGGTGCAGT	ACCAACGGCA	ACTACGACAC	CGACGACCGG	TTTGGCTTCT	GCCCCAGCGA	840
	GAGACTCTAC	ACCCGGGACG	GCAATGCTGA	TGGGAAACCC	TGCCAGTTTC	CATTCACTTT	900
	CCAAGGCCAA	TCCTACTCCG	CTCTGACACC	GGACGGTCGC	TCCAGCGGCT	ACCGCTGGTG	960
	CGCCACCACC	GCCAACGGCA	ACCGGGACAA	GCTCTTCGGC	TTCTGCCCCA	CCCGAGCTGA	1020
20	CTCGACGGTG	ATGGGGGGCA	ACTCGGCGGG	GGAGCTGTGC	GTCTTCCCCT	TCACTTTCCT	1080
	GGGTAAAGAG	TACTCGACCT	GTACACGCGA	GGGCCGCGGA	GATGGGCGCC	TCTGGTGCGC	1140
	TACCACCTCG	AACCTTGACA	GCGACAAGAA	GTGGGGCTTC	TGCCCGGACC	AAGGATACAG	1200
	TTTGTTCCTC	GTGGCGGCGC	ATGAGTTCGG	CCACGCGCTG	GGCTTAGATC	ATTCTCAGT	1260
	GCCGGAGGCG	CTCATGTACC	CTATGTACCG	CTTCACTGAG	GGGCCCCCTC	TGCATAAGGA	1320
25	CGACGTGAAT	GCCATCGGCG	ACCTCTATGG	TCCTCGCCCT	GAACCTGAGC	CACGGCCTCC	1380
	AACCACCACC	ACACCGCAGC	CCACGGCTCC	CCGACGGTTC	TGCCCCACCG	GACCCCCCAC	1440
	TGTCCACCCC	TCAGAGCGCC	CCACAGCTGG	CCCCACAGGT	CCCCCTCAG	CTGGCCCCAC	1500
	AGGTCCCCCC	ACTGCTGGCC	CTTCTACGGC	CACTACTGTG	CCTTTGAGTC	CGGTGGACGA	1560
	TGCTTGCAAC	GTGAACATCT	TCGACGCCAT	CGCGGAGATT	GGGAACCAAG	TGTATTTGTT	1620
30	CAAGGATGGG	AAGTACTGGC	ATTCTCTGA	GGGCAGGGGG	AGCCGCGCCG	AGGGCCCCCT	1680
	CCTTATCGCC	GACAAGTGGC	CGCGCTGCGC	CGCAAGCTG	GACTCGGTCT	TTGAGGAGCC	1740
	GCTCTCCAAG	AAGCTTTTCT	TCTTCTCTGG	GCGCCAGGTG	TGGGTGTACA	CAGGCGCGTC	1800
	GGTGTCTGGC	CCGAGGCGTC	TGGACAAGCT	GGGCTGGGGA	GCCGACGTGG	CCGAGGTGAC	1860
35	CGGGGCCCTC	CGGAGTGGCA	GGGGGAAGAT	GCTGCTGTTT	AGCGGGCGCG	GCCTCTGGAG	1920
	GTTCGACGTG	AAGGCGCAGA	TGGTGGATCC	CCGGAGCGCC	AGCGAGGTGG	ACCGGATGTT	1980
	CCCCGGGGTG	CCTTTGAGCA	GCGACGACGT	CTTCCAGTAC	CGAGAGAAAG	CCTATTTCTG	2040
	CCAGGACCGC	TTCTACTGGC	CGGTGAGTTC	CCGGAGTGAG	TTGAACCAAG	TGGACCAAGT	2100
	GGGCTACGTG	ACCTATGACA	TCCTGCACTG	CCCTGAGGAC	TAGGGCTCCC	GTCTGCTTTT	2160
	GCAGTGCCAT	GTAATATCCC	ACTGGGACCA	ACCCTGGGGA	AGGAGCCAGT	TTGCCGGATA	2220
40	CAAACTGSTA	TTCTGTCTTG	GAGGAAAGGG	AGGAGTGGAG	GTGGGCTGGG	CCCTCTCTTC	2280
	TCACCTTGT	TTTTTGTGG	AGTGTCTCTA	ATAAACTTGG	ATTCTCTAAC	CTTT	

Seq ID NO: 126 Protein sequence:
Protein Accession #: NP_004985.1

	1	11	21	31	41	51	
	MSLWQPLVLV	LLVLGCCFAA	PRQRQSTLVL	FPGDLRLNLT	DRQLAEEVLY	RYGYTRVAEM	60
	RGESKSLGPA	LLLLQKQLSL	PETGELDSAT	LKAMRTPRCG	VPDLGRFQTF	EGDLKWHHHN	120
50	ITYWIQNYSE	DLPRVIDDA	FARAFALWSA	VTPLTFTRVY	SRDADIVIQF	GVAEHGDGYP	180
	FDGKDGLLAH	AFPPGPGIQG	DAHFDDDELW	SLGKGVVVPT	RFGNADGAAC	HFPFIFEGRS	240
	YSACTTDGRS	DGLFWCSTTA	NYTDDRFGF	CPSERLYTRD	GNADGKPCQF	PFIFQGQSYS	300
	ACTTDRSDG	YRWCAATTANY	DRDKLFGFCP	TRADSTVMGG	NSAGELCVFP	FTPLGKEYST	360
55	CTSEGRGDGR	LWCATTNFD	SDKKWGFCPD	QGYSLFLVAA	HEFGHALGLD	HSSVPEALMY	420
	PMYRFTGPP	LHKDDVNGIR	HLYGPRPEPE	PRPPTTTTPQ	PTAPPTVCPT	GPPTVHPSER	480
	PTAGPTGPPS	AGPTGPPTAG	PSTATTVPLS	PVDDACNVNI	FDIAIEIGNQ	LYLPKDGKYW	540
	RFSEGRGSRP	QGPFLLADKW	PALPRKLDV	FEEPLSKKLF	FFSGRQVWVY	TGASVLGPRR	600
	LDKLGGLADV	AQVTGALRS	RGMMLFSGR	RLWRFDVKAQ	MVDPRSASEV	DRMFPVPLD	660
60	THDVQYREK	AYFQDRFYV	RVSRSSELNQ	VDQVGYVTYD	ILQCPED		

Seq ID NO: 127 DNA sequence
Nucleic Acid Accession #: NM_004181
Coding sequence: 32-670

	1	11	21	31	41	51	
	GCAGAAATAG	CCTAGGGAGA	TCAACCCCGA	GATGCTGAAC	AAAGTGCTGT	CCCGGCTGGG	60
	GGTCGCGGCG	CAGTGGCGCT	TCGTGGACGT	GCTGGGGCTG	GAAGAGGAGT	CTCTGGGCTC	120
70	GGTGCCAGCG	CCTGCCTGCG	CGCTGCTGCT	GCTGTTTCCC	CTCACGGCCC	AGCATGAGAA	180
	CTTCAGGAAA	AAGCAGATTG	AAGAGCTGAA	GGGACAAGAA	GTTAGTCCTA	AAGTGTACTT	240
	CATGAAGCAG	ACCATTGGGA	ATTCTGTGG	CACAATCGGA	CTTATTACAG	CAGTGGCCAA	300
	TAATCAAGAC	AAACTGGGAT	TTGAGGATGG	ATCAGTTCTG	AAACAGTTTC	TTTCTGAAAC	360
	AGAGAAAATG	TCCCTGAAG	ACAGAGCAAA	ATGCTTTGAA	AAGAATGAGG	CCATACAGGC	420
75	AGCCCATGAT	AGCGTGGCAC	AGGAAGGCCA	ATGTCGGGTA	GATGACAAGG	TGAATTTCCA	480
	TTTTATTCTG	TTTAACAACG	TGATGGGCCA	CCTCTATGAA	CTTGATGGAC	GAATGCCTTT	540
	TCCGTGAAC	CATGGCGCCA	GTTCAAGGGA	CACCTGCTG	AAGGACGCTG	CCAAGGTGTG	600
	CAGAGAATTG	ACCGAGCGTG	AGCAAGGAGA	AGTCCGCTTC	TCTGCCGTGG	CTCTCTGCAA	660
	GGCAGCCTAA	TGCTCTGTGG	GAGGGACTTT	GCTGATTTC	CCTCTTCCCT	TCAACATGAA	720
80	AATATATACC	CCCATGACG	TCTAAAATGC	TTCACTACTT	GTGAAACACA	GCTGTTCTTC	780
	TGTTCTGCAG	ACCGCCTTTC	CCCTCAGCCA	CACCCAGGCA	CTTAAGCACA	AGCAGAGTGC	840
	ACAGCTGTCC	ACTGGGCCAT	TGTGGTGTGA	GCTTCAGATG	GTGAAGCATT	CTCCCCAGTG	900
	TATGTCTTGT	ATCCGATATC	TAACGCTTTA	AATGGCTACT	TTGGTTTCTG	TCTGTAAAGT	960
85	AAGACCTTGG	ATGTGGTTAT	GTGTCTCTAA	AGAATAAATT	TTGCTGATAG	TAGC	

Seq ID NO: 128 Protein sequence:
Protein Accession #: NP_004172

1	11	21	31	41	51	
MLNKVLSRLG	VAGQWRFDV	LGLEESLGS	VPAPACALLL	LPPLTAQHEN	FRKKQIEELK	60
GQEVSPKVPYF	MKQITIGNSCG	TIGLIHAVAN	NQDKLGFEDG	SVLKQFLSET	EKMSPEDRAX	120
CFEKNEAIIQA	AHDAVAQEGQ	CRVDDKVNFIH	FILENNVDGH	LYELDGRMPF	PVNHGASSED	180
TLLKDAAKVC	REFTEREQGE	VRFSAVALCK	AA			

Seq ID NO: 129 DNA sequence
Nucleic Acid Accession #: NM_000213
Coding sequence: 127-5385

15	1	11	21	31	41	51	
	CGCCCGCGCG	CTGCAGCCCC	ATCTCCTAGC	GGCAGCCAG	GCGCGGAGGG	AGCGAGTCCG	60
	CCCCGAGGTA	GGTCCAGGAC	GGGCGCACAG	CAGCAGCCGA	GGCTGGCCGG	GAGAGGGAGG	120
	AAGAGGATGG	CAGGSCCAGC	CCCCAGCCCA	TGGGCCAGGC	TGCTCCTGGC	AGCCTTGATC	180
	AGCGTCAGCG	TCTCTGGGAC	CTTGGCAAAAC	CGCTGCAAGA	AGGCCCCAGT	GAAGAGCTGC	240
	ACGGAGTGTG	TCCGTGTGGA	TAAGGACTGC	GCCTACTGCA	CAGACGAGAT	GTTCAGGGAC	300
20	CGCGCGTGA	ACACCCAGGC	GGAGCTGCTG	GCCGCGGGCT	GCCAGCGGGA	GAGCATCGTG	360
	GTCAATGGAG	GCAGCTTCCA	AATCACAGAG	GAGACCCAGA	TTGACACCAC	CCTGCGGCGC	420
	AGCCAGATGT	CCCCCAAGG	CCTGCGGGTC	CGTCTGCGGC	CCGGTGAGGA	GCGGCATTTT	480
	GAGCTGGAGG	TGTTTGAGCC	ACTGGAGAGC	CCCGTGGACC	TGTACATCCT	CATGGACTTC	540
	TCCAACCTCA	TGTCGATGA	TCTGGACAAC	CTCAAGAAGA	TGGGCGAGAA	CCTGGCTCGG	600
25	GTCCCTGAGCC	AGCTCACCAG	CGACTACACT	ATTGGATTGT	GCAAGTTTGT	GGACAAAGTC	660
	AGCGTCCCCG	AGACGGACAT	GAGGCCTGAG	AAGCTGAAGG	AGCCCTGGCC	CAACAGTGAC	720
	CCCCCTTCT	CCTTCAAGAA	CGTCATCAGC	CTGACAGAAG	ATGTGGATGA	GTTCCGGAAT	780
	AAACTGCAGG	GAGAGCGGAT	CTAGGCCAAC	CTGGATGCTC	CTGAGGGCGG	CTTCGATGCC	840
	ATCCTGCAGA	CAGCTGTGTG	CACGAGGGAC	ATTGGCTGGC	GCCCGGACAG	CACCCACCTG	900
30	CTGGTCTTCT	CCACCGAGTC	AGCCTTCCAC	TATGAGGCTG	ATGGCGCCAA	CGTCTGGCT	960
	GGCATCATGA	GCCGCAACGA	TGAACGGTGC	CACCTGGACA	CCACGGGCAC	CTACACCCAG	1020
	TACAGGACAC	AGGACTACCC	GTCCGTGCC	ACCCTGGTGC	GCCTGCTCGC	CAAGCACAAC	1080
	ATCATCCCCA	TCTTTGTGTG	CACCAACTAC	TCTATAGCT	ACTACGAGAA	GCTTCAACAC	1140
	TATTTCCCTG	TCTCTCACT	GGGGTGTCTG	CAGGAGGACT	CGTCCAACAT	CGTGGAGCTG	1200
35	CTGGAGGAGG	CCTTCAATCG	GATCCGCTCC	AACCTGGACA	TCCGGGCCCT	AGACAGCCCC	1260
	CGAGGCCTTC	GGACAGAGGT	CACCTCCAAG	ATGTTCCAGA	AGACGAGGAC	TGGGTCCTTT	1320
	CACATCCGGC	GGGGGGAAGT	GGGTATATAC	CAGGTGCAGC	TGCGGGCCCT	TGAGCACGTG	1380
	GATGGGACGC	ACGTGTGCCA	GCTGCCGGAG	GACCAGAAGG	GCAACATCCA	TCTGAAACCT	1440
	TCCTTCTCCG	ACGGCCTCAA	GATGGACGCG	GGCATCATCT	GTGATGTGTG	CACCTGCGAG	1500
40	TCGCAAAAAG	AGGTGCGGTG	AGCTCGCTGC	AGCTTCAACG	GAGACTTCGT	GTGCGGACAG	1560
	TGTGTGTGCA	GCGAGGGCTG	GAGTGGCCAG	ACCTGCAACT	GCTCCACCGG	CTCTCTGAGT	1620
	GACATTGAGC	CCTGCCTGCG	GGAGGGCGAG	GACAAGCCGT	GCTCCGGCCG	TGGGAGTGTG	1680
	CAGTGCGGGC	ACTGTGTGTG	CTACGGCGAA	GGCCGCTACG	AGGGTCAGTT	CTGCGAGTAT	1740
	GACAACTTCC	AGTGTCCCGG	CACITCCGGG	TTCCTCTGCA	ATGACCGAGG	ACGCTGCTCC	1800
45	ATGGGCCAGT	GTGTGTGTGA	GCCTGGTTGG	ACAGGCCCAA	GCTGTGACTG	TCCCTTCAGC	1860
	AATGCCACCT	GATCCGACAG	CAATGGGGGC	ATCTGTAATG	GACGTGGCCA	CTGTGAGTGT	1920
	GGCCGCTGCC	ACTGCCACCA	GCAGTCGCTC	TACACGGACA	CCATCTGCGA	GATCAACTAC	1980
	TCGGCGATCC	ACCCGGGCGT	CTGCGAGGAC	CTACGCTCCT	GCGTGCACTG	CCAGGCGTGG	2040
50	GGCACCGGGC	AGTGCAGTGT	GCGCACGTGT	GAGGAATGCA	ACTTCAAGGT	CAAGATGGTG	2100
	GACGAGCTTA	AGAGAGCCGA	GGAGGTGGTG	GTGCGCTGCT	CCTTCCGGGA	CGAGGATGAC	2160
	GACTGCACCT	ACAGCTACAC	CATGGAAGGT	GACGGCGCCC	CTGGGCCCAA	CAGCACTGTC	2220
	CTGGTGACA	AGAAAGAAAG	CTGCCCTCCG	GGCTCCTTCT	GGTGGCTCAT	CCCCCTGCTC	2280
	CTCCTCCTCC	TGCCGCTCCT	GGCCCTGCTA	CTGCTGCTAT	GCTGGAAGTA	CTGTGCTGCT	2340
	TGCAAGGCCT	GCCTGGCCT	TCTCCCGTGC	TGCAACCGAG	GTCAATGGT	GGGCTTTAAG	2400
55	GAAGACCACT	ACATGCTCGG	GGAGAACCTG	ATGGCCTCTG	ACCACTTGGG	CACGCCCATG	2460
	CTGCGCAGCG	GGAACTCAA	GGGCGGTGAC	GTGGTCCGCT	GGAAGGTCAC	CAACAACATG	2520
	CAGCGGCCTG	GCTTTGCCAC	TCATGCCGCC	AGCATCAACC	CCACAGAGCT	GGTGCCCTAC	2580
	GGGCTGTCTC	TGGCGCTGGC	CCGCCTTTGC	ACCGAGAACC	TGCTGAAGCC	TGACACTCGG	2640
	GAGTGCGCC	AGCTGCGCCA	GGAGGTGGAG	GAGAACCTGA	ACGAGGTCTA	CAGGCAGATC	2700
60	TCGGGTGTAC	ACAAGCTCCA	GCAGACCAAG	TTCCGGCAGC	AGCCCAATGC	CGGGAATAAG	2760
	CAAGACCA	CAATGTCTGA	CACAGTGTCTG	ATGGCGCCCC	GCTCGGCCAA	GCGGCCCATG	2820
	CTGAAGCTTA	CAGAGAAGCA	GGTGGAACAG	AGGGCCTTCC	ACGACCTCAA	GGTGGCCCCC	2880
	GGCTACTACA	CCCTCACTGC	AGACCAGGAC	GCCCGGGGCA	TGGTGGAGTT	CCAGGAGGGC	2940
	GTGAGCTGG	TGGAGCTAGC	GGTGCCCTCT	TTTATCCGGC	CTGAGGATGA	CGACGAGAAG	3000
65	CAGCTGCTGG	TGGAGGCCAT	CGAGTGCCCC	GCAGGCACTG	CCACCTCTCG	CCGCGCCTG	3060
	GTAAACATCA	CCATCATCAA	GGAGCAAGCC	AGAGACGTGG	TGTCCTTTGA	GCAGCTGAG	3120
	TTCTCGGTCA	GCCGCGGGGA	CCAGGTGGCC	CGCATCCCTG	TCATCCGGCG	TGTCCTGGAC	3180
	GGCGGGAAGT	CCCAGGTCTC	CTACCGCACA	CAGGATGGCA	CCGCGCAGGG	CAACCGGGAC	3240
	TACATCCCGG	TGGAGGGTGA	GCTGCTGTTT	CAGCCTGGGG	AGGCCCTGGA	AGAGCTGCAG	3300
70	GTGAAGCTCC	TGGAGCTGCA	AGAAGTTGAC	TCCCTCCTGC	GGGGCCGCCA	GGTCCGCCGT	3360
	TTCCACGTCC	AGCTCAGCAA	CCCTAAGTTT	GGGGCCCAAC	TGGGCCAGCC	CCACTCCACC	3420
	ACCATCATCA	TCAGGACCCC	AGATGAACTG	GACCGGAGCT	TCACGAGTCA	GATGTTGTCA	3480
	TCACAGCCAC	CCCCTCACGG	CGACCTGGGC	GCCCCGAGCA	ACCCCAATGC	TAAGGCCCGT	3540
	GGGTCCAGGA	AGATCCATT	CAACTGGCTG	CCCCCTTCTG	GCAAGCCAAT	GGGGTACAGG	3600
75	GTAAAGTACT	GGATTCAAGG	TGACTCCGAA	TCCGAAGCCC	ACCTGCTCGA	CAGCAAGGTG	3660
	CCCTCAGTGG	AGTTCAACAA	CCTGTACCCG	TATGCGACT	ATGAGATGAA	GGTGTGCGCC	3720
	TACGGGGCTC	AGGGCGAGGG	ACCCTACAGC	TCCCTGGTGT	CCTGCGGCAC	CCACCAAGGA	3780
	GTGCCAGCG	AGCCAGGGCG	TCTGGCCTTC	AATGTCGTCT	CCTCCACGGT	GACCCAGCTG	3840
80	AGCTGGGCTG	AGCCGCGCTG	GACCAACGGT	GAGATCACAG	CTACGAGGTT	CTGCTATGGC	3900
	CTGGTCAACG	ATGACAACCG	ACCTATTGGG	CCCATGAAGA	AAGTGCTGGT	TGACAACCTT	3960
	AAGAACCCGA	TGCTGCTTAT	TGAGAACCTT	CGGGAGTCCC	AGCCCTACCG	CTACACGGTG	4020
	AAGGCGCGCA	ACGGGGCGCT	GAGCGGGGCT	GAGCGGGAGG	CCATCATCAA	CCTGGCCACC	4080
	CAGCCCAAGA	GGCCCATGTC	CATCCCCATC	ATCCCTGACA	TCCCTATCGT	GGACGCCACG	4140
	AGCGGGGAGG	ACTACGACAG	CTTCCTTATG	TACAGCGATG	ACGTTCTACG	CTCTCCATCG	4200
85	GGCAGCCAGA	GCCGACGCGT	CTCCGATGAC	ACTGAGCACC	TGGTGAATGG	CCGGATGGAC	4260
	TTTGCCCTTC	CGGGCAGCAC	CAACTCCCTG	CACAGGATGA	CCACGACCAG	TGCTGCTGCC	4320
	TATGGCACCC	ACCTGAGCCC	ACAGTGCCCC	CACCGCGTGC	TAAGCACATC	CTCCACCTTC	4380

	ACACGGGACT	ACAACTCACT	GACCCGCTCA	GAACACTCAC	ACTCGACCAC	ACTGCCGAGG	4440
	GACTACTCCA	CCCTCACCTC	CGTCTCCTCC	CACGACTCTC	GCCTGACTGC	TGGTGTGCC	4500
	GACACGCCCA	CCCGCTGGT	GTTCTCTGCC	CTGGGGCCCA	CATCTCTCAG	AGTGAGCTGG	4560
5	CAGGAGCCGC	GGTGCAGCG	GCCGTGTCAG	GGCTACAGTG	TGGAGTACCA	GCTGCTGAAC	4620
	GGCGGTGAGC	TGCATCGGCT	CAACATCCCC	AACCTGCCCC	AGACCTCGGT	GGTGGTGGAA	4680
	GACCTCTGTC	CCAACCACTC	CTACGTGTTT	CGCGTGCCTG	CCCAGAGCCA	GGAAGGCTGG	4740
	GGCCGAGAGC	GTGAGGGTGT	CATCACCATT	GAATCCAGG	TGCACCCGCA	GAGCCCACTG	4800
	TGTCCCTGTC	CAGGCTCCGC	CTTCACTTTG	AGCACTCCCA	GTGCCCCAGG	CCCGCTGGTG	4860
10	TTCACTGCCC	TGAGCCACGA	CTCGCTGCAG	CTGAGCTGGG	AGCGGCCACG	GAGGCCCAAT	4920
	GGGGATATCG	TCGGCTACCT	GGTGACCTGT	GAGATGGCCC	AAGGAGGAGG	GCCAGCCACC	4980
	GCATTCCGGG	TGGATGGAGA	CAGCCCCGAG	AGCCGGCTGA	CCGTGCCGGG	CCTCAGCGAG	5040
	AACGTGCCCT	ACAAGTTCAA	GGTGCAGGCC	AGGACCACTG	AGGGCTTCGG	GCCAGAGCGC	5100
	GAGGGCATCA	TCACCATAGA	GTCCCAGGAT	GGAGGACCTT	TCCCGCAGCT	GGGCAGCCGT	5160
15	GCCGGGCTCT	TCCAGCACCC	GCTGCAAAGC	GAGTACAGCA	GCATCACCAC	CACCCACACC	5220
	AGCGCCACCC	AGCCCTTCTT	AGTGGATGGG	CCGACCTCTG	GGGCCCAGCA	CCTGGAGGCA	5280
	GGCGGCTCCC	TGACCCGGCA	TGTGACCCAG	GAGTTTGTGA	GGCGGACACT	GACCCACAGC	5340
	GGAAACCTTA	GCACCCACAT	GGACCAACAG	TTCTTCCAAA	CTTGACCGCA	CCCTGCCCCA	5400
	CCCCCGCCAT	GTCCCACTAG	CGCTCCTCCC	GACTCCTCTC	CCGGAGCCTC	CTCAGCTACT	5460
20	CCATCCTTGC	ATCCCTGGGG	GCCACGCCCA	CCCGCATGCA	CAGAGCAGGG	GCTAGGTGTC	5520
	TCCTGGGAGG	CATGAAGGGG	GCAAGGTCCG	TCCTCTGTGG	GCCCAAACCT	ATTGTGAACC	5580
	AAAGAGCTGG	GAGCAGCACA	AGGACCCAGC	CTTTGTCTTG	CACCTAATAA	ATGGTTTTGC	5640
	ACTG						

25 Seq ID NO: 130 Protein sequence:
Protein Accession #: NP_000204

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30	MAGPRPSPWA	RLLLAALISV	SLSGTLANRC	KKAPVKSCTE	CVRVDKDCAY	CTDEMFRDRR	60
	CNTQAEALLA	GQQRRESIVM	ESSFQITEET	QIDTTLRRSQ	MSPQGLRVRL	RPGEERHFEL	120
	EVFEPLESPV	DLVYILMDFSN	SMSDDLNLK	KMGQNLARVL	SQLTSDYTIG	FGKFVDKVS	180
	PQTMDRPEKL	KEPWNSSDP	FSFKNVISLT	EDVDEFRNKL	QGERISGNLD	APEGGFDAIL	240
	QTAVCTRDIG	RKPDSTHLLV	FSTESAFHYE	ADGANVLAGE	MSRNDERCHL	DTTGTYTQVR	300
35	TQDYPSPVPT	VRLLAKHNII	PIFAVTNYSY	SYYEKLHTYF	PVSSLGVLQE	DSSNIVELLE	360
	EAFNRIRSNL	DTRALDSPRG	LRTEVTSKMF	QKTRTGSFHI	RRGEVGYQV	QLRALEHVDG	420
	THVCQLPEDQ	KGNHILKPSF	SDGLKMDAGI	ICDVCTCELO	KEVRSARCSF	NGDFVCGQCV	480
	CSEGWSGQTC	NCSTGSLSDI	QPCLEGEEDK	PCSGRGECQC	GHCVCYGEGR	YEGQFCEYDN	540
40	FQCPRTSGFL	CNDRGRCSMG	QCVCPEGWG	PSCDCPLSNA	TCIDSNGGIC	NGRGHCECGR	600
	CHCQQQLSVT	DTICEINYSY	IHPGLCEDLR	SCVQCQAWGT	GEKKGRTECE	CNFKVKMVDG	660
	LKRAEEVVVR	CSFRDEDDDC	TYSYTMEDDG	APGPNSTVLV	HKKKDCPPGS	FWWLIPLLLL	720
	LPLLLALLLL	LCWKYCACCK	ACLALLPCCN	RGHMVGFED	HYMLRENLM	SDHLDTPLMR	780
	SGNLKGRDVV	RKKNVTNNQV	PGFATHAASI	NPTLVVPYGL	SLRLARLCTE	NLLKPDTRC	840
45	AQLRQEVEEN	LNEVYRQISG	VHKLQQTFR	QQPNAGKKQD	HTIVDTVLMA	PRSAKPALLK	900
	LTEKQVEQAG	PHDLVAPVY	YTLTADQDAR	GMVEFQEGVE	LVDVVRVPLFI	RPEDDDEKQL	960
	LVEAIDVPAQ	TATLGRRLVN	ITIIKEQARD	VVSFEQPEFS	VSRGDQVARI	PVIRVLDGG	1020
	KSQVSRYTQD	GTAQGNRDI	PVEGELLFQP	GEAWKELQVK	LLELQEVDSL	LRGRQVRRFH	1080
	VQLSNPKFPA	HLGQPHSTTI	IIRDPDELDR	SFTSQMLSSQ	PPPHGDLGAP	QNPNAKAAGS	1140
50	RKIHFNWLLP	SGKPNMYRVK	YWIQDSESE	AHLDSKVPS	VELTNLYPYC	DYEMKVCAYG	1200
	AQGEQPYSSL	VSCRTHQEVF	SEPGRLAFNV	VSSVTQLSW	AEPATNGEI	TAYEVCYGLV	1260
	NDDNRPIGPM	KKVLVDNPKN	RMLLIENLRE	SQPYRYTVKA	RNGAGWGPER	EAIINLATQP	1320
	KRFMSIPIIP	DIPIVDNPKN	EDYDSFLMYS	DDVLRSPSGS	QRPVSDDTE	HLVNGRMDFA	1380
	FPGSTNSLHR	MTTTSAAAYG	THLSPHVPHR	VLSTSSLTTR	DYNSLTRSEH	SHSTTLPRDY	1440
	STLTSVSSHD	SRLTAGVPDT	PTRLVFSALG	PTSLRVSWQE	PRCERPLQGY	SVEYQLLNGG	1500
55	ELHRLNIPNP	AQTSVVVEDL	LPHNSYVFRV	RAQSQEGWGR	EREGVITIES	QVHPQSPCLP	1560
	LPQSAFTLST	PSAPGPLVFT	ALSPDSLQLS	WERPRRPNGD	IVGYLVTCEM	AQGGGPATAF	1620
	RVDGDSPEER	LTVPLGSENV	PYKFKVQART	TEGFGPEREG	IITIESQDGG	PFPQLGSRAG	1680
	LFQHPQLQSEY	SSITTTHTSA	TEPFLVDGPT	LGAQHLEAGG	SLTRHVTQEF	VSRTLITSTGT	1740
60	LSTHMDQQFF	QT					

Seq ID NO: 131 DNA sequence
Nucleic Acid Accession #: BC004372
Coding sequence: 132..2231

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65	CCTCGTCCGC	CGGACCCAG	CCTCTGCCAG	GTTCCGTCGG	CCATCCTCGT	CCCGTCTCTC	60
	GCCGGCCCCCT	GCCCCGCGCC	CAGGGATCCT	CCAGCTCCTT	TCGCCCGCGC	CCTCCGTTTG	120
70	CTCGGACAC	CATGGACAAG	TTTGGTGGC	ACGCAGCCTG	GGGACTCTGC	CTCGTGCCGC	180
	TGAGCCTGGC	GCAGATCGAT	TTGAATATAA	CCTGCCGCTT	TGCAGGTGTA	TTCCACGTGG	240
	AGAAAAATGG	TGCTACAGC	ATCTCTCGGA	CGGAGGCCGC	TGACCTCTGC	AAGGCTTTCA	300
	ATAGCACCTT	GCCCCAATG	GCCCAGATGG	AGAAAGCTCT	GAGCATCGGA	TTTGAGACCT	360
	GCAGGTATGG	GTTCTAGAA	GGGCATGTGG	TGATTCCTCC	GATCCACCCC	AACTCCATCT	420
75	GTGCAGCAAA	CAACACAGGG	GTGTACATCC	TCACATCCAA	CACCTCCCAG	TATGACACAT	480
	ATTGCTTCAA	TGCTTCAGCT	CCACCTGAAG	AAGATTGTAC	ATCAGTCACA	GACCTGCCCA	540
	ATGCTTTTGA	TGCACCAATT	ACCACTAATA	TTGTTAACCG	TGATGGCACC	CGCTATGTCC	600
	AGAAAGGAGA	ATACAGAAGC	AATCCTGAAG	ACATCTACCC	CAGCAACCCT	ACTGATGATG	660
	ACGTGAGCAG	CGGCTCCTCC	AGTGAAAGGA	GCAGCACTTC	AGGAGGTTAC	ATCTTTTACA	720
80	CCTTTTCTAC	TGCACACCCC	ATCCAGACG	AAGACAGTCC	CTGGATCACC	GACAGCACAG	780
	ACAGAATCCC	TGCTACCACT	ACGTCTTCAA	ATACCATCTC	AGCAGGCTGG	GAGCCAAATG	840
	AAGAAAAATGA	AGATGAAAGC	GACAGACACC	TCAGTTTTTC	TGGATCAGGC	ATTGATGATG	900
	ATGAAGATT	TATCTCCAGC	ACCATTTCAA	CCACACCAGC	GGCTTTTGAC	CACACAAAC	960
	AGAACCAGGA	CTGAGCCAG	TGGAACCCAA	GCCATTCAAA	TCCGGAAGTG	CTACTTCAGA	1020
85	CACCCACAAG	GATGACTAGT	GTAGACAGAA	ATGGCACCAC	TGCTTATGAA	GGAAACTGGA	1080
	ACCCAGAAGC	ACACCTCTCC	CTCATTCACC	ATGAGCATCA	TGAGGAAGAA	GAGACCCAC	1140
	ATTCTACAAG	CACAAATCCAG	GCAACTCCTA	GTAAGTACAAC	GGAAGAAACA	GCTACCCAGA	1200
	AGGAACAGTG	GTTTGGCAAC	AGATGGCATG	AGGATATCG	CCAAACACCC	AGAGAAGACT	1260

5
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CCCATTCGAC AACAGGGACA GCTGCAGCCT CAGCTCATAC CAGCCATCCA ATGCAAGGAA 1320
GGACAACACC AAGCCCAGAG GACAGTTCCT GGACTGATTT CTTCACCCCA ATCTCACACC 1380
CCATGGGACG AGGTCATCAA GCAGGAAGAA GGATGGATAT GGACTCCAGT CATAGTACAA 1440
CGCTTCAGCC TACTGCAAAAT CCAAAACACAG GTTTGGTGGG AGATTGGAC AGGACAGGAC 1500
CTCTTTCAAT GACAACGAG CAGAGTAATT CTCAGAGCTT CTCTACATCA CATGAAGGCT 1560
TGGAAGAAGA TAAAGACCAT CCAACAACCT CTACTCTGAC ATCAAGCAAT AGGAATGATG 1620
TCACAGGTGG AAGAAGAGAC CCAAAATCATT CTGAAGGCTC AACTACTTTA CTGGAAGGTT 1680
ATACCTCTCA TTACCCACAC ACGAAGGAAA GCAGGACCTT CATCCCAGTG ACCTCAGCTA 1740
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GTTCTTTATC AGGAGACCAA GACACATTCC ACCCCAGTGG GGGGTCCCAT ACCACTCATG 1860
GATCTGAATC AGATGGACAC TCACATGGGA GTCAAGAAGG TGGAGCAAAC ACAACCTCTG 1920
GTCCTATAAG GACACCCCAA ATTCCAGAAT GGCTGATCAT CTTGGCATCC CTCTTGGCCT 1980
TGGCTTTGAT TCTTTCAGTT TGCATTGACG TCAACAGTCG AAGAAGTGT GGGCAGAAGA 2040
AAAAGCTAGT GATCAACAGT GGCAATGGAG CTGTGGAGGA CAGAAAGCCA AGTGGACTCA 2100
ACGGAGAGGC CAGCAAGTCT CAGGAAATGG TGCATTGGT GAACAAGGAG TCGTCAGAAA 2160
CTCCAGACCA GTTTATGACA GCTGATGAGA CAAGGAACCT CGAAGTGTG GACATGAAGA 2220
TTGGGGTGTA ACACCTACAC CATTATCTTG GAAAGAAACA ACCGTGGAA ACATAACCAT 2280
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TTTTTAGCAT AAAATTTTCT ACTCTTAAAA AAAAAA AAAA

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Seq ID NO: 132 Protein sequence:
Protein Accession #: AAH04372

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1 11 21 31 41 51
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PTMAQMEKAL SIGFETCRYG PIEGHVVIPR IHPNSICAAN NTGVYILTSN TSQYDYTCFN 120
ASAPPEEDCT SVTDLPNADF GPITITIVNR DGTRYVQKGE YRNPEDIYP SNPTDDDVSS 180
GSSSERSSTS GGYIFYTFTST VHPIDEDSP WITDSTDRIP ATSTSSNTIS AGWEPNEENE 240
DERDRHLSFS GSGIDDDDEF ISSTISTTFR AFDHTKQND WTQWNPSSHN PEVLLQTTR 300
MTDVRNGTT AYEGRWNPEA HPPLIHHEHH EEEETPHSTS TIQATPSSTT EETATQKEQW 360
FGRNWHGYSR QTPREDSSHT TGTAASAHT SHPMQGRTP SPEDSSWTF FNPISHPMGR 420
GHQAGRMDM DSSHSTTLQP TANPNTGLVE DLDRTGPLSM TTQSNVSQSF STSHEGLEED 480
KDHPPTSTLT SSNRNDVTGG RRDPNHSEGS TTLLEGYTS YPHTKESRTF IPVTSAKTGS 540
FGTAVTVGD SMSNVNRLS GDQDTFHPSG GSHTHGSES DGHSHGSQEG GANTTSGPIR 600
TPQIPEWLI LSLALALALI LAVCIAVNSR RRCGQKKLV INSGNGAVED RKP SGLNGEA 660
SKSQEMVHLV NKESSETPDQ FMTADETRNL QNVDMKIGV

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Seq ID NO: 133 DNA sequence
Nucleic Acid Accession #: NM_002882
Coding sequence: 150-755

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1 11 21 31 41 51
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GCGGAGGAA GGAGCTACGA GTAGCCGCCG AGAGGCCGCG GAGCCAGCGA CGACCCAGCC 120
AGCCGAGCCG CCGCCGCCGC CGCGCCCCCA TGGCGGCCGC CAAGGACACT CATGAGGACC 180
ATGATACTTC CACTGAGAA ACAGACGAGT CCAACCATGA CCCTCAGTTT GAGCCAATAG 240
TTTCTCTTCC TGAGCAAGAA ATTAAACAC TGAAGAAGA TGAAGAGGAA CTTTTTAAAA 300
TGCGGGCAAA ACTGTCCGA TTTGCCTCTG AGAACGATCT CCCAGAATGG AAGGAGCGAG 360
GCACTGGTGA CGTCAAGCTC CTGAAGCACA AGGAGAAAGG GGCCATCCGC CTCTCATGC 420
GGAGGGACAA GACCCTGAAG ATCTGTGCCA ACCACTACAT CACGCCGATG ATGGAGCTGA 480
AGCCCAACGC AGGTAGCGAC CGTGCCTGGG TCTGGAACAC CCACGCTGAC TTCGCCGACG 540
AGTGCCCAA GCCAGAGCTG CTGGCCATCC GCTTCCTGAA TGCTGAGAAT GCACAGAAAT 600
TCAAAACAAA GTTTGAAGAA TGCAGGAAAG AGATCGAAGA GAGAGAAAG AAAGCAGGAT 660
CAGGCAAAAA TGATCATGCC GAAAAAGTGG CGGAAAAGCT AGAAGCTCTC TCGGTGAAGG 720
AGGAGACCAA GGAGGATGCT GAGGAGAAGC AATAAATCGT CTTATTTTAT TTTCTTTTCC 780
TCTCTTCTCT TCTCTTTCTT TAAAAAATT TACCCTGCCC CTCTTTTTCG GTTTGTTTTT 840
ATTCTTTTCT TTTTACAAGG GACGTTATAT AAAGAACTGA ACTC

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Seq ID NO: 134 Protein sequence:
Protein Accession #: NP_002873

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70

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1 11 21 31 41 51
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ENDLPEWKER GTGDVKLLKH KEKGAILRLM RRDKTLKICA NHYITPMEL KPNAGSDRAW 120
VWNTHADPAD ECPKPELLAI RFLNAENAQK PKTKFEECRK EIEEREKAG SGKNDHAEKV 180
AEKLEALSVK EETKEDAEK Q

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Seq ID NO: 135 DNA sequence
Nucleic Acid Accession #: NM_000077.2
Coding sequence: 277-742

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80
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1 11 21 31 41 51
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GGATTGTAGG GACAGGTCAG GAGGGGGCTC TTCCGCCAGC ACCGAGGAA GAAAGAGGAG 180
GGGCTGGCTG GTCACCAGAG GGTGGGGCGG ACCGCGTGGC CTCGGCGGCT GCGGAGAGGG 240
GGAGAGCAGG CAGCGGGCGG CGGGGAGCAG CATGGAGCCG GCGGCGGGGA GCAGCATGGA 300
GCCTTGGGCT GACTGGCTGG CACGGCGCGC GGCGCGGGGT CGGGTAGAGG AGGTGCGGGC 360
GCTGCTGGAG GCGGGGGCGC TGCCCAACGC ACCGAATAGT TACGGTCGGA GGCCGATCCA 420
GGTCATGATG ATGGGCAGCG CCCGAGTGGC GGAGCTGCTG CTGCTCCAGC GCGCGGAGCC 480

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CAACTGCGCC GACCCCGCCA CTCTCACCAG ACCCGTGCAC GACGCTGCCC GGGAGGGCTT 540
 CCGTGACACG CTGGTGGTGC TGACACGGGC CGGGGCGCGG CTGGACGTGC GCGATGCCTG 600
 GGGCGGTCTG CCCGTGGACC TGGCTGAGGA GCTGGGCCAT CGCGATGTGC CACGGTACCT 660
 GCGCGCGGCT GCGGGGGGCA CCAGAGGCAG TAACCATGCC CGCATAGATG CCGCGGAAGG 720
 TCCCTCAGAC ATCCCGGATT GAAAGAACCA GAGAGGCTCT GAGAAACCTC GGGAAACTTA 780
 GATCATCACT CACCGAAGGT CCTACAGGGC CACAAC TGCC CCGCCACAA CCCACCCCGC 840
 TTTCGTAGTT TTCATTAGTA AAATAGAGCT TTTAAAAATG TCCTGCCTTT TAACGTAGAT 900
 ATATGCCTTC CCCCACTACC GTAATATGCC ATTTATATCA TTTTATATAT ATCTTATATA 960
 AATGTAAAA AAGAAAAACA CCGCTTCTGC CTTTCTACTG TGTGGAGTT TTTGGAGTG 1020
 AGCACTCAGC CCTAAGCGC ACATTTCATGT GGGCATTCTT TGGAGGCTC GCAGCCTCCG 1080
 GAAGCTGTGC ACTTCATGAC AAGCATTTTG TGAAC TAGGG AAGCTCAGGG GGGTTACTCG 1140
 CTTCTCTTGA GTCACACTGC TAGCAATGG CAGAACCAAA GCTCAATAA AATAAAAAA 1200
 ATTTTCATTC ATTCATC

Seq ID NO: 136 Protein sequence:
 Protein Accession #: NP_000068.1

1 11 21 31 41 51
 MEPAAGSSME PSADWLATAA ARGVVEEVRA LLEAGALPNA PNSYGRRIQ VMMMG SARVA 60
 ELLLLHGAEP NCADPATLTR PVHDAAREGP LDTLVVLHRA GARLDVRDAW GRLPVDLAE 120
 LGHRDVARYL RAAAGGTRGS NHARIDA AEG PSDIPD

Seq ID NO: 137 DNA sequence
 Nucleic Acid Accession #: NM_058196.1
 Coding sequence: 104-421

1 11 21 31 41 51
 TGTGTGGGGG TCTGCTTGGC GGTGAGGGGG CTCTACACAA GCTTCCTTTC GTTCATGCCG 60
 GCCCCCACC TGCTCTGAC CATCTGTTC TCTCTGGCAG GTCATGATGA TGGGCAGCGC 120
 CCGAGTGGCG GAGCTGCTGC TGCTCCACGG CGCGGAGCCC AACTGCGCGC ACCCGCCAC 180
 TCTCACCCGA CCCGTGCAGC ACGCTGCCCG GGAGGGCTTC CTGGACACGC TGGTGGTGCT 240
 GCACCGGGCC GGGGCGCGGC TGGACGTGCG CGATGCCCTGG GCGCGTCTGC CCGTGGACCT 300
 GGCTGAGGAG CTGGGCCATC GCGATGTGCG ACGGTACCTG CGCGCGGCTG CCGGGGGCAC 360
 CAGAGGCAGT AACCATGCCC GCATAGATGC CGCGGAAGGT CCCTCAGACA TCCCGGATTG 420
 AAAGAACCAG AGAGGCTCTG AGAAACCTCG GGAAACTTAG ATCATCAGTC ACCGAAGGTC 480
 CTACAGGGCC ACAACTTGCCC CCGCCACAAC CCACCCGCT TCTGTAGTTT TCATTAGAA 540
 AATAGAGCTT TAAAAATGT CCTGCCCTTT AACGTAGATA TAAGCCTTCC CCCACTACCG 600
 TAAATGTCCA TTTATATCAT TTTTATATA TTCTTATAAA AATGTAAAAA AGAAAAACAC 660
 CGCTTCTGCC TTTTCTGCT GTTGGAGTTT TCTGGAGTGA GCACTCAGCG CCTAAGCGCA 720
 CATTTCATGT GGCATTTCTT GCGAGCCTCG CAGCCTCCGG AAGCTGTGCA CTTTCATGACA 780
 AGCATTTTGT GAAC TAGGGA AGCTCAGGGG GGTACTGGC TTCTCTTGG TCACTGTGCT 840
 AGCAATGGC AGAACCAAG CTCAAATAAA AATAAAATAA TTTTCATTCA TTCCTC

Seq ID NO: 138 Protein sequence:
 Protein Accession #: NP_478103.1

1 11 21 31 41 51
 MMMGSARVAE LLLLHGAEPN CADPATLTRP VHDAAREGFL DTLVVLHRA G ARLDVRDAWG 60
 RLPVDLAEEL GHRDVARYLR AAGGTRGSN HARIDA AEGP SDIPD

Seq ID NO: 139 DNA sequence
 Nucleic Acid Accession #: NM_058197.1
 Coding sequence: 272-684

1 11 21 31 41 51
 CCCAACCTGG GCGCACTTCA GGTGTGCCAC ATTCGCTAAG TGCTCGGAGT TAATAGCACC 60
 TCCTCCGAGC ACTCGCTCAC GGCCTCCCTT TGCTGGAAA GATACCGCG TCCCTCCAGA 120
 GGATTGAGG GACAGGGTCG GAGGGGGCTC TTCCGCCAGC ACCGGAGGAA GAAAGAGGAG 180
 GGGCTGGCTG GTCACAGAG GGTGGGGCGG ACCCGTGGC CTGGCGGCT GCGGAGAGGG 240
 GGAGAGCAGG CAGCGGGCGG CGGGGAGCAG CATGGAGCCG GCGCGGGGA GCAGCATGGA 300
 GCGCGCGCGG GGGAGCAGCA TGGAGCCTTC GGCTGACTGG CTGGCCACGG CCGCGGCCCG 360
 GGGTGGGTA GAGGAGGTGC GGGCGCTGCT GGAGGCGGGG GCGCTGCCCA ACGCACCGAA 420
 TAGTTACGGT CGGAGGCCGA TCCAGGTGGG TAGAAGTCT GCAGCGGAG CAGGGGATGG 480
 CCGGCGACTC TGGAGGACGA AGTTTGACAG GGAATTGGAA TCAGGTAGCG CTTTCGATTCT 540
 CCGAAAAAG GGGAGGCTTC CTGGGGAGTT TTCAGAAAGG GTTTGTAATC ACAGACCTCC 600
 TCCTGGCGAC GCCCTGGGGG CTTGGGAAAC CAAGGAAGAG GAATGAGGAG CCACGCGCGT 660
 ACAGATCTCT CGAATGCTGA GAAGATCTGA AGGGGGGAAC ATATTGTAT TAGATGGAAG 720
 TCATGATGAT GGGCAGCGCC CGAGTGGCGG AGCTGCTGCT GCTCCACGCG GCGGAGCCCA 780
 ACTGCGCGGA CCCGCGCTC CTCACCGAC CCGTGACGCA CGCTGCCCG GAGGGCTTCC 840
 TGGACACGCT GGTGGTGTG CACCGGGCGG GGGCGCGGCT GGACGTGCGC GATGCCTGGG 900
 GCGCTGTGCC CGTGGACCTG GCTGAGGAGC TGGGCCATCG CGATGTGCGA CGGTACCTCG 960
 GCGCGGCTGC GGGGGGCCA AGAGGAGTA ACCATGCCCG CATAGATGCC GCGGAAGGTC 1020
 CCTCAGACAT CCCGATTGTA AAGAACCAGA GAGGCTCTGA GAAACCTCGG GAACTTAGAT 1080
 CATCAGTCA CAGAGGCTCT ACAGGGCCAC AACTGCCCCC GCCACAACCC ACCCGCTTT 1140
 CGTAGTTTTC ATTTAGAAAA TAGAGCTTTT AAAAAATGCC TGCCTTTTAA CGTAGATATA 1200
 TGCCTTCCCC CACTACCGTA AATGTCCATT TATATCATTT TTTATATATT CTTATAAAAA 1260
 TGTAAAAAG AAAACACCG CTTCTGCCTT TCACTGTGT TGGAGTTTTC TGGAGTGAGC 1320
 ACTCAGCCCC TAACGCGCA TTTCTGTGGG CATTCTTGC GAGCCTCGCA GCCTCCGGAA 1380
 GCTGTGACT TCATGACAAG CATTTTGTGA ACTAGGGAAG CTCAGGGGGG TTA CTGGCTT 1440
 CTCTTGAGTC ACAC TGCTAG CAAATGGCAG AACCAAGCT CAAATAAAAA TAAATAAATT 1500

Seq ID NO: 140 Protein sequence:
Protein Accession #: NP_478104.1

1	11	21	31	41	51	
MEPAAGSSME	PAAGSSMEPS	ADWLATAAAR	GRVEEVALL	EAGALPNAPN	SYGRRPIQVG	60
RRSAAGAGDG	GRLWRKFAG	ELESGSASIL	RKKGRLPGEF	SEGVNHRPP	PGDALGAWET	120
KEEE						

Seq ID NO: 141 DNA sequence
Nucleic Acid Accession #: NM_058195.1
Coding sequence: 163-684

1	11	21	31	41	51	
CCTCCCTACG	GGCGCCTCCG	GCAGCCCTTC	CCGCGTGCGC	AGGGCTCAGA	GCCGTTCCGA	60
GATCTTGGAG	GTCCGGGTGG	GAGTGGGGGT	GGGGTGGGGG	TGGGGGTGAA	GGTGGGGGGC	120
GGGCGCGCTC	AGGGAAGCGC	GGTGC CGCC	TGCGGGGCGG	AGATGGGCAG	GGGCGGCTGC	180
GTGGGTCCCA	GTCTGCAGTT	AAGGGGCGAG	GAGTGGCGCT	GCTCACCTCT	GGTGCCAAAG	240
GGCGGCGCAG	CGGCTGCCGA	GCTCGGCCCT	GGAGGCGGCG	AGAACATGGT	GCGCAGGTTC	300
TTGGTGACCC	TCCGATTTCG	GCGCGCGTGC	GGCCCGCGCG	GAGTGAGSGT	TTTCGTGGTT	360
CACATCCCGC	GGCTCACGGG	GGAGTGGGCA	GCGCCAGGGG	CGCCCGCGCG	TGTGGCCCTC	420
GTGCTGATGC	TACTGAGGAG	CCAGCGTCTA	GGGCAGCAGC	CGCTTCCTAG	AAGACCAGGT	480
CATGATGATG	GGCAGCGCCC	GAGTGGCGGA	GCTGCTGCTG	CTCCACGGCG	CGGAGCCCAA	540
GTGCGCGCAG	CCCGCCATCT	TCACCCGACC	CGTGACGACG	GCTGCCCGGG	AGGGCTTCCT	600
GGACAGCTCG	GTGGTGCTGA	ACCGGGCCGG	GGCGGCGCTG	GACGTGCGCG	ATGCTTGGGG	660
CCGTCTGCCC	GTGGACCTGG	CTGAGGAGCT	GGGCCATGCG	GATGTCGCAC	GGTACCTGCG	720
CGCGGCTGCG	GGGGGACCCA	GAGGCAGTAA	CCATGCCCGC	ATAGATGCCG	CGGAAGGTCC	780
CTCAGACATC	CCGATTGAA	AGAACCAGAG	AGGCTCTGAG	AAACCTCGGG	AAACTTAGAT	840
CATCAGTCAC	CGAAGTCTCT	ACAGGGCCAC	AACTGCCCCC	GCCACAACCC	ACCCCGCTTT	900
CGTAGTTTTC	ATTAGAAAAA	TAGAGCTTTT	AAAAATGTCC	TGCCTTTTAA	CGTAGATATA	960
TGCTTCCCCC	CACTACCGTA	AATGTCCATT	TATATCATTT	TTTATATATT	CTTATAAAAA	1020
TGTAATAAAG	AAAAACACCG	CTTCTGCCTT	TTCAGTGTGT	TGGAGTTTTC	TGGAGTGAGC	1080
ACTCAGCGCC	TAAGCGCACA	TTCATGTGGG	CATTTCTTGC	GAGCCTCGCA	GCCTCCGGAA	1140
GCTGTGAGCT	TCATGACAAG	CATTTGTGA	ACTAGGGAAG	CTCAGGGGGG	TTACTGGCTT	1200
CTCTTGAGTC	ACACTGCTAG	CAAAATGGCAG	AACCAAGCT	CAATAAAAAA	TAAATAAATT	1260
TTCATTCACT	CACTC					

Seq ID NO: 142 Protein sequence:
Protein Accession #: NP_478102.1

1	11	21	31	41	51	
MGRGRVCGPS	LQLRGQEWRC	SPLVPKGGAA	AAELGPGGGE	NMVRRLVLT	RIRRACGPPR	60
VRVFFVHIIP	LTGEWAAPGA	PAVALVLM	LRSQRLGQQP	LPRRPGHDDG	QRPSSGAAAA	120
PRRGAQLRRP	RHSHPTRARR	CPGGLPGHAG	GAAPGRGAAG	RARCLGPSAR	GPG	

Seq ID NO: 143 DNA sequence
Nucleic Acid Accession #: NM_018131
Coding sequence: 412..1107

1	11	21	31	41	51	
GAAATTGCAC	ACTTAAAGAC	ATCAGTGGAT	GAAATCACAA	GTGGGAAAGG	AAAGCTGACT	60
GATAAAGAGA	GACAGAGACT	TTTGAGAGAA	ATTCGAGTCC	TTGAGGCTGA	GAAGGAGAAG	120
AATGCTTATC	AACTCACAGA	GAAGGACAAA	GAAATACAGC	GACTGAGAGA	CCAAGTGAAG	180
GCCAGATATA	GTACTCCGCG	ATTGCTTGAA	CAGCTGGAAG	AGACAACGAG	AGAAGGAGAA	240
AGGAGGGAGC	AGGTGTTGAA	AGCCTTATCT	GAAGAGAAAG	ACGTATTGAA	ACAACAGTTG	300
TCTGCTGCAA	CCTCAGCAAT	TGCTGAACTT	GAAAGCAAAA	CCAATACACT	CCGTTTATCA	360
CAGACTGTGG	CTCCAACTG	CTTCAACTCA	TCAATAAATA	ATATTCATGA	AATGGAAATA	420
CAGCTGAAAG	ATGCTCTGGA	GAAAAATCAG	CAGTGGCTCG	TGTATGATCA	GCAGCGGGAA	480
GTCTATGTAA	AAGGACTTTT	AGCAAGATC	TTTGAGTTGG	AAAAGAAAAC	GGAAACAGCT	540
GCTCATTAC	TCCCACAGCA	GACAAAAAAG	CCTGAATCAG	AAGGTTATCT	TCAAGAAGAG	600
AAGCAGAAAT	GTTACAACTG	TCTCTTGGCA	AGTGCAAAAA	AAGATCTTGA	GGTTGAACGA	660
CAAAACATAA	CTCAGCTGAG	TTTGAACCTG	AGTGAATTTT	GAAGAAAATA	TGAAGAAACC	720
CAAAAAGAAG	TTCACAATT	AAATCAGCTG	TGTATTACAC	AAAGAAGGGC	AGATGTGCAA	780
CATCTGGAAG	ATGATAGGCA	TAAAACAGAG	AAGATACAAA	AACTCAGGGA	AGAGAATGAT	840
ATTGCTAGGG	GAAAACTTGA	AGAAGAGAAG	AAGAGATCCG	AAGAGCTCTT	ATCTCAGGTC	900
CAGTCTCTTT	ACACATCTCT	GCTAAAGCAG	CAAGAAGAAC	AAACAAGGGT	AGCTCTGTTG	960
GAACAACAGA	TGCAGGCATG	TACTTTAGAC	TTTGAATAATG	AAAAACTCGA	CCGTCAACAT	1020
GTGCAGCATC	AATTGCTATG	AATCTTAAAG	GAGCTCCGAA	AAGCAAGAAA	AAATAACACA	1080
GTTGGAATCC	TTGAAACAGC	TTCATGAGTT	TGCCATCACA	GAGCCATTAG	TCACTTTCCA	1140
AGGAGAGACT	GAAAAACAGAG	AAAAAGTTGC	CGCCTCACCA	AAAAGTCCCA	CTGCTGCACT	1200
CAATGGAAGC	CTGGTGGAA	GTCCCAAGTG	CAATATACAG	TATCCAGCCA	CTGAGCATCG	1260
CGATCTGCTT	GTCCATGTGG	AATCTGTTT	AAAGTAGCAA	AATAAGTATT	TGTTTGTATA	1320
TTAAAGGATT	CAATAGTGTA	TTTTCTGTTA	GCTTGTGGGC	ATTTTGAATT	ATATATTTC	1380
CATTTTGCTT	AAAAGTGCCT	ATCTACCTTT	GACACTCCAG	CATGCTAGTG	AATCATGTAT	1440
CTTTTAGGCT	GCTGTGCTAT	TCTCTTGGCA	GTGATACCTC	CCTGACATGG	TTCATCATCA	1500
GGCTGCAATG	ACAGAAATG	GTGAGCAGCG	TCTACTGAGA	TACTAACATT	TTGCACTGTC	1560
AAAACTACTG	GTGAGGAAAA	GATAGCTCAG	GTTATTGCTA	ATGGGTTAAT	GCACCAGCAA	1620
GCAAAATATT	TATATGTTTC	GGGGTTTGA	AAAATCAAAG	ATAATTAACC	AAGGATCTTA	1680
ACTGTGTTCC	CATTTTATAT	CCAAGCACTT	AGAAAACCTA	CAATCCTAAT	TTTGATGTCC	1740
ATTGTTAAGA	GGTGGTGATA	GATACATATT	TTTTTTCATA	TTGTATAGCG	GTTATTAGAA	1800

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AAAGTTGGGA TTTTCTTGAT CTTTATTGCT GCTTACCATT GAAACTTAAC CCAGCTGTGT 1860
TCCCAACTC TGTTCTGCGC ACGAAACAGT ATCTGTTTGA GGCATAATCT TAAGTGGCCA 1920
CACACAATGT TTCTCTTAT GTTATCTGGC AGTAACTGTA ACTTGAATTA CATTAGCACA 1980
TTCTGCTTAG TAAATAATGT TAAATAAAC CCATGTAGCC CTCTCATTTG 2040
ATTGACAGTA TTTTAGTTAT TTTTGGCATT CTAAAGCTG GGCAATGTAA TGATCAGATC 2100
TTTGTGTTGC TGAACAGGTA TTTTATACA TGCTTTTGT AAACCAAAAA CTTTTAAATT 2160
TCTTCAGGTT TCTAACATG CTTACCACGT GGCTACTGTA AATGAGAAAA GAATAAAATT 2220
ATTTAATGTT TT
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Seq ID NO: 144 Protein sequence:
Protein Accession #: NP_060601

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1 11 21 31 41 51
| | | | |
MEIQLKDALE KNQQLVLYDQ QREVVYKGLL AKIFELEKKT ETAHSLPQQ TKKPESEGYL 60
QEEKQKCYND LLASAKDLLE VERQTITQLS FELSEFRKRY EETQKEVHNL NQLLYSQRRR 120
DVQHLEDDRH KTEKIQLKRE ENDIARGKLE EEKRRSEELL SQVQSLYTSL LKQEEQTRV 180
ALLEQQMQAC TLDPFENEKLD RQHVQHQLHV ILKELRKARK NNTVGILETA S
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Seq ID NO: 145 DNA sequence
Nucleic Acid Accession #: NM_001168
Coding sequence: 50..478

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1 11 21 31 41 51
| | | | |
CCGCCAGATT TGAATCGCGG GACCCGTTGG CAGAGGTGGC GCGCGCGGCA TGGGTGCCCC 60
GACGTTGCCC CTGCGCTGGC AGCCCTTTCT CAAGGACCAC CGCATCTCTA CATTCAAGAA 120
CTGGCCCTTC TTGGAGGGCT GCGCTGCAC CCGGAGCGG ATGGCCGAGG CTGGCTTCAT 180
CCACTGCCCC ACTGAGAACG AGCCAGACTT GGCCAGTGT TTCTTCTGCT TCAAGGAGCT 240
GGAAGGCTGG GAGCCAGATG ACGACCCCAT AGAGGAACAT AAAAAGCATT CGTCCGGTTG 300
CGCTTTCTCT TCTGTCAAGA AGCAGTTTGA AGAATTAACC CTTGGTGAAT TTTTGAAACT 360
GGACAGAGAA AGAGCCAAGA ACAAATTGTC AAAGGAAACC AACATAAGA AGAAAGAATT 420
TGAGGAAACT GCGAAGAAAG TGCGCCGTGC CATCGAGCAG CTGGCTGCCA TGGATTGAGG 480
CCTCTGGCCG GAGCTGCCTG GTCCAGAGT GGCTGCACCA CTTCCAGGGT TTATTCCCTG 540
GTGCCACCAG CCTTCTGTGT GGCCCTTAG CAATGTCTTA GGAAAGGAGA TCAACATTTT 600
CAAAATTAGAT GTTCAACTGT TGCTCCTGTT TTGTCTTGAA AGTGGCACA GAGGTGCTTC 660
TGCTGTGCA GCGGCTGCTG CTGGTAACAG TGGCTGCTTC TCTCTCTCTC TCTCTTTTTT 720
GGGGGCTCAT TTTTGTGTTT TTGATTCCCG GGCTTACCAG GTGAGAAGTG AGGGAGGAAG 780
AAGGCAGTGT CCTTTTGCT AGAGCTGACA GCTTTGTTCG CGTGGGCAGA GCCTTCCACA 840
GTGAATGTGT CTGGACTCTA TGTGTTGAG GCTGTACAG TCCTGAGTGT GGACTTGGCA 900
GGTGCTGTGT GAATCTGAGC TGCAGGTTCC TTATCTGTCA CACCTGTGCC TCCTCAGAGG 960
ACAGTTTTTT TGTGTTGTGT TTTTGTGTT TTTTGTGTT GGTAGATGCA TGACTTGTGT 1020
GTGATGAGAG AATGGAGACA GAGTCCCTGG CTCCTCTACT GTTAAACAAC ATGGCTTTCT 1080
TATTTTGTGT GAATTGTTAA TTCACAGAAT AGCACAACT ACAATTAAAA CTAAGCACAA 1140
AGCCATTCTA AGTCATTGGG GAAACGGGGT GAACTTCAGG TGGATGAGGA GACAGAATAG 1200
AGTGATAGGA AGCGTCTGGC AGATACTCCT TTGCGCACTG CTGTGTGATT AGACAGGCC 1260
AGTGAGCCGC GGGGCACATG CTGGCCGCTC CTCCTCAGA AAAAGGCAGT GGCCTAAATC 1320
CTTTTAAAT GACTTGGCTC GATGCTGTGG GGGACTGGCT GGGCTGCTGC AGGCCGTGTG 1380
TCTGTACGCC CAACTTTCAG ATCTGTACG TTCTCCACAC GGGGAGAGA CGCAGTCCGC 1440
CCAGGTCCCC GCTTTCTTTG GAGGCAGCAG CTCGCGCAGG GCTGAAGTCT GGCCTAAGAT 1500
GATGGAATTT ATTCGCCCTC CTCCTGTCA TAGAGCTGCA GGGTGGATTG TTACAGCTTC 1560
GCTGGAACC TCTGAGGTC ATCTCGGCTG TTCCTGAGAA ATAAAAAGCC TGTCATTTT
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Seq ID NO: 146 Protein sequence:
Protein Accession #: NP_001159

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1 11 21 31 41 51
| | | | |
MGAPTLPPAW QPFLKDHRS TFKNWPFLG CACTPERMAE AGFIHCPTEN EPDLAQCFPC 60
FKELEGWEPD DDPIEHHKH SSGCAFLSVK KQFEBELTGE FLKLDREKAK NKIAKETNNK 120
KKEFEETAKK VRRAIQLAA MD
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Seq ID NO: 147 DNA sequence
Nucleic Acid Accession #: NM_014176.1
Coding sequence: 127-720

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1 11 21 31 41 51
| | | | |
GCGCGCAGCG CTGGTACCCC GTTGGTCCGC GCGTTGCTGC GTTGTGAGGG GTGTGAGTCT 60
AGTGCATCCC AGGCAGCTCT TAGTGTGGAG CAGTGAACG TGTGTGGTTC CTCTACTTTG 120
GGGATCATGC AGAGAGCTTC ACGTCTGAAG AGAGAGCTGC ACATGTTAGC CACAGAGCCA 180
CCCCAGGCA TCACATGTTG GCAAGATAAA GACCAATGG ATGACCTGCG AGCTCAAATA 240
TTAGGTGGAG CCAACACACC TTATGAGAAA GGTGTTTTTA AGCTAGAAGT TATCATTCCT 300
GAGAGGTACC CATTGGAACC TCCTCAGATC CGATTCTCA CTCGAATTTA TCATCCAAAC 360
ATTGATTCTG CTGGAAGGAT TTGTCTGGAT GTTCTCAAAT TGCCACCAAA AGGTGCTTGG 420
AGACCATCCC TCAACATCGC AACTGTGTTG ACCTCTATTC AGCTGCTCAT GTCAGAACCC 480
AACCTGTATG ACCCGCTCAT GGCTGACATA TCCTCAGAAT TTAATATAA TAAGCCAGCC 540
TTCTCAAGA ATGCCAGACA GTGGACAGAG AAGCATGCAA GACAGAAACA AAAGGCTGAT 600
GAGGAAGAGA TGCTTGATAA TCTACCAGAG GCTGGTGACT CCAGAGTACA CAACTCAACA 660
CAGAAAAGGA AGGCCAGTCA GCTAGTAGGC ATAGAAAAGA AATTTTCATC TGATGTTTGT 720
GGGACTTGTC CTGGTTCATC TTAGTTAATG TGTCTTTGTC CAAGGTGATC TAAGTTGCCT 780
ACCTTGAATT TTTTTTAA TATATTTGAT GACATAATTT TTGTGTAGTT TATTTATCTT 840
GTACATATGT ATTTTGAAAT CTTTAAACC TGAAAAATAA ATAGTCATTT AATGTTGAAA 900
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Seq ID NO: 148 Protein sequence:
 Protein Accession #: NP_054895.1

1	11	21	31	41	51	
MQRASRLKRE	LHMLATEPPP	GITCWQDKDQ	MDDLRAQILG	GANTPYEKG	VFKLEVIIPER	60
YFPFPPQIRF	LTPIYHPNID	SAGRICLDVL	KLPPKGAWRP	SLNIATVLTS	IQLLMSEPNP	120
DDPLMADISS	EPFKYNKPAFL	KNARQWTEKH	ARQKQKADEE	EMLDNLPEAG	DSRVHNSTQK	180
RKASQLVGIE	KKFHPDV					

Seq ID NO: 149 DNA sequence
 Nucleic Acid Accession #: NM_003812
 Coding sequence: 224-2722

1	11	21	31	41	51	
TCCTCTGCGT	CCCGCCCCGG	GAGTGGCTGC	GAGGCTAGGC	GAGCCGGGAA	AGGGGGCGCC	60
GCCCAGCCCC	GAGCCCCCGG	CCCCGTGCCC	CGAGCCCGGA	GCCCCCTGCC	CGCGGCGGCA	120
CCATGCGCGG	CGAGCCGGCG	TGACCGGGTC	CGCCCGCGGC	CGCCCCGCGC	CTAGCCCGGC	180
GCTCTCGCGG	GCCACACGGA	GCGGCGCCCG	GGAGCTATGA	GCCATGAAGC	CGCCCGCGAG	240
CAGCTCGCGG	CAGCCGCCCC	TGGCGGGCTG	CAGCCTTGCC	GGCGCTTCTT	GCGGCCCCCA	300
ACGCGGCCCC	GCGCGCTCGG	TGCCTGCCAG	CGCCCGCGCC	CGCACGCGCG	CCTGCCCGCT	360
GCTTCTGCTC	CTTCTCTCTG	TGCCTCCGCT	CGCCGCGCTG	TCCGCGCCCC	GCGCCTGGGG	420
GGCTGCTGCG	CCCAGCGCTC	CGCATTGGAA	TGAAACTGCA	GAAAAAAATT	TGGGAGTCCT	480
GGCAGATGAA	GACAATACAT	TGCAACAGAA	TAGCAGCAGT	AATATCAGTT	ACAGCAATGC	540
AATGCAGAAA	GAATCACAC	TGCCTTCAAG	ACTCATATAT	TACATCAACC	AAGACTCGGA	600
AAGCCCTTAT	CACGTCTTGT	ACACAAAGGC	AAGACACCAG	CAAAAACATA	ATAAGGCTGT	660
CCATCTGGCC	CAGGCAAGCT	TCCAGATTGA	AGCCTTCGGC	TCCAAATTCA	TTCTTGACCT	720
CATCTGGAAC	AATGGTTTGT	TGTCTTCTGA	TTATGTGGAG	ATTCACACG	AAAATGGGAA	780
ACCACAGTAC	TCTAAGGGTG	GAGAGCACTG	TTACTACCAT	GGAAGCATCA	GAGGCGTCAA	840
AGACTCCAAG	TGGGCTCTGT	CAACCTGCAA	TGGACTTCAT	GGCATGTTTG	AAGATGATAC	900
CTCTGCTGAT	ATGATAGAGC	CACATAGAGC	GGTTCATGAT	GAGAAAAGCA	CAGGTCGACC	960
ACATATAATC	CAGAAAACCT	TGGCAGGACA	GTATTCTAAG	CAATGAAGA	ATCTCACTAT	1020
GGAAAGAGGT	GACCACTGGC	CCTTCTCTCT	TGAATTACAG	TGGTTGAAAA	GAAGGAAGAG	1080
AGCATGGAAT	CCATCAGCTG	GTATATTGGA	AGAAATGAAA	TATTTGGAAC	TTATGATTGT	1140
TAATGATCAC	AAAACGTATA	AGAAGCATCG	CTCTTCTCAT	GCACATACCA	ACAACCTTGC	1200
AAAGTCCGTG	GTCAACCTTG	TGGATTCTAT	TTACAAGGAG	CAGCTCAACA	CCAGGGTTGT	1260
CCTGCTGGCT	TAGAGACACT	GGACTGAGAA	GGATCAGATT	GACATCACCA	CCAACCTCTG	1320
GCAGATGCTC	CATGAGTTCT	CAAAATACCG	GCAGCGCATT	AAGCAGCATG	CTGATGCTGT	1380
GCACCTCATC	TCGCGGGTGA	CATTTCACTA	TAAGAGAAGC	AGTCTGAGTT	ACTTTGGAGG	1440
TGCTCTTTCT	CGCACAAAGG	GAGTTGGTGT	GAATGAGTAT	GGTCTTCCAA	TGGCAGTGGC	1500
ACAAGTATTA	TCGCAGAGCC	TGGCTCAAAA	CCTTGGAAATC	CAATGGGAAC	CTTCTAGCAG	1560
AAAGCCAAAA	TGTGACTGCA	CAGAAATCCTG	GGGTGGCTGC	ATCATGGAGG	AAACAGGGGT	1620
GTCCATTCTT	CGAAAATTTT	CAAAAGTGCA	CATTTTGGAG	TATAGAGACT	TTTACAGAG	1680
AGGAGGTGGA	GCCTGCCTTT	TCAACAGGCC	AACAAAGCTA	TTTGAGCCCA	CGGAATGTGG	1740
AAATGGATAC	GTGGAAGCTG	GGGAGGAGTG	TGATTGTGGT	TTTCATGTGG	AATGCTATGG	1800
ATTATGCTGT	AAGAAATGTT	CCCTCTCCAA	CGGGGCTCAC	TGCAGCGACG	GGCCCTGCTG	1860
TAACAATACC	TCATGTCTTT	TTCAGCCACG	AGGGTATGAA	TGCCGGGATG	CTGTGAACGA	1920
GTGTGATATT	ACTGAATATT	GTACTGGAGA	CTCTGGTCAG	TGCCCCACCA	ATCTTCATAA	1980
GCAAGACGGA	TATGCATGCA	ATCAAAATCA	GGGCGCTGTC	TACAATGGCG	AGTGCAAGAC	2040
CAGAGACAAC	CAGTGTCACT	ACATCTGGGG	AACAAAGGCT	GCAGGGTCTG	ACAAGTTCTG	2100
CTATGAAAAG	CTGAATACAG	AAGGCACTGA	GAAGGGAAGC	TGCCGGGAAG	ATGGAGACCG	2160
GTGGATTTCAG	TGCAGCAAA	ATGATGTGTT	CTGTGGATTTC	TTACTCTGTA	CCAATCTTAC	2220
TCGAGCTCCA	CGTATTGGTC	AACCTCAGGG	TGAGATCATT	CCAACCTCCT	TCTACCATCA	2280
AGGCCGGGTG	ATTGACTGCA	GTGGTGCCCA	TGTAGTTTAA	GATGATGATA	CGGATGTGGG	2340
CTATGTAGAA	GATGGAACGC	CATGTGGCCC	GTCTATGATG	TGTTTAGATC	GGAAGTGCCT	2400
ACAAATTCAA	GCCCTAAATA	TGAGCAGCTG	TCCACTCGAT	TCCAAGGGTA	AAGTCTGTTC	2460
GGGCCATGGG	GTGTGTAGTA	ATGAAGCCAC	CTGCATTGTG	GATTTCACCT	GGGCAGGGAC	2520
AGATTGCGAGT	ATCCGGGATC	CAGTTAGGAA	CCTTCACCCC	CCCAAGGATG	AAGGACCCAA	2580
GGTCTCTAGT	GCCACCAATC	TCATAATAGG	CTCCATCGCT	GGTGCCATCC	TGGTAGCAGC	2640
TATGTCTCTT	GGGGGACAGC	GCTGGGGATT	TAAAAATGTC	AAGAAGAGAA	GGTTCGATCC	2700
TACTCAGCAA	GGCCCCATCT	GAATCAGCTG	CGCTGGATGG	ACACCGCCTT	GCACTTTTGG	2760
ATTCTGGGTA	TGACATACTC	GCAGCAGTGT	TACTGGAACT	ATTAAGTTTG	TAAACAAAAC	2820
CTTTGGGTGG	TAATGACTAC	GGAGCTAAAG	TGGGGGTGAC	AAGGATGGGG	TAAAGAAAAA	2880
CTGTCTCTTT	TGGAATAAAT	GTCAAAAGAAC	ACCTTTCACC	ACCTGTCACT	AAACGGGGGA	2940
GGGGGCAAAA	GACCATGCTA	TAAAAAGAAC	TGTTCCAGAA	TCTTTTTTTT	TCCCTAATGG	3000
ACGAAGGAAC	AACACACACA	CAAAAATTAA	ATGCAATAAA	GGAATCATTAA	AAAA	

Seq ID NO: 150 Protein sequence:
 Protein Accession #: NP_003803

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MKPPGSSSRQ	PPLAGCSLAG	ASCPQQRGPA	GSVPASAPAR	TPPCRLLLV	LLLPLLAASS	60
RPRAWGAAAP	SAPHWNETAE	KNLGLVADED	NTLQONSSSN	ISYSNAMQKE	ITLPSRLIYY	120
INQDESFPYH	VLDTKARHQ	KHNAVHLAQ	ASFQIEAFGS	KFILDLLNN	GLLSSDYVEI	180
HYENGKPYQS	KGGEHCYHYH	SIRGVKDSKV	ALSTCNGLHG	MFEDDTFVYM	IEPLELVHDE	240
KSTGRPHIQ	KTLAGQYSKQ	MKNLTMERGD	QWPLSELQW	LKRRKRAVNP	SRGIFEMMY	300
LELMIVNDHK	TYKKHRSSHA	HTNFAKSVV	NLVDISIYKEQ	LNTRVVLVAV	ETWTEKDQID	360
ITTNPVQMLH	EPISKYRRIK	QHADAHLIS	RVTFFHYKRSS	LSYFGGVCSR	TRGVGVNEYG	420
LPMAVAQVLS	QSLAQNGLIQ	WEPSSRKPKC	DCTESWGGCI	MEETGVSHSR	KFSKCSILEY	480
RDFLRGGGA	CLFNRPTKLF	EPTECGNGYV	EAGEECDGCF	HVECYGLCK	KCSLSNGAHC	540
SDGPCCNNTS	CLFQPRGYEC	RDVNECDIT	EYCTGDSGQC	PPNLHKQDGY	ACNQNGRCRY	600
NGECKTRDQ	CQYINGTKAA	GSDKFCYEKL	NTEGTEKGNC	GKDGDRWIOC	SKHDVFCGFL	660

LCTNLTRAPR IGQLQGEIIP TSFYHQGRVI DCSGARHVLD DTDVGVYVED GTPCGPSMMC 720
 LDRKCLQIQIA LNMSSCPLDS KGVKCSGHGV CSNEATCICD FTWAGTDCSI RDPVRNLHPP 780
 KDEGPKGPSA TNLIIGSIAG AILVAAIVLG GTGWGFKNVK KRRFDPTQQG PI

5 Seq ID NO: 151 DNA sequence
 Nucleic Acid Accession #: NM_023915
 Coding sequence: 250-1326

10 1 11 21 31 41 51
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 GGCACGAGGG TTTCGTTTTC ATGCTTTACC AGAAAATCCA CTTCCTGCC GACCTTAGTT 60
 TCAAAGCTTA TTCTTAATTA GAGACAAGAA ACCTGTTTCA ACTTGAAGAC ACCGTATGAG 120
 GTGAATGGAC AGCCAGCCAC CACAATGAAA GAAATCAAAC CAGGAATAAC CTATGCTGAA 180
 15 CCCACGCCTC AATCGTCCCC AAGTGTTTCC TGACACGCAT CTTTGCTTAC AGTGCATCAC 240
 AACTGAAGAA TGGGGTTCAA CTGACGCTT GCAAAATTAC CAAATAACGA GCTGCACGGC 300
 CAAGAGAGT CAAGATTCAGG CAACAGGAGC GACGGGCCAG GAAAGAACAC CACCTTCAC 360
 AATGAATTG ACACAATTGT CTTGCCGGTG CTTTATCTCA TTATATTGT GGCAGCATC 420
 TTGCTGAATG GTTTAGCAGT GTGGATCTTC TTCCACATTA GGAATAAAC CAGCTTCATA 480
 20 TTCTATCTCA AAAACATAGT GGTTCGAGAC CTCATAATGA CGCTGACATT TCCATTTCGA 540
 ATAGTCCATG ATGCAGGATT TGGACCTTGG TACTTCAAGT TTATTTCTCTG CAGATACACT 600
 TCAGTTTGTG TTTATGCAAA CATGTATACT TCCATCGTGT TCCTTGGGCT GATAAGCATT 660
 GATCGCTATC TGAAGTGTGT CAAGCCATTG GGGGACTCTC GGATGTACAG CATAACCTTC 720
 ACGAAGGTTT TATCTGTTTG TGTGTTGGTG ATCATGGCTG TTTTGTCTTT GCCAACATC 780
 ATCTCTGACAA ATGGTCAGCC AACAGAGGAC AATATCCATG ACTGCTCAAA ACTTAAAAAGT 840
 25 CCTTTGGGGG TCAATGGCA TACGGCAGTC ACCTATGTGA ACAGCTGCTT GTTTGTGGCC 900
 GTGCTGGTGA TTCTGATCGG ATGTTACATA GCCATATCCA GGTACATCCA CAAATCCAGC 960
 AGGCAATTCA TAAGTCAGT AAGCCGAAAG CGAAAACATA ACCAGAGCAT CAGGGTTGTT 1020
 GTGGCTGTGT TTTTACCTG CTTTCTACCA TATCACTTGT GCAGAATTCC TTTTACTTTT 1080
 30 AGTCACTTAG ACAGGCTTTT AGATGAATCT GCACAAAAA TCCTATATTA CTGCAAGAA 1140
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 ATCAGATCAC TGCAAGTGT GAGAAGATCG GAAGTTCGCA TATATTATGA TTACACTGAT 1320
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 35 TTCATTATCC TTAATAAAAA AA

Seq ID NO: 152 Protein sequence:
 Protein Accession #: NP_076404

40 1 11 21 31 41 51
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 MGFNLTLAKL PNNELHQGES HNSGNRSDGP GKNTTLHNEF DTIVLPVLYL IIFVASILLN 60
 GLAVWIFPHI RNKTSIFLYL KNIVVADLIM TLTFFPRIVH DAGFGPWYFK FILCRYTSVL 120
 45 FYANMYTSIV FLGLISIDRY LKVVKPFQDS RMYSTFTKV LSVCVWVIMA VLSLPNIILT 180
 NQOPTEDNIH DCSKLKSPLG VKWHTAVTVV NSCLFVAVLV ILIGCYIAIS RYIHKSSRQF 240
 ISQSSRRKXH NQSIIRVVAV FPTCFLPYHL CRIPFTFSLH DRLLESAQK ILYYCKEITL 300
 FLSACNVCLD PIYFFMCRS PSRRLPKXSN IRTRESIRS LQSVRRSEVR IYYDYTDV

50 Seq ID NO: 153 DNA sequence
 Nucleic Acid Accession #: D80008.1
 Coding sequence: 149-739

55 1 11 21 31 41 51
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 CGAGCTGCAT CGCGCGCCCG AAGGCCAACT GCCTGCCCTC AACGAGGATG GACTCAGACA 240
 60 AGTTCTGGAG GAGATGAAAG CTTTGTATGA ACAAACCAG TCTGATGTGA ATGAAGCAAA 300
 GTCAAGTGGA CGAAGTGATT TGATACCAAC TATCAAATT CGACACTGTT CTCTGTTAAG 360
 AAATCGACGC TGACATGTAG CATACCTGTA TGACCGCTTG CTTGGATCA GAGCACTCAG 420
 ATGGGAATAT GGTAGCGTCT TGCCAAATGC ATTACGATT CACATGGCTG CTGAAGAAAT 480
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 65 TGAAGGTTTG GACATTACAC AGGATATGAA ACCACCAAAA AGCCTATATA TTGAAGTCCG 600
 GTGTCTAAAA GACTATGGAG AATTTGAAGT TGATGATGGC ACTTCAGTCC TATTAATAAA 660
 AAATAGCCAG CACTTTTAC CTCGATGGAA ATGTGAGCAG CTGATCAGAC AAGGAGTCCCT 720
 GGAGCACATC CTGTCATGAC CATGCGCGGA GGCACCTCCA GGCCTCACTC AACTCATGGA 780
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 70 TAGACATTGT TTAAGATAAC TAAGAATACT TGGCTAAGAA GTATAATTG CTAACATTA 900
 AGGACTTTCT TTTTCTAATG TTGTACACTA TTCTTCCTAC TCTTTTGGG TTTTGGTTT 960
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 AGTCCTCCCA CCTTAGCTTC TCAAAGTGT GAGATCACAG GCGTGAGCCA CTGACCCCG 1080
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 75 GTGTGTTTTT TAAATGAAAG TAAACATGGT TACATTGAA TCTCTTAAAT AAGCAGTCAC 1200
 TTGGCTGGAC AGGAAGAAGG TAGATCCTGT GTGTCTTGT TCTGGTCAT GTGTATTGTA 1260
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 CACTGCAATC TCTATCCCT GGGTTCAGT GATTCTCTTG TCTCAGCCTC CCAAGTAGCT 1920
 GGGATTACAG GCACAGGCCG CCACGCTCG CTAATTTTGT TATTTTGTAGT AGAGACAGAG 1980

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TTTTACCATG TTGGCCAGGC TGTTTCAAA CTCCTGACCT CAAGTGACCC ACCTTGGCCT 2040
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GAATTTTATA TATGTTGCAA GGTGTCAATC CACCTTCACT TTTTCTTGGG AATATAGATA 2160
TCCAGCTGTT TCACTACCAT TTTTGAAGG GACTGCCCTT TGCTCTATCA CCTTTGCATT 2220
TTTGTAAAAA AGTAGTTGTC AATGTATATG TGGGTTTATT TCAGGACTCT GTTTTGTTC 2280
ATTGACCTGT TTTTCTCTCC TGAATGCCAA TACCATATTT GTATGTAGTG TATGTAATTT 2340
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TTTGTAGAGA TGGGGTTTCA CCGTGTGGC CAGGCTGTGT TGAACCTCTG AGCTAAAGCA 2460
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GTGAAATTGT GGAAACAGGA GGGTGTGGTG GCTTATGCCT GTAATCCTAG AACTTTGGGA 2640
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AACTCCGTCT CTACAAAAA TAGAAAAAAT TAGCCAGGTG TGGTGGTGCA TGCCGTGATG 2760
CACAGTTACA CGGCAGGCTG AGGTGGGAGG ATCACTTGAA CCCAGAGGT CAAGACTGCA 2820
GTGAGCTGAG ATCACACCAC TGTACTCCAG CCTGGGTGAC AAAGTGAGAC TCTATCTCAA 2880
AAAGAAATTA GGATCAATTT GTCATTTCT ACAACAACAA CAACAAAAAC CCCTGTTGGG 2940
CACCTTGATT GAGATTGCAT TGAATTTATA TAAACCTGTT GGGAGAATTG ACATCTTAAT 3000
AATATTGAGT CTTCTGGCCT ATAAACAAGG TCTGTCTTCC TAGGTATTAA TGTTTTGTCT 3060
TCTATTTCTC TTAATAATCT TTTGTAGTTT TCAGTGATCA GGTCTACCAT GTCAGCATT 3120
CATAGTTTGT ATGCTAAATG GTATTTTAAA ATTTCAAATT CTAACCACTT GTTGCTAGTA 3180
AATAGAAATA CAATTGATGT TGAACCTGTA TCCTTCAGCC TTGCTAAACT GTGAGTTCTC 3240
ATGGTGTGTT TGTAAATTAC ATCAACAGTC ATGTGTTCTA TGAATAAAGA GTTTTACTCC 3300
TTC
  
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Seq ID NO: 154 Protein sequence:
Protein Accession #: BAA11503.1

1 11 21 31 41 51
 MFCEKAMELI RELHRAPEQG LPAFNEGLR QVLEEMKALY EQNQSDVNEA KSGGRSDLIP 60
 TIKFRHCSLL RNRRCTVAYL YDRLLRIRAL RWEYGSVLPN ALRFHMAAEE MEWFNNYKRS 120
 LATYMRSLGG DEGLDITQDM KPPKSLYIEV RCLKDYGEFE VDDGTSVLLK KNSQHPLPRW 180
 KCEQLIRQGV LEHILS

Seq ID NO: 155 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 149-709

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GTTCGGCGCC AAAGCGCGGA GCGGAGGCCG AGGCGAGAGC CTGGCGCTGT AGGACTAGAA 60
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AAGGCCGCGG GAGTGGGAAG CGTCCGCCAT GTTCTGCGAA AAAGCCATGG AACTGATCCG 180
CGAGCTGCAT CGCGCGCCCG AAGGGCAACT GCCTGCCTTC AACGAGGATG GACTCAGACA 240
AGTTCTGGAG GAGATGAAAG CTTGTATGTA ACAAACCCAG TCTGATGTGA ATGAAGCAAA 300
GTCAGGTGGA CGAAGTGATT TGATACCAAC TATCAAAATTT CGACACTGTT CTCTGTTAAG 360
AAATCGACGC TGCACGTAG CATACCTGTA TGACCGCTTG CTTGGATCA GAGCACTCAG 420
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TGAAGGTTTG GACATTACAC AGGATATGAA ACCACCAAAA AGCCTATATA TTGAAGCTGG 600
ATGCAGTGGC GCGATCTCGG CTCACCTGTC AACCTCCACC TCCCAGGTTT ACCTCAACTG 660
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GCACTTCAGT CCTATTAATA AAAAATAGCC AGCACTTTT ACCTCGATGG AAATGTGAGC 780
AGCTGATCAG ACAAGGAGTG CTGGAGCACA TCCTGTGATG ACCATGCGCC GAGGCACCTC 840
CAGGCTTCAC TCAACTCATG GACTCCTCTG TACTCACTCT CTCACCACT CCCTTCACTT 900
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ACTCTTTTCT GTGTTTGTGT TGTGTTTGTG GAGACTGTCT CACTATGTTG CCCAAGCTGG 1080
TCTCAAACCT CTGGCCTCAA GCAGTCTCTC CACCTTAGCT TCTCAAAGTG TTGAGATCAC 1140
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ACATACTAAT TTATCATCTG GCTATTTGGG AAGGAAGGAC ACACATGGAT TTTGCACATT 1500
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GCATCCGAGA AATCTTTTCC CATCCCAAGA TCACAAATTT TTTTCTTTT TACTTCTAGA 1800
AGTGTATAAA TTTTAAGCTT TATACTTTGG TCTATGACCC GTTTTTTTTT TTGTTTGTG 1860
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GTGCAGTGGC GTGATCTTGG CTCACCTGCA TCTCTATCCC CTGGGTTCAA GTGATTCTCT 1980
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CTCAAGTGAC CCACCTTGGC TCCCAAAGT TTTGGGATTA CAAGTGTGGG CCACCGCGGG 2160
CAGCCTATGA TCCATTTTGA ATGAATTTT TATATGGTGC AAGGTGTCAA TCCACCTTCA 2220
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GACCAGCCCG GGCCTATGSC AAAATCTCGT CTCTACAAAA AATAGAAAAA ATTAGCCAGG 2820
  
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TGTGGTGGTG CATGCCCTGTA GTCACAGTTA CACGGCAGGC TGAGGTGGGA GGATCACTTG 2880
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 CCTAGGTATT AATGTTTTGT CTCTATTTC TCTTAATAAT CTTTGTAGT TTTCACTGTA 3180
 CAGGTCTACC ATGTGAGCAT TTCATAGTTT TGATGCTAAA TGGTATTTTA AAATTTCAAA 3240
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Seq ID NO: 156 Protein sequence:
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 MFCEKAMELI RELHRAPEQG LPAFNEDGLR QVLEEMKALY EQNQSDVNEA KSGGRSDLIP 60
 TIKFRHCSLL RNRRTVAVYL YDRLLRIRAL RWEYGSVLPN ALRFHMAAEE MEWFNNYKRS 120
 LATYMRSLGG DEGLDITQDM KPPKSLYIEA GCSGAISAQP ATSTSQVHLN CNLHLP GPVS 180
 KRLWRI

Seq ID NO: 157 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 148-621

1 11 21 31 41 51
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 GAGCTGCATC GCGCGGCCGA AGGGCAACTG CCTGCCTTCA ACGAGGATGG ACTCAGACAA 240
 GTTCTGGAGG AGATGAAGCC TTTGTATGAA CAAAACCACT CTGATGTGAA TGAAGCAAAG 300
 TCAGGTGGAC GAAGTGATTT GATACCAACT ATCAAATTTT GACACTGTTC TCTGTTAAGA 360
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 TGGGAATATG GTAGCGTCTT GCCAAATGCA TTACGATTTC ACATGGCTGC TGAAGAAGTC 480
 CGGTGTCTAA AAGACTATGG AGAATTTGAA GTTGATGATG GCACCTTCAGT CCTATTAAAA 540
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Seq ID NO: 158 Protein sequence:
 Protein Accession #: Eos sequence

1 11 21 31 41 51
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MFCEKAMELI RELHRAPEGO LPAFNEGLR QVLEEMKALY EQNQSDVNEA KSGGRSDLIP 60
 TIKFRHCSLL RNRRTVAYL YDRLLRIRAL RWEYGSVLPN ALRPHMAAEE VRCLKDYGEF 120
 EVDGTSVLL KNSQHPLPR WKCEQLIRQG VLEHILS

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Seq ID NO: 159 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 149-229

10 1 11 21 31 41 51
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 CGAAAGGAGT GAGGCGCCGA GAGCCAGAT ACCATTTTGG CGTGAGAGCT GGTGGTTGGC 120
 AAGGCCGCGG GAGTGGGAAG CGTCCGCCAT GTTCTGCGAA AAAGCCATGG AACTGATCCG 180
 CGAGCTGCAT CGCGCGCCCG AAGGGCAACT GCCTGCCTTC AACAAATTAGC TGGGTGTGGT 240
 15 GGCACACACC TGTAGTCCCA GCAACTTAGG AGGCTGAAAT GAGAGGATTG CATGGCTCCA 300
 GGAAGTTGAA ACTGCAGTGA ACTGTGGTCA CGCTATTACA CTCCAGCCTG GGTGACAGAC 360
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 AAGCTTTGTA TGAACAAAAC CAGTCTGATG TGTCTCTGT TAAGAAATCG ACGCTGCACT 480
 20 GTAGCATACC TGTATGACCG CTGCTTCGG ATCAGAGCAC TCAGATGG

Seq ID NO: 160 Protein sequence:
 Protein Accession #: Eos sequence

25 1 11 21 31 41 51
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 ATGTTCTGCG AAAAAGCCAT GGAAGTATC CGCGAGCTGC ATCGCGCGCC CGAAGGGCAA 60
 CTGCCTGCCT TCAACAATTA G

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Seq ID NO: 161 DNA sequence
 Nucleic Acid Accession #: U10694
 Coding sequence: 1333-2280

35 1 11 21 31 41 51
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 AGGAACCTAA GGGAGGATCG AGGGTACCTC CAGGCCAGAG AAACCTCTCAG ATCAAGAGAG 180
 TTTGGCCCTGC CCTACTGTC ACCCCAGAGA GCCCGGGCAG GGCTGTCTGC TGAGGTGCTC 240
 CCTTTATCCT GGGATCATCG GTGTGCGGGA GGGCTGCGCT TGGTCTGAGG GGGCTGCACT 300
 40 CAGTTCAGCA GAGGGAGGGT CCCAGGCCCT GCCAGGAGTC CAGGTGCAGA CTGAGGGGAC 360
 CCCACTCACC AAACACAGAG GACCTAGCCC CACCCTGCCC CTTGTGTGTA CTGAGGGGAG 420
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 45 CTACCCCGAG GACACATGGA CCCATTGAA TTTAGACATC TCTTACTGTA CTTCCGAGGA 600
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 CTTGGTCTGA GACAGTGTCC TCAGGTGCGA GAGCAGAGGA GACCCAGGCA GTGTGAGCAG 960
 TGAAGGTGAA GTGTTACACC TGAATGTGCA CCAAGGGCCC CACCTGCCCC AGCACACATG 1020
 GGACCCCATG GCACCTGGCC CCATTCCCCC TACTGTCACT CATAGAGCCT TGATCTCTGC 1080
 AGGCTAGCTG CAGCTGAGT GAGCTGTGCT CTTCTCTCTC CAGGTCTCTG GGACAGGCTA 1140
 55 ACCAGGAGGA CAGGAGCCCC AAGAGGCCCC AGAGCAGCAC TGACGAAGAC CTGTAAGTCA 1200
 GCCTTTGTTA GAACCTCCAA GGTTCGGTTC TCAGCTGAAG TCTCTCACAC ACTCCCTCTC 1260
 TCCCGAGGCC TGTGGGTCTC CATGCCCCAG CTCCTGCCCA CGCTCCAGAC TGCTGCCCTG 1320
 ACCAGAGTCA TCATGTCTCT CGAGCAGAGG AGTCCGCACT GCAAGCCTGA TGAAGACCTT 1380
 GAAGCCCAAG GAGAGGAGT GGGCCTGATG GGTGCACAGG AACCCACAGG CGAGGAGGAG 1440
 60 GAGACTACCT CCTCTCTGA CAGCAAGGAG GAGGAGGTGT CTGCTGCTGG GTCATCAAGT 1500
 CCTCCCCAGA GTCTCAGGG AGGCGCTTCC TCCTCCATT TCCGTCTACTA CACTTTATGG 1560
 AGCCAAATTC ATGAGGGCTC CAGCAGTCAA GAAGAGGAAG AGCCAAAGCTC CTGGGTGAGC 1620
 CCAAGTCAAG TGGAGTTTAT GTTCCAAGAA GCACTGAAAT TGAAGGTGGC TGAGTTGGTT 1680
 CATTTCTGCT TCCACAAATA TCGAGTCAAG GAGCCGCTCA CAAAGGCAGA AATGCTGGAG 1740
 AGCGTCATCA AAAATTACAA GCGCTACTTT CCTGTGATCT TCGGCAAGGC CTCGAGTTTC 1800
 65 ATGCAGGTGA TCTTTGGCAC TGATGTGAAG GAGGTGGACC CCGCCGGCCA CTCCTACATC 1860
 CTTGTCACTG CTCTGGCCT CTCGTGCGAT AGCATGCTGG GTGATGGTCA TAGCATGCCC 1920
 AAGGCCGCCC TCTGTATCAT TGTCTGGGT GTGATCCTAA CCAAGACAA CTGCGCCCTG 1980
 GAAGAGGTTA TCTGGGAAGC GTTGTGTGTG ATGGGGGTGT ATGTTGGGAA GGAGCACATG 2040
 70 TTCTACGGGG AGCCAGGAA GCTGCTCACC CAAGATTGGG TGCAGGAAAA CTACCTGGAG 2100
 TACCGGCAGG TGCCCGGAG TGATCCTCGC CACTACGAGT TCCTGTGGGG TTCCAAGGCC 2160
 CACGCTGAAA CCAGCTATGA GAAGGTGATA AATTATTTGG TCATGCTCAA TGCAAGAGAG 2220
 CCCATCTGCT ACCATCCCT TTATGAAGAG GTTTTGGGAG AGGAGCAGA GGGAGTCTGA 2280
 GCACAGCCCG CAGCCGGGGC CAAAGTTTGT GGGGTGAGG CCCCATCCAG CAGCTGCCCT 2340
 75 GCCCATGTG ACATGAGGCC CATCTTCCG TCTGTGTTTG AAGAGAGCAA TCAGTGTCTT 2400
 CAGTGGCAGT GGGTGAAGT GAGCACACTG TATGTCTCT CTGGGTCTCT TGTCTATTGG 2460
 GTGATTTGGA GATTATCTCT TGCTCCCTTT TGAATTTGTT CAAATGTTCT TTTAATGGTC 2520
 AGTTTAAATGA ACTTCACCAT CGAAGTTAAT GAATGACAGT AGTCACACAT ATTGCTGTTT 2580
 ATGTTATTTA GGAGTAAGAT TCTTGCTTTT GAGTCACATG GGGAAATCCC TGTATTTTG 2640
 TGAATTGGGA CAGATAAACA TAGCAGAGGA ATTAATAATT TTTTGAAGAC TTGAAGTTAG 2700
 80 TGAACAAATA GAGCTCATAA AGAAATAGTG AAATGAAAT GTAGTTAATT CTGCTCTTAT 2760
 ACCCTCTTCT CTCTCCTGTA AAATTAAGAC ATATACATGT ATACCTGGAT TTGCTTGGCT 2820
 TCTTTGAGCA TGAAGAGGAA ATAAATATG AAAGAATAAT TTTTCTGTT CACTGGCTCA 2880
 TTTTCTTCTC AGACACGCAC TGAACATCTG TTATTCGGAA CACCCTGGGT T

85

Seq ID NO: 162 Protein sequence:
 Protein Accession #: AAA68877.1

1	11	21	31	41	51	
MSLEQRSPHC	KPDEDLEAQQ	EDLGLMGAQE	PTGEEEBETTS	SSDSKEEEVS	AAGSSSPPOS	60
PQGGASSSIS	VYYTLWSQFD	EGSSSQEEEE	PSSSVDPQAL	EFMFQEALKL	KVAELVHFL	120
HKYRVKEPVT	KAEMLSEVIK	NYKRYFPVIF	GKASEFMQVI	FGTDVKEVDP	AGHSYILVTA	180
LGLSCDSMLG	DGHSMFKAAL	LIIVLGVILT	KONCAPEEVI	WEALSVMGVY	VGKEHMFYGE	240
PRKLLTQDWW	QENYLEYRQV	PGSDPAHYEF	LWGSKAHAET	SYEKVINYL	MLNAREPICY	300
PSLYEEVLGE	EQEGV					

Seq ID NO: 163 DNA sequence
Nucleic Acid Accession #: AF292100
Coding sequence: 30-809

1	11	21	31	41	51	
GGGGGGGGAG	AGGCCTGGAG	GACACCAACA	TGAACAAAGT	GAAATCATCG	CAGAAGGATA	60
AAGTTCGTCA	GTTTATGATC	TTACACAAT	CTAGTGAAAA	AACAGCAGTA	AGTTGTCTTT	120
CTCAAAATGA	CTGGAAGTTA	GATGTTGCAA	CAGATAATTT	TTTCCAAAT	CCTGAACTTT	180
ATATACGAGA	GAGGTGAAAA	GGATCATGG	ACAGGAAGAA	GTTAGAACAG	CTGTACAATA	240
GATACAAAGA	CCCTCAAGAT	GAGAATAAAA	TTGGAATAGA	TGGCATAACG	CAGTTCTGTG	300
ATGACCTGGC	ACTCGATCCA	GCCAGCATT	GTGTGTGAT	TATTGCGTGG	AAGTTCAGAG	360
CAGCAACACA	GTGCGAGTTC	TCCAAACAGG	AGTTCATGGA	TGGCATGACA	GAATTAGGAT	420
GTGACAGCAT	AGAACAACCT	AAGGCCAGAG	TACCCAAGAT	GGAACAAGAA	TTGAAAGAAC	480
CAGGACGATT	TAAAGATTTT	TACCAGTTTA	CTTTTAATTT	TGCAAGAAT	CCAGGACAAA	540
AAGGATTAGA	TCTAGAAATG	GCCATTGCCT	ACTGGAACCT	AGTGCTTAAT	GGAAGATTTA	600
AATTCTTAGA	CTTATGGAAT	AAATTTTGT	TGGAACATCA	TAAACGATCA	ATACCAAAAG	660
ACACTTGGA	TCTTCTTTTA	GACTTCAGTA	CGATGATTGC	AGATGACATG	TCTAATTATG	720
ATGAAGAAGG	AGCATGGCCT	GTCTTATTG	ATGACTTTGT	GGAATTGCA	CGCCCTCAAA	780
TTGCTGGGAC	AAAAGTACA	ACAGTGTAGC	ACTAAAGGAA	CCTTTTAGAA	TGTACATAGT	840
CTGTACAATA	AATACAACAG	AAAATTGCAC	AGTCAATTTT	TGCTGGCTGG	ACTGAACTGA	900
AGATCAATCC	TACAAGTTCA	GACTGAGGGT	TGAGACAAAA	CTTTAAGGAT	ACATCTTGGA	960
CCATATCGTA	TTTCATTCTT	CTAATGTGG	TTTGGGCTTG	TCTTCTAGTC	TGGGCGGCTC	1020
TAAACATTTA	TAATTCACAC	ATTGTGGATT	TCATCTTATA	TCTGTGGACC	ATCCTAGTTT	1080
ATTCTCCCAT	AAGTCTTAGA	AGCTTTATGG	TGATTATTTT	GAGGTTTTCA	TTCTCGCATA	1140
AAGCAAAATG	CTGTCTTCAT	CAGAAAACAG	TTGGCATAAG	AATTAAACAT	ATGAACATCA	1200
CAAAACAATT	TATAAAAAT	TCTTAAATAT	ACGCTTTGGG	CTAGTTGCAA	AGACTATGCT	1260
AATAGCACTT	CCAGTGAGAG	TGATATATTT	AAGTGTACTG	GATCTGGAAT	GGTGTTTTGG	1320
TTTGGGGGGA	ATTTTTTTTT	TTTCTTGCCA	AATCACATAT	GTGTGTGATG	TGAGTATCTG	1380
ATGAAAAAAC	AATGTACGAA	TAACCGACAT	GAAAAATTTT	TAGGATAACT	TGGTGCCCTAC	1440
CTGAAAAATG	TATTGTGTGT	TAGACTCTTG	ATTTCAAAAG	GTTCACAGAG	ACTAGTCTGC	1500
GCTTACCTTA	CCCATGTTTA	TATATAGCTG	TCCTACAGGG	AGCTTTTATT	TAGAAAAATG	1560
CTGCATAATG	TTAGATTCTT	CTCCTGTCTA	CATTATGCAC	TACATAATTG	GACTTCATTA	1620
TGCTTTTGAA	ATGCTTATCT	GCCTGTACAC	TAAGTTAAAC	TATTTAATTT	GTTTTGAATG	1680
TTTTGGATTG	CTACACAATA	CAATATTCTA	AATTTAGGCA	TGAGGGTTTT	TTTGTTTTAT	1740
TTTTACTTTT	TTTTTGTTCAT	TGCACTATGG	AACACAAATG	AAATCTCTTT	AATTTATAAG	1800
AAGATAGTAG	GAGTTTATGG	TTGAAATGG	TTGTGATGAG	CCACGAAAT	CAATCTTTAT	1860
AATATAGGTA	CTGCTCTTTC	AGACAAACAG	TCCATTTTAA	ATGACTTCTT	ATTTTGTGTA	1920
AATTACTTTA	ACTGCTAATC	ACTGTGGTTG	CCAAATATTT	ACTTCAGAA	CAAAGATTTT	1980
CAAAACAAGCA	TACACATGAC	AAATACACAG	TCTGGCTTCT	AGTCTATTTA	CTGTTTGTGT	2040
TCACTCAGAT	TAGCTCAGTT	TTCTCATCAA	AGCAGAAATG	TATCTTGCGT	GTGTGTGTGT	2100
GTGTGTGTGT	GTGTGTGTGT	GTATGTGTGT	ATATATATAT	ATATATATAT	ATATATATTT	2160
TTTTTTTTTT	TTTTTTTTTA	ATACAAAAAG	CCATGAGCTG	CTTTTATGCT	GAAAAATGGT	2220
ATTTCCCTGT	TCACCTACTG	ACATGTGAAG	AAGGGTTTCT	TGCTTCTCTA	AACATTTCCG	2280
TAAGGCAGGC	TAGAAATGTA	ATACCTCAAA	TGTTTGATGA	TTATGGTCTT	TTGATAGGAA	2340
TAGATTCTGC	TGGGATATA	TATCCAGGCA	CTCTCTAAGG	TCTAGGGTTG	ATATTAACAA	2400
AGGAATGTAC	TTAGAATAGC	AGTACATTTT	ATGCAAAAT	GGAATTAATT	TTAAGAAACA	2460
ATGACATATC	AAAACGTGCT	TTTACATGAT	TTTGAAATAG	ACTAGAAAGC	TTTCCCTATA	2520
GACATATTAA	TATTTCCAACT	ATAACTTTAA	TTCAAGAAATG	CAGTTTACC	AAAAGAAAAA	2580
TTTGAAAAAT	TCTATTACAG	CTACTGGAAT	TGGTTATTAA	AAGAAAAAGG	AAAAAGAGA	2640
ATCTTGCTGC	TTTCAGTATT	TCCTGATTTT	TTTGAAATA	TAAAGAGGAA	CTTCAATTAT	2700
GAAAAATTTT	TAAAGATAT	ATATATCTAT	ATATCTATAT	ATATGTACTG	TTTGTTTTCC	2760
TGTCTTGAAG	ATTTGAGTT	ATGGTTATTG	GTTTCAGATT	GATTAAATCA	CATATGCTGT	2820
GTTTTCTTTA	AAAGTCATAT	GGGTTCTGGG	CCTAATGCCT	TGGATTTTAC	ATATTTTCT	2880
TTTTAAATGC	AAAACTTTT	CAACAAAAATA	GTGTTTGTCA	TCAGGTGGT	ACTAAACATT	2940
TATAAATACT	GTGTAATTAT	AAACAAAAAT	ACATAAAGCT	TTGAATATAA	TTATGTAGCA	3000
TAAAGTTAA	GGTTGTTTAC	TATGATGGCA	TCTTAGAATT	AAACAAAACT	TTTACTAGGG	3060
CTGAAAAAGAG	AAGACTGATT	TAATGTGGTG	TGATTATTCT	GAAGATAAAT	GTCTGGCTAC	3120
AGGGAAATAT	TTGTAATAAA	AAATGATTAC	ACATATGGCT	GTGTGTGTTT	GAGTCTGTGT	3180
CTGTGAGAGA	GCCAGAGAGA	GTGAGAGAGA	TTGACAGAGA	AAGGGAGAGA	CACACACACG	3240
CCCCTTGAAT	TGCTTTAACT	CCTAAGTGT	TCAGTCTCTCA	TTCCGGTAAA	CTCCCATGTC	3300
TGATTCTTTG	TTTTAAACTG	AACCATAGGT	ACAGTTTCTT	TTTTGCCAAA	TGTCAAAACA	3360
GGTACAAATT	TTAAATGTA	ATGCTTTTAA	AATAGAAAAA	TGTATAAAAT	TAGAAGTGCC	3420
CACATATAAA	AAATACTTGA	GATGAAGATT	ATCTTTAGTG	AATATCATCT	GCATATCTCT	3480
GTAAGTTCAA	TTGTGTTTCT	TACAGTCCCT	GTCATATTAC	CAACAGAGGC	AATAAAAGCT	3540
GCAGTGAAT	TG					

Seq ID NO: 164 Protein sequence:
Protein Accession #: AAG00606

1	11	21	31	41	51	
MNKLKSSQKD	KVRQFMIFTO	SSEKTAVSCL	SQNDWKLDVA	TDNFFQNP	YIRESVKGSL	60
DRKKLEQLYN	RYKDPQDENK	IGIDGIQFQC	DDLALDPASI	SVLIIAWKFR	AATQCEPSKQ	120
EFMDGMTLGL	CDSIEQLKAQ	IPKMEQELKE	PGRPKDFYQF	TFNFAKNPQ	KGLDLEMAIA	180
YWNVLNLRFR	KFLDLWNKFL	LEHMKRSIPK	DTWNLLLDPS	TMIAADMSNY	DEEGAWPVLI	240
DDFVEFARPO	IAGTKSTTV					

Seq ID NO: 165 DNA sequence
Nucleic Acid Accession #: AF256215
Coding sequence: 220-2028

5	1	11	21	31	41	51	
	CTCCAGTCCG	CATGCTCAGT	AGCTGCTGCC	GGCCGGGGCTG	GGGGGGGGCG	TCCGCTGCGC	60
10	GCCTACGGGC	TGCGGTGGCG	GCCGCCCGCG	CACCCGGCAG	GGCCCGCCAG	TCCCCGCTTC	120
	CTGTCTCCAG	AGCCGCCGCC	TGGGCCGGGG	CAGGGCGGGC	CCGGGGCTCC	TCCATGCTGC	180
	CAGCCGCCGG	GCTGCGGAGC	CGACCAAGTG	GCTCCTGCGA	TGGCGGCGGA	AGAGGAGGCT	240
	GCGCGGGGAG	GTAAAGTGTT	GAGAGAGGAG	AACCAAGTGA	TTGCTCTCTG	GGTTTCCAGC	300
	CGCGTGAGTC	CAGGGACAAG	ACCAACAGCT	ATGGGGTCTT	TCAGCTCACA	CATGACAGAG	360
15	TTTCCACGAA	AACGCAAAAG	AAGTGATTCA	GACCCATCCC	AAGTGAAGA	TGGTGAACAC	420
	CAAGTTAAAA	TGAAGGCCTT	CAGAGAAGCT	CATAGCCAAA	CTGAAAAGCG	GAGGAGAGAT	480
	AAATGAATA	ACCTGATTGA	AGAACTGTCT	GCAATGATCC	CTCAGTGCAA	CCCCATGGCG	540
	CGTAAACTGG	ACAAACTTAC	AGTTTAAAGA	ATGGCTGTTC	AACACTTGAG	ATCTTTAAAA	600
	GGCTTGACAA	ATTCTTATGT	GGGAAGTAAT	TATAGACCAT	CATTCTTCTA	GGATAATGAG	660
20	CTCAGACATT	TAATCTTAA	GACTGCAGAA	GGCTTCTTAT	TTGTGGTTGG	ATGTGAAAGA	720
	GGAAAAATTC	TCTTCGTTTC	TAAGTCAGTC	TCCAAAATAC	TTAATTATGA	TCAGGCTAGT	780
	TTGACTGGAC	AAAGCTTATT	TGACTTCTTA	CATCCAAAAG	ATGTTGCCAA	AGTAAAGGAA	840
	CAACTTCTCT	CTTTTGATAT	TTCACCAAGA	GAAAAGCTAA	TAGATGCCAA	AACCTGGTTG	900
	CAAGTTCACA	GTAATCTCCA	CGCTGGAAGG	ACACGTGTGT	ATTCTGGCTC	AAGACGATCT	960
25	TTTTTCTGTC	GGATAAAGAG	TTGTAATAATC	TCTGTCAAAG	AAGAGCATGG	ATGCTTACCC	1020
	AACTCAAAGA	AGAAAAGACA	CAGAAAATTC	TATACTATCC	ATTGCCTGGG	TTACTTGAGA	1080
	AGCTGGCCTC	CAAAATATTGT	TGGAATGGAA	GAAGAAAGGA	ACAGTAAGAA	AGACAACAGT	1140
	AATTTTACCT	GCCTTGTGGC	CATTGGAAGA	TTACAGCCAT	ATATTGTCTC	ACAGAACAGT	1200
	GGAGAGATTA	ATGTGAAACC	AACCTGAATT	ATAACCCGGT	TTGCAGTGAA	TGGAAAATTT	1260
30	GTCTATGTAG	ATCAAAGGGC	AACAGCGATT	TTAGGATATC	TGCCTCAGGA	ACTTTTGGGA	1320
	ACTTCTTGTT	ATGAATATTT	TCATCAAGAT	GACCACAATA	ATTTGACTGA	CAAGCACAAA	1380
	CGAGTTCTAC	AGAGTAAGGA	GAAAATACTT	ACAGATTCCCT	ACAAATTCAG	AGCAAAAGAT	1440
	GGCTCTTTTG	TAACCTTAAA	AAGCCAATGG	TTTAGTTTCA	CAAAATCCTG	GACAAAAGAA	1500
	CTGGAATATA	TTGTATCTGT	CAACACTTTA	GTTTGGGAC	ATAGTGAGCC	TGGAGAAGCA	1560
35	TCATTTTATC	CTTGAGCTCT	TCAATCATCA	GAAGAATCCT	CTAGACAGTC	CTGTATGAGT	1620
	GTACCTGGAA	TGCTACTGGG	AACAGTACTT	GGTGCTGGTA	GTATTGGAAC	AGATATTGCA	1680
	AATGAAATTC	TGGATTATCA	GAGGTTACAG	TCTTCTTCAT	ACCTTGATGA	TTGAGTCCA	1740
	ACAGGTTTAA	TGAAGATACA	TCATACTGTA	AACCTGCAGG	GTATGTCAAA	TAAGGAGTTG	1800
	TTTCCACCAA	GTCCTTCTGA	AATGGGGGAG	CTAGAGGCTA	CCAGGCAAAA	CCAGAGTACT	1860
40	GTTGCTGTCC	ACAGCCATGA	GCCACTCTCT	AGTGATGGTG	CACAGTTGGA	TTTCGATGCC	1920
	CTATGTGACA	ATGATGACAC	AGCCATGGCT	GCATTTATGA	ATTACTTAGA	AGCAGAGGGG	1980
	GGCTGGGAG	ACCCCTGGGA	CTTCAGTGAC	ATCCAGTGGA	CCCTCTAGCC	TTTGATTTTT	2040
	AACTCCAAAA	ATGAGAAAAC	TTTTAAAGCA	TTATTACGA	AAAAACTGTC	TCAACTATTC	2100
	TTAAGTACTG	TATTGATATT	GTTTGTATCT	TTTATTAATG	TTCTACCACT	TTTATAGAT	2160
45	TTGCATCTTC	TGCTCACAGG	GATGTGGGGA	AATACGTTTT	CCTCCCAAGA	GAACCAAGTT	2220
	TATTATAGAT	TCCTTTATTC	AGTGAAATGG	CTTATAATCC	ACTAGTTGCC	ATATTTTTCG	2280
	TAAATATTT	CTAACCAAGA	ATACTACTTA	CATATTGTTT	TGGCTTTGTT	TTATTTTGA	2340
	TGCAGTTTTT	TTTAGTTGAG	GTAATGTAAT	ATATTGATGT	TTTCTTTGTT	GTCTAAGATT	2400
	GATTATATAAT	AGTAGGTTTG	TATAATTTGG	AACATTTTCC	ATGCCCTGCG	AAATTCCTTA	2460
50	ATTGAGGATA	GGGCTTACAC	ACTTTAAGAA	AACAGTGAGT	ACTTGAACAT	TTAAAGGGAC	2520
	AGTGCAATTT	ATAGTCATAA	TCACATTGAA	TACTGTATTT	GATCTTTGGA	GACTTAGGCA	2580
	AGCACAGAGC	TGGGATATTT	ATGCTCAGTT	GAGCACTTTA	AGATGAATTT	TAAGTGAGAT	2640
	GATTTCTTGC	TTAAACTCA	GAAAGTCAAA	AGAGTTTCAG	CTTTCTTAC	AGAAAAGGAA	2700
	GGATCTTGGG	CCCTAGATCT	TGGGGATTAA	CCTCTGCATA	TAAGATTTAC	TCTTAATAGG	2760
55	CCAGACGTGG	TGCTCACGCC	TGTAATCCCA	GTACTTTGGG	AGGCTGAGAC	GGGCAGATCA	2820
	CTTGAGGTCA	GGAGTTCAG	ACCAGCCTGG	CCAATATGGT	GAAACCCCGT	TTCTACTAAA	2880
	AATACAAAAA	AAATTTACCA	GGCACTCACT	CTTGAGGTAA	CTAACCAACT	CCCACGATAA	2940
	TGACAGTCCA	TTCATGAGCG	CAAGGCCCTC	ATGACCTAAT	GGCACACACC	TGTAATCCCA	3000
	ACTGCTTGGG	AGGCTGAGGC	GAGAGGATTG	CTTGAACCTG	GGAGGCAGAG	GTTGCACTGA	3060
60	GCGGAGATCG	CACCACTGCA	CTCCAGTCTG	GGCAACAGAG	TGAGACTTCA	TCTCAAAAAA	3120
	AGTAAAAAAA	AAGATTATAT	ATAATCACTG	AAGATCTCTA	TTATAGATAG	ATTAGGTTTT	3180
	TGACATTGGA	AACATACTTA	GGGATAGATT	TGCTCTAAAG	GAAAAAAGTA	GGCCCGGGCA	3240
	GATTAAATGT	CTTGTGTAAA	GTCACACATT	AAATTCAGTC	ACACATTAAA	TTCATAGAGT	3300
	TTTAAATGTT	TAATGTATAT	AAACCAAGTT	CTTTATACAC	ATTTGGGAAA	ACATTGGTCT	3360
	CACAGATTAA	ATGATTAACT	AACTGACCCA	GGAAGTAGTT	GTAGCTTTCT	AAGTAATTAG	3420
65	GCAATTACAG	TTATTGCCCT	TAACCAAGGG	TAATAAAACA	AAATGACAAG	TACATGTTTA	3480
	AAATTATGAG	GCAATGAGAA	ATAATTAAAA	AACCAATTTT	CTAGTTATAA	TTTAAATTTT	3540
	GGAGAGCATT	TTTAAACAGT	ATTAATCCAG	AGGTGGCTCA	AATTGAGTAT	AAGAAATTAAG	3600
	ATTATTAAAA	ATACTGCATG	TCTACCTTCT	CGGGGATCAT	ACTTTATAAC	ACTTTCTGCT	3660
70	TCAGTAGCTC	TTCATAGCTT	GCCAAAGTATG	CTCCCATATT	TTCTCTCTCG	TGCCTCGCAA	3720
	ATGAAAGTCA	GATAGGCTGG	GAACCTCATGG	GGCAGCCCTC	AGACTTCAAT	GTGGGCTTCA	3780
	AAATCCAGTT	CCTGTTCTAT	ATGGTGCTAC	ATCTTTCCAG	AAAATTTCCC	TCAGAGCCCC	3840
	TCGCCAAAAA	AAAGCATTAT	TTTGACCCCTG	CATGCTATTT	CTTTAGCTGT	AGGTGATAGA	3900
	TTAGAACTTC	TGTCAGACAT	GTTAATGACA	AACATACCAG	CAGACAATAA	CCAAAGCAAA	3960
75	TGTTTCCCTC	AAGTGTAAG	TGTGACGGGG	CTCGTGGGCA	AGGATGTATT	GGCACACTGT	4020
	CCTCTTGAAC	TGATAGTGTC	CCAGCAATGT	TGGAGGTTGG	CACCATTCCT	GGTCCGACAC	4080
	TTGAGGACCT	GAGAGACATC	AGGTTTAGAA	TGAGCCAAAG	AAATCCTTACA	AGATGGGGAG	4140
	AAATGGTGTC	CAGCAGCCTA	AGTGTATAG	TTAAGTCTAA	AGAAGTATGA	AAGATCCCCCT	4200
	GTGTTCTCTA	AAATGAGCAG	AGGGGCCTGC	CTACCAATAT	CACTTTTATG	GGGACTGAAC	4260
	CATTGCAAGT	TAGACTTGGC	TTCCAAAGAG	TCTGCCTAAG	CCAGGGGTGG	CAGGGTAGGC	4320
80	CATCATAGCT	GGATGGCCCT	AAAAGCAGAT	GGGGGCAGAC	TTGCCCTCGT	GATGCCAGGA	4380
	TTTGAGAGGC	AGAGTTTCTA	GAGGGAGACC	AGTGCTGCCT	CTCACAGTGG	CAGTTTTCCT	4440
	TCTTTGCAAG	AGGAGGGGCT	GTTCAATTCC	ATAGACCAGT	GGGCAGATAG	CCAGTTGAAT	4500
	ACTCTGTGCA	TGGTTTGATG	CTTTATTAGT	TCGCTCTAAT	ATTTTCTGCT	AGATCCTTTT	4560
	GTCTCTGACT	CAAAATCTAA	TCCATGCATT	GTATGATACC	GTAGCTCTCC	TAAGGTTTGT	4620
85	GTTTCCCTCA	AAATGTTTTA	GTTTTCTTCA	ACTAAATTTG	ATTTTCTGCT	TTAGAAGTGA	4680
	CATATTTTTA	TGGTATACAC	TATGTTCTCT	TTTCTACTG	CGAGTCAATT	TTTTGAATTT	4740
	TCGTGAGAAA	GAATATATCT	ACAAATTGCA	CGAAAGTATC	ATAAAAAACG	TACTCTAGAG	4800

	CAGGCGTGT	CAATAGAAAT	ATAATCTGAG	CCACATGTAT	AATTTTATTT	TCTTCTAGCC	4860
	ACATTAAAGA	AGTAAAAAGA	TACAAGTAGA	ACTAATTTTA	ATGTTTTAAT	TCAGTATATC	4920
	CAAAATATCA	TTTGAACATG	TAATTAATAT	AAAATTATTA	ATGTGATATT	TTACATTTCT	4980
5	TTGGTAATAC	TAGTCTTCAA	AATCTGGTAT	GTATCTTACA	TTGATAGCAC	ATCTCACTTT	5040
	GTACTAGCCA	CATTGCAAGT	GCTCAGTAGC	CACATGTGGC	TAGTGGCTAC	TGCACTGGAC	5100
	AGCACAGTTC	TAGGTTCCAC	CCTAACACCC	AAGTCTGTG	GATTAGAATC	CCAGAATCAG	5160
	AGCTGGAAGT	AAACATAGAG	ATCAAACTTC	CTTTTAAAAA	TGAGGACGCT	GAGGCACAGA	5220
	GTTTAAATGG	CTTGCAATGAG	GTACATACAGC	TAAATTCAGC	CTCAACAGGG	TCTTCTGATT	5280
10	CCAGGCACCT	TTCCCACTCC	ACTACATTAC	TGTAGTGGTA	ATTCCTTAGGG	TTAAAAAAG	5340
	TGTAGAGTAG	GCCGGGCGCA	GTGGCTCATG	CCTGTAATCC	CAGCACTTTG	GGAGGCCGAA	5400
	GTGGGCGGAT	CACGAGGTCA	GGAGATCGAG	ACCATCCTGG	CCAACATGGT	GAAACCCCGT	5460
	CTCTACTGAA	AATACAAAGC	AAAATTAGCC	AGGTGTGGTG	GCGGGCGCCT	GTGGTCCCAG	5520
	CTGCTCTGGA	GGCTGAGGCA	GAATGGCGTG	AACCCAGGAG	GCAGAGATGG	CAGTGAGCCA	5580
15	AGATCGCGCC	ACTGCACCCC	AGCCTGGGCG	ACAGAGCGAG	ACTCCATCTC	AAAAAAGAAA	5640
	AAAAAAGAAA	AAGAAAAGAA	AAGAAAAGTC	TAGAGAACAT	TATATTAAGT	GGTTATTATT	5700
	GAAGTAGACC	AAAGTTTATA	CCATAAGGAT	ATTTTTCCTT	AAATACCATG	TTTGAAGAAC	5760
	AATTATTAT	TGATCCTGTA	ATCTGTAAGA	TCAAATAACA	AGTCTCTATC	CATGTTACCA	5820
	AAITTTAACCT	TTTGAATAA	ATAAACTTTA	AAATATCAGA	TGTGTTATTA	CAGGATGATA	5880
20	CTTGGAATCA	AGTGAATGA	GTTATATGGT	CATCACTAAA	TTTAGAAATC	TATTGTGAAA	5940
	CAAAGACAAA	CAGGAAAGTA	CAGAAATAGAG	ACTTTTAGTA	AATAAATGGA	ATTTAAAGA	6000
	AAGTGTTTAT	TTACAGTGTG	ACGACAGAAA	AGGATGTCTT	TGTTGTCTATA	GTCTTTGAGG	6060
	GATCTCCGTA	AAATCTGGGG	CACAGGTACA	AGAAATAGCC	AATATTTAGT	TCCCAGACCA	6120
	TGTTTAGTAG	TGTTCAGTTT	CAGATCATGC	TGCCAAGAGG	TATCTCCCCC	TCAGGTGGGT	6180
25	CATCACTGAG	CCCTGGAATT	GGAGACTCAT	ACTTGCCGAG	CACAATGTTA	CGGGCAGACA	6240
	GGCCGACATC	TATGATTAGC	TAGAAGCCAT	AAAGAAAAGC	TGCTAAGTGG	CCACTAGGTG	6300
	CCACTTTTCT	GTTTTGTGTA	TGCTTTCATT	AGCAGATCTT	TTTTTTCCAA	GCTCCATGGG	6360
	GCCTATGAGA	GGCATTTATG	ATTTTGTGTC	CTACAATAAG	TCAGCCTGTC	TGGTGTGAGT	6420
	TGTTTATGA	GAATGCTTTT	CCAAGGGAGG	TCTAGGAAGA	TCTTGACACA	TAAGAACTTT	6480
30	GGCTTAGAGA	GCTTTCCAGG	TGTAGTGCCA	ATAAAACTG	ACCTGGAAAG	AAAACTGCC	6540
	CAGCAGGAA	CATGCTTTCT	GAACCTCACT	GAGAGTGTAT	GGTGTATGTC	ACTTCTCATA	6600
	TATTCTTGAG	TTTAGATTGT	TCTTTTATAC	AATTTTATAGC	TCTTTTCCAG	TTCACTTTGT	6660
	CTCGTCTGTA	TATTGCTATT	TTTAAATTTT	TGTGGTAAAT	AATGAAAGA	GTGAAATTAT	6720
	ATTTTATAAT	TACTCATTG	TAGTTTTTTT	TTTAAATTTA	ATAAACTTCC	TCCAAAAGT	6780
35	GTCCCTTAA	AA					

Seq ID NO: 166 Protein sequence:
Protein Accession #: AAG34652

40	1	11	21	31	41	51	
	MAAEEBAAG	GKVLREENQC	IAPVVSSRVS	PGTRPTAMGS	FSSHMTFEPF	KRKGSDSDPS	60
	QVEDGEHQVK	MKAFFREAHQ	TEKRRRDKNM	NLIEELSAMI	PQCNPMARKL	DKLTVLRMAV	120
	QHLRSKGLT	NSYVGSNYRP	SPLQDNELRH	LILKTAEGFL	FVVGCEGKI	LFVSKSVSKI	180
45	LNVDQASLTG	QSLFDFLHPK	DVAKVKEQLS	SFDISPREKL	IDAKTGLQVH	SNLHAGTRTV	240
	YSGSRRSFFC	RIKSKISVK	EEHGCPLNSK	KKEHRKFYTI	HCTGYLRSWP	PNIVGMEEER	300
	NSKKNNSNFT	CLVAIGRLQP	YIVPQNSGEI	NVKPTEFITR	FAVNGKFVYV	DQRATAILGY	360
	LPQELLGTSC	YEFVHQDDHN	NLTDKHKAVL	QSKEKILTDS	YKFRKAGDSF	VTLSQWFSF	420
50	TNPWTKELEY	IVSVNLTVLG	HSEPEASFL	PCSSQSSEES	SRQSCMSVPG	MSTGTVLGAG	480
	SIGTDIANEI	LDLQRLQSSS	YLDSSPTGL	MKDTHTVNCR	SMSNKLEFPF	SPSEMGELEA	540
	TRQNQSTVAV	HSHEPLSDG	AQLDFDALCD	NDDTAMAAFM	NYLEAEGGLG	DPGDFSDIQW	600
	TL						

Seq ID NO: 167 DNA sequence
Nucleic Acid Accession #: NM_014400
Coding sequence: 86-1126

60	1	11	21	31	41	51	
	GGTTACTCAT	CCTGGGCTCA	GGTAAGAGGG	CCCGAGCTCG	GAGGCGGCAC	ACCCAGGGGG	60
	GACGCCAAGG	GAGCAGGAGC	GAGCCATGGA	CCCCGCCAGG	AAAGCAGGTG	CCCAGGCCAT	120
	GATCTGGACT	NSYVGSNYRP	TGCTGCTGCT	GCTGCTTCGC	GGAGGAGCGC	AGGCCCTGGA	180
	GTGCTACAGC	TGCGTGACAG	AAGCAGATGA	CGGATGCTCC	CCGAACAAGA	TGAAGACAGT	240
	GAAAGTGCAG	CCGGGCGTGG	ACGTCTGCAC	CGAGGCCGTG	GGGGCGGTGG	AGACCATCCA	300
65	CGGACAATTG	TCCGTGGCAG	TGCSGGGTG	CGGTTCCGGA	CTCCCCGCGA	AGAATGACCG	360
	CGGCCTGGAT	CTTCACGGGC	TTCTGGCGTT	CATCCAGCTG	CAGCAATGCG	CTCAGGATCG	420
	CTGCAACGCC	AAGCTCAACC	TCACTCGCG	GGCGCTCGAC	CCGGCAGGTA	ATGAGAGTGC	480
	ATACCCGCC	AACGGCGTGG	AGTGCTACAG	CTGTGTGGGC	CTGAGCCGGG	AGGCGTGCCA	540
	GGGTACATCG	CGCCCGGTG	TGAGCTGCTA	CAACGCCAGC	GATCATGTCT	ACAAGGGCTG	600
70	CTTCGACGGC	AACGTCAACT	TGACGGCAGC	TAATGTGACT	GTGTCCTTGC	CTGTCCGGGG	660
	CTGTGTCCAG	GATGAATTCT	GCACTCGGGA	TGGAGTAACA	GGCCCAAGGT	TCACGCTCAG	720
	TGGCTCCTGT	TGCCAGGGGT	CCCGCTGTAA	CTCTGACCTC	CGCAACAAGA	CCTACTTCTC	780
	CCCTCGAATC	CCACCCCTTG	TCCGGCTGCC	CCCTCCAGAG	CCCACGACTG	TGGCCTCAAC	840
75	CACATCTGTC	ACCACCTTCA	CCTCGGCC	AGTGAGACCC	ACATCCACCA	CCAAACCCAT	900
	GCCAGCGCCA	ACCAGTCAGA	CTCCGAGACA	GGGAGTAGAA	CACGAGGCCT	CCCGGATGA	960
	GGAGCCCAGG	TTGACTGGAG	GCGCCGCTGG	CCACCAGGAC	CGCAGCAATT	CAGGGCAGTA	1020
	TCCGTCAAAA	GGGGGGCCCC	AGCAGCCCCA	TAATAAAGGC	TGTTGGCTC	CCACAGCTGG	1080
	ATTGGCAGCC	CTTCTGTTGG	CGTGGCTGTC	TGGTGTCTTA	CTGTGAGCTT	CTCCACCTGG	1140
80	AAATTTCCCT	CTCACCTACT	TCTCTGGCCC	TGGGTACCCC	TCTTCTCATC	ACTTCTGTT	1200
	CCCACTACTG	GACTGGGCTG	GCCAGCCCC	TGTTTTTCCA	ACATTCACCA	GTATCCCCAG	1260
	CTTCTGCTGC	GCTGGTTTGC	GGCTTTGGGA	AATAAATAC	CGTTGTATAT	ATTCTGGCAG	1320
	GGGTGTTCTA	GCTTTTGTAG	GACAGCTCCT	GTATCCTTCT	CATCCTTGTC	TCTCCGCTTG	1380
	TCCTCTTGTG	ATGTTAGGAG	AGAGTGAGAG	AAGTCAGCTG	TCACGGGGAA	GGTGAGAGAG	1440
85	AGGATGCTAA	GCTTCTACT	CACTTTCTCC	TAGCCAGCCT	GGACTTTGGA	GCGTGGGGTG	1500
	GGTGGGACAA	TGGTCCCCCA	CTCTAAGCAC	TGCCTCCCCC	ACTCCCCGCA	TCTTTGGGGA	1560
	ATCGGTTCCC	CATGTTCTT	CCTTACTAGA	CTGTGAGCTC	CTCAGGGGCA	GGGACCGTGC	1620
	CTTATGTCTG	TGTGTGATCA	GTTTCTGGCA	CATAAATGCC	TCAATAAAGA	TTTAATTACT	1680

TTGTATAGTG AAAAAAA

Seq ID NO: 168 Protein sequence:
Protein Accession #: NP_055215

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1      11      21      31      41      51
|      |      |      |      |      |
MDPARKAGAG AMIWTAGWLL LLLLRGGAQA LECYSCVQKA DDGCSFNKMK TVKCAPGV DV      60
CTEAVGAVET IHQQFSLAVX GCGSGLPGKN DRGLDLHGLL AFIQLQCCAQ DRGNALNLT      120
SRALDPAGNE SAYPPNGVEC YSCVGLSREA CQGTSPFVVS CYNASDHVYK GCFDGNVTLT      180
AANVTVSLPV RGCVDQDEFCT RDGVTGPGFT LSGSCCQGSR CNSDLRNKTY FSPRIPLVLR      240
LPPPEPTTVA STTSVTSTST APVRPTSTTK PMPAPTSQTP RQGVHEEASR DEEPRLTGGA      300
AGHQDRNSNG QYPAKGGPQQ PHNKGCVAPT AGLAALLLAV AAGVLL

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Seq ID NO: 169 DNA sequence
Nucleic Acid Accession #: NM_006875
Coding sequence: 186-1190

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1      11      21      31      41      51
|      |      |      |      |      |
GAATTCGGCA CGAGCGCGCG GCGAATCTCA ACGCTGCGCC GTCTGCGGGC GCTTCCGGGC      60
CACCAGTTTC TCTGCTTTCC ACCCTGGCGC CCCCCAGCCC TGGCTCCCCA GCTGCGCTGC      120
CCCGGGCGTC CACGCCCTGC GGGCTTAGCG GGTTCAGTGG GCTCAATCTG CGCAGCGCCA      180
CCTCCATGTT GACCAAGCCT CTACAGGGGC CTCCGCGGCC CCGCGGGACC CCCACGCGCG      240
CGCCAGGAGG CAAGGATCGG GARGCGTTCC AGGCCGAGTA TCGACTCGGC CCCCTCCTGG      300
GTAAAGGGGGG CTTTGGCACC GTCTTCGCAG GACACCGCCT CACAGATCGA CTCAGGTGG      360
CCATCAAAGT GATTCGCCCG AATCGTGTGC TGGGCTGGTC CCCCTGTGCA GACTCAGTCA      420
CATGCCCACT CGAAGTCGCA CTGCTATGGA AAGTGGGTGC AGGTGGTGGG CACCCTGGCG      480
TGATCCGCGT GCTTGACAGG TTTGAGACAC AGGAAGGCTT CATGCTGGTC CTCGAGCGGC      540
CTTTGCCCGC CAGGATCTCT TTTGACTATA TCACAGAGAA GGGCCCACTG GGTGAAGGCC      600
CAAGCGCGTG CTTCCTTGGC CAAGTAGTGG CAGCCATCCA GCACCTGCCA TCCCGTGGAG      660
TTGTCCATCG TGACATCAAG GATGAGAACA TCCTGATAGA CTTACGCGGT GGCTGTGCCA      720
AACTCATTGA TTTTGGTTCT GGTGCCCTGC TTCATGATGA ACCCTACACT GACTTTGATG      780
GGACAAGGGT GTACAGCCCC CCAGAGTGGG TCTCTCGACA CCAGTACCAT GCACTCCCGG      840
CCACTGTCTG GTCACTGGGC ATCCTCTCTC ATGACATGGT GTGTGGGGAC ATTCCCTTTG      900
AGAGGGACCA GGAGATTCTG GAAGCTGAGC TCCACTTCCC AGCCCATGTC TCCCAGACT      960
GCTGTGCCCT AATCCGCGCG TGCCCTGGCC CCAAACCTTC TTCCCGACCC TCACTGGAAG      1020
AGATCCTGCT GGACCCCTGG ATGCAAAACAC CAGCCGAGGA TGTATCCCTC CAACCCCTCC      1080
AAAGGAGGCC CTGCCCTTTT GGCTGGTCC TTGCTACCTT AAGCTGGGCC TGGCTGGGCC      1140
TGGCCCCCAA TGGTCAGAAG AGCCATCCCA TGGCCATGTC ACAGGGATAG ATGGACATTT      1200
GTTGACTTGG TTTTACAGGT CATTACCACT CATTAAAGT CAGTATTACT AAGGTAAGGG      1260
ATTGAGGATC AGGGGTAGA AGACATAAAC CAAGTTTGCC CAGTCCCTT CCCAATCTA      1320
CAAAGGAGCC TTCTCCAG AACCTGTGGT CCCTGATTTT GGAGGGGGAA CTTCTTGCTT      1380
CTCATTTTGC TAAGGAGGTT TATTTTGGTG AAGTTGTTCC CATTITGAGC CCGGGGACTC      1440
TTATTTTGAT GATGTGTAC CCACATTTG CACCTCTAC TACCACCACA CAACTTAGT      1500
TCATATGCTT TTAATGGGCG AAGGGTGCTT TCCTTCCAAT ACCCCAGTAG CTTTATTTT      1560
AGTAAAGGGA CCCTTTCCCG TAGCCTAGG TCCCATATTG GGTCAAGCTG CTTACCTGCC      1620
TCAGCCAGG ATTTTATT TTTGGGGAGG TAATGCCCTG TTGTTACCCC AAGCTTCTT      1680
TTTTTTTTTT TTTTTTTT GGTGAGGGGA CCTACTTTG TTATCCCAAG TGCTCTTATT      1740
CTGGTGAGAA GAACCTTAAT TCCATAATT GGAAGGAAT GGAAGATGGA CACCACCGGA      1800
CACCACAGA CAATAGGATG GATGATGAG TTTTGGGG GATGGGCTAG GGGAAATAAG      1860
GCTTGCTGTT TGTTTTCCCT GGGCGCTCCC TCCAATTTG CAGATTTTGG CAACCTCCTC      1920
CTGAGCGGGG ATTTGCTCAAT TACTAAATG TAAATAATCA CGTATTGTGG GGAGGGGAGT      1980
TCCAAGTGTG CCTCTCTTT TTTCTCTGCC TGGATTATTT AAAAAGCCAT GTGTGGAAC      2040
CCACTATTTA ATAAAGTAA TAGAATCAGA AAAAAA AAAAAA

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Seq ID NO: 170 Protein sequence:
Protein Accession #: NP_006866

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1      11      21      31      41      51
|      |      |      |      |      |
MLTKPLQGP APPGTPTPPP GKDREAFEA EYRLGPLLGK GFGTVFAGH RLTDRLQVAI      60
KVIPRNRVLG WSPLSDSVTC PLEVALLWKV GAGGGHPGVI RLLDWFTQE GFMLVLERPL      120
PAQDLPHYIT EKGPLGEGPS RCFFGQVVA IQHCHSRGVV HRDIKDENIL IDLRRCAGKL      180
IDFGSALLH DEPYTFDGT RVYSPPEWIS RHQYHALPAT VWSLGILLYD MVEGDIPIFER      240
DQEILEAELH FPAHVSPDCC ALIRRLAPK PSSRPSLEBI LLDPMWQTPA EDVTPQLQR      300
RPFPGVLVA TSLANPGLA PNGQKSHMPA MSQG

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Seq ID NO: 171 DNA sequence
Nucleic Acid Accession #: NM_003646
Coding sequence: 89..2875

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GCCCTCGGCC GGCCTGGGCT AGGGCCGGAT GGAGCCGCGG GACCGTAGCC CCGAGGCCCCG      120
GAGCAGCGAC TCCGAGTCGG CTTCGCGCTC GTCCAGCGGC TCCAGCGCGC ACGCGGCTCC      180
CGAGCCGGAC AAGGCGCGCG GCGGACTCAA CAAGCGGCGC TTCCCGGGGC TCGGGCTCTT      240
CGGGCAGAGC AAAGCATCA CCAAGTCGGG CCTCCAGCAC CTGGCCCCCC CTCGCGCCAC      300
CCCTGGGGCC CCGTGCAGCG AGTCAGAGCG GCAGATCCGG AGTACAGTGG ACTGGAGCGA      360
GTCAGCGACA TATGGGAGC ACATCTGGTT CGAGACCAAC GTGTCCGGGG ACTTCTGCTA      420
CGTTGGGGAG CAGTACTGTG TAGCCAGGAT GCTGAAGTCA GTGTCTCGAA GAAAGTGCGC      480
AGCTGCAAG ATTGTGTG ACACGCCCTG CATCGAGCAG CTGGAGAAGA TAAATTTCCG      540
CTGTAAGCCG TCCTTCGGTG AATCAGGCTC CAGGAATGTC CGCAGGCCAA CCTTTGTACG      600
GCACCACTGG GTACACAGAC GACGCCAGGA CGCAAGTGT CGGCACTGTG GGAAGGGATT      660
CCAGCAGAAG TTCACCTTCC ACAGCAAGGA GATTGTGGCC ATCAGCTGCT CGTGGTGCAA      720

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	GCAGGCATAC	CACAGCAAGG	TGTCCTGCTT	CATGCTGCAG	CAGATCGAGG	AGCCGTGCTC	780
	GCTGGGGGTC	CACGAGCCG	TGGTCATCCC	GCCACCTGG	ATCCTCCGG	CCCGAGGGCC	840
	CCAGAAATCT	CTGAAGACAA	GCAAGAAGAA	GAAGAGGGCA	TCCTTCAAGA	GGAAAGTCCAG	900
5	CAAGAAAGGG	CTTAGGAGG	GCCGCTGGAG	ACCTTTCATC	ATCAGGCCCC	CCCCCTCCCC	960
	GCTCATGAAG	CCCTGCTGG	TGTTTGTGAA	CCCCAAGAGT	GGGGGCAACC	AGGGTGCAAA	1020
	GATCATCCAG	TCTTCTCTCT	GGTATCTCAA	TCCCGACAA	GTCTTCGACC	TGAGCCAGGG	1080
	AGGGCCCAAG	GAGGCGCTGG	AGATGTACCG	CAAAGTGAC	AACCTGGGGA	TCCTGGCGTG	1140
	CGGGGCGGAC	GGCAGGTGG	GCTGGATCCT	CTCCACCTG	GACCAGCTAC	GCCTGAAGCC	1200
10	GCCACCCCT	GTTCGCATCC	TGCCCTGGG	TACTGGCAAC	GACTTGGCCC	GAACCTCAA	1260
	CTGGGGTGGG	GGCTACACAG	ATGAGCCTGT	GTCCAAGATC	CTCTCCACG	TGGAGGAGGG	1320
	GAACGTGGTA	CAGCTGGACC	GCTGGACCT	CCACGCTGAG	CCCAACCCCG	AGGCAGGGCC	1380
	TGAGGACCGA	GATGAAGGCG	CCACGACCG	GTTCGCCCTG	GATGTCTTCA	ACAACCTACT	1440
	CAGCCTGGGG	TTTGACGCCC	AGCTACCCCT	GGAGTTCCAC	GAGTCTCGAG	AGGCCAACCC	1500
15	AGAGAAATTC	AACAGCCGCT	TTCCGAATAA	GATGTTCTAC	GCCGGGACAG	CTTCTCTGTA	1560
	CTTCCTGATG	GGCAGCTCCA	AGGACCTGGC	CAAGCACATC	CGAGTGGTGT	GTGATGGAAT	1620
	GGACTTGACT	CCCAAGATCC	AGGACCTGAA	ACCCAGTGT	GTGTGTTTCC	TGAACATCCC	1680
	CAGGTACTGT	GCGGGCACCA	TGCCCTGGGG	CCACCTGGG	GAGCACCACG	ACTTTGAGCC	1740
	CCAGCGGCAT	GACGACGGCT	ACCTCGAGGT	CATTGGCTTC	ACCATGACGT	CGTTGGCCGC	1800
20	GCTGCAGGTG	GGCGGACAG	GCGAGCGGCT	GACGAGTGT	GCGAGGTGG	TGCTCACCAC	1860
	ATCCAAGGCC	ATCCCGGTGC	AGGTGGATGG	CGAGCCCTGC	AAGCTTGAC	CCTCAGCAT	1920
	CCGCTCGCC	CTGCGCAAC	AGGCCACCAT	GGTGACAGAG	GCCAAAGCGC	GGAGCGCCGC	1980
	CCCTCTGCAC	AGCGACGCG	AGCCGGTGCC	AGAGCAGTTG	CGCATCCAGG	TGAGTCGCGT	2040
	CAGCATGCAC	GACTATGAGG	CCCTGCACTA	CGACAAGGAG	CAGCTCAAGG	AGGCCTCTGT	2100
	GCCGCTGGGC	ACTGTGGTGG	TCCAGGAGA	CAGTGACCTA	GAGCTCTGCC	GTGCCACAT	2160
25	TGAGAGACTC	CAGCAGATGC	CCGATGTTGC	TGGAGCCAAG	TCCCGACAT	GCCAGAACT	2220
	GTCCCCCAAG	TGGTGCTTCC	TGGACGCCAC	CACCTGCCAGC	CGCTTCTACA	GGATCGACCG	2280
	AGCCCAAGG	CACCTCAACT	ATGTGACTGA	GATCGACAG	GATGAGATTT	ATATCTGGA	2340
	CCCTGAGCTG	CTGGGGCAT	CGGCCCGGCC	TGACCTCCCA	ACCCCACTT	CCCTCTCCC	2400
30	CACCTCACCC	TGCTCACCCA	CGCCCGGTC	ACTGCAAGGG	GATGCTGCAC	CCCCTCAAGG	2460
	TGAAGAGCTG	ATTGAGGCTG	CCAAGAGGAA	CGACTTCTGT	AAGCTCCAGG	AGCTGCACCG	2520
	AGCTGGGGGC	GACCTCATGC	ACCGAGACGA	GCAGAGTCGC	ACGCTCTGTC	ACCAACGAGT	2580
	AGCACTGGC	AGCAAGGATG	TGGTCCGCTA	CCTGCTGGAC	CAGCCCCCCC	CAGAGATCCT	2640
	TGATGCGGTG	GAGGAAAACG	GGGAGACCTG	TTTGACACAA	GCAGCGGCC	TGGGCCAGCG	2700
35	CACCATCTGC	CATCATATGC	TGGAGGCCGG	GGCCTCGCTC	ATGAAGACAG	ACCAGCAGGG	2760
	CGACACTCCC	CGGACGCGG	CTGAGAAAGC	TCAGGACACC	GAGCTGGCCG	CCTACTGGA	2820
	GAACCGGCAG	CATACACAGA	TGATCCAGCG	GGAGGACCAG	GAGACGGCTG	TGTAGCGGGC	2880

Seq ID NO: 172 Protein sequence:
Protein Accession #: NP_003637

40	1	11	21	31	41	51	
	MEPRDGSPEA	RSSDSESASA	SSSGSERDAG	PEPDKAPRRL	NKRRFPGLRL	FGHRKAITKS	60
	GLQHLAPPPP	TPGAPCSESE	RQIRSTVDWS	ESATYGEHIW	FETNVSGDFC	YVGEQYCVAR	120
45	MLKSVSRRC	AACKIVVHTP	CIEQLEKINF	RCKPSFRESG	SRNVREPTFV	RHHVWHRRRQ	180
	DGKCRHCGKG	FQKQFTFSK	EIVAISSWC	KQAYHSKVSC	FMLQIEBPC	SLGVHAAVVI	240
	PPTWILRARR	PQNTLKAASK	KKRASFPRKS	SKKGPEEGRW	RPFIIRPTPS	PLMKPLLVFV	300
	NPKSGNQGA	KIQSFLWYL	NPRQVFDLSQ	GGPKAEALMY	RKVHNLRLA	CGDGTGVGWI	360
50	LSTLDQLRLK	PPPPVAILPL	GTGNDLARTL	NWGGGYTDEP	VSKILSHVEE	GNVVQLDRWD	420
	LHAEPNPEAG	PEDRDGATD	RLPLDVFNRY	FSLGFDHVT	LEFHESREAN	PEKFNSRFRN	480
	KMFYAGTAFS	DPLMGSSKDL	AKHIRVVC DG	MDLTPKIQDL	KPQC VVFLNI	PRYAGTMPW	540
	GHPGEHDFE	PQRHDDGYLE	VIGFTMTSLA	ALQVGGHGER	LTQCREVVL T	TSKAIPVQVD	600
	GEPCKLAA SR	IRIALRNQAT	MVQAKRRSA	APLHSDQQPV	PEQLRIQVSR	VSMHDEYALH	660
55	YDKEQLKEAS	VPLGTVVVPG	DSDELCRAH	IERLQQEPDG	AGAKSPTCQK	LSPKWCFLDA	720
	TTASRFYRID	RAQEHNLNYT	EIAQDEIYIL	DPELLGASAR	FDLPTPTSPL	PTSPCSPTPR	780
	SLQGDAAFPQ	GEELIEAAKR	NDFCKLQELH	RAGGDLMHRD	EQSRTLHHA	VSTGSKDVVR	840
	YLLDHAPPET	LDAVEENGET	CLHQAAALGQ	RTICHYIVEA	GASLMKTDQQ	GDTPRQRAEK	900
	AQDTLAAAYL	ENRQHYQMIQ	REDQETAV				

Seq ID NO: 173 DNA sequence
Nucleic Acid Accession #: AF232772
Coding sequence: 1-1662

65	1	11	21	31	41	51	
	ATGCCCGTGC	AGCTGACGAC	AGCCCTGCGT	GTGGTGGGCA	CCAGCCTGTT	TGCCCTGGCA	60
	GTGCTGGGTG	GCATCCTGGC	AGCCTATGTG	ACGGGCTACC	AGTTATCCA	CACGGAAAAG	120
	CACCTACCTGT	CCTTCGGCCT	GTACGGCGCC	ATCCTGGGCC	TGCACCTGCT	CATTACAGAGC	180
70	CTTTTTCGCT	TCCTGGAGCA	CGGGCGCATG	CGAGCTGCCG	GCCAGGCCCT	GAAGCTGCC	240
	TCCCCCGGCG	GGGGCTCGGT	GGCACTGTGC	ATTGCCGCAT	ACCAGGAGGA	CCCTGACTAC	300
	TTGCGCAAGT	GCTGCGCTC	GGCCAGCGC	ATCTCCTTCC	CTGACCTCAA	GGTGGTCATG	360
	GTGGTGGATG	GCAACCGCCA	GGAGGACGCC	TACATGCTGG	ACATCTTCCA	CGAGGTGCTG	420
	GGCGGCACCG	AGCAGGCCGG	CTTCTTTGTG	TGGCGCAGCA	ACTTCCATGA	GGCAGGCGAG	480
75	GGTGAGACGG	AGGCCAGCTG	GCAGGAGGGC	ATGGAACGTG	TGCGGGATGT	GGTGCGGGCC	540
	AGCACCTTCT	CGTGATCAT	GCAGAAAGTG	GGAGGCAAGC	GCGAGGTCT	GTACACGGCC	600
	TTCAAGGCC	TCGGCGATTC	GGTGGACTAC	ATCCAGGTGT	GCGACTCTGA	CACTGTGCTG	660
	GATCCAGCCT	GCACATCGA	GATGCTTCGA	GTCTGGAGG	AGGATCCCCA	AGTAGGGGGA	720
	GTCCGGGGAG	ATGTCAGAT	CCTCAACAAG	TACGACTCAT	GGATTTCCTT	CCTGAGCAGC	780
80	GTGCGGTACT	GGATGGCCTT	CAACGTGGAG	CGGGCCTGCC	AGTCCTACTT	TGGCTGTGTG	840
	CAGTGATATTA	GTGGGCCCTT	GGGCATGTAC	CGCAACAGCC	TCCTCCAGCA	GTTCCTGGAG	900
	GACTGGTACC	ATCAGAAATT	CCTAGGCAGC	AAGTGCAGCT	TCCGGGATGA	CCGGCACCTC	960
	ACCAACCGAG	TCCTGAGCCT	TGGCTACCGA	ACTAAGTATA	CCGCGCGCTC	CAAGTGCCTC	1020
	ACAGAGACCC	CACCTAAGTA	CCTCCGGTGG	CTCAACAGC	AAACCCGCTG	GAGCAAGTCT	1080
85	TACTCCGGG	AGTGCTCTA	CAACTCTCTG	TGGTTCATA	AGCACCACCT	CTGGATGACC	1140
	TACGAGTCAG	TGGTCACGGG	TTTCTTCCCC	TTCTTCTCTA	TTGCCACGGT	TATACAGCTT	1200
	TTTACCCGGG	CGGCAGCTCG	GAACTTCTC	CTCTTCTGTC	TGACGGTGCA	GCTGGTGGGC	1260
	ATTATCAAGG	CCACCTACGC	CTGCTTCTT	CGGGGCAATG	CAGAGATGAT	CTTCATGTCC	1320

	CTCTACTCCC	TCCTCTATAT	GTCCAGCCTT	CTGCCGGCCA	AGATCTTTGC	CATTGCTACC	1380
	ATCAACAAAT	CTGGCTGGGG	CACCTCTGGC	CGAAAAACCA	TTGTGGTGAA	CTTCATTGGC	1440
	CTCATTCCCTG	TGTCCATCTG	GGTGGCAGTT	CTCCTGGAGG	GGCTGGGCTA	CACAGCTTAT	1500
5	TGCCAGGACC	TGTTCACTGA	GACAGAGCTA	GCCTTCCTTG	TCCTCGGGGC	TATACTGTAT	1560
	GGCTGCTACT	GGGTGGCCCT	CCTCATGCTA	TATCTGGCCA	TCATCGCCCG	GCGATGTGGG	1620
	AAGAAGCCGG	AGCAGTACAG	CTTGGCTTTT	GCTGAGGTGT	GACATGGCCC	CCAAGCAGAG	1680
	CGGGTAAAGT	GCAATGGGTA	AGGGAGGGAA	GGGGAATGGA	AGAGAAAAGA	CAGGGTGGGA	1740
	GGGAGGAGGG	AGTGCTGTGT	TTTAGTCTCT	TAATGGTCCA	AAGGACAAAT	CTAAAAATGCA	1800
10	AAGAACGGTG	ATGTAGTATG	GCCTGACAGC	TCTGTTTAGA	GGAGGCAACA	CTGATCCCCC	1860
	AGATGCGAGG	CTGCAGGGGA	TTCTGTGTTT	TCAGACTGCC	TGCTGTCTTG	CATCTGCACA	1920
	TAGGCAGTAG	CCTCCTCCTG	GGCTCCAGAG	GGCACTCAGA	AGTTGTGCTA	AACCAAGTTA	1980
	AGTCCCATTC	AGTGGCAACT	TGTGATAGGT	ACCTGAGTGA	CGGCAACCTG	CGGAAGGAGG	2040
	TTCTCCCAGC	CCATCTGAAC	ACAACCAGAG	GTGGCAGGAG	AATTTCTACT	GAGCGAGGTG	2100
15	GGCCGGTTAG	TGTATGTCTC	CCCCACCCCA	CCCATAAGTA	GTCAATCAATG	CAATAAGATT	2160
	GCCGCTGAGA	TACAAGGCC	AGAAAGCCTGA	TCTTTGGGCA	TCAGAAAACA	GGGTCCAGGA	2220
	ATGGTGCTTT	ATGTGAGATA	CCCCACTCCA	CATCAACATT	CCAGGGATGA	GCCAAACCAG	2280
	CAGGAGGTTA	GCACTGAAGT	GCTTTTAAAA	GTGCACATTA	AAAAGGAAAG	TTTGGCAGGA	2340
	GGAAACAAAGA	GATTGTGGTG	GTGCTAAAGG	AGGCCATAAG	CTACACAGAG	GCCTTGGGTG	2400
20	TTCCACCTGG	AAACTGCTCA	GACGTCTAGA	TGGGTTCCTA	GCTTGTCTGT	GATCTCTGCT	2460
	GGGGAGATAA	AAAGATTAAAG	CCCCAACATG	TTCAAGAAAG	AAGTGAAGTC	TTGGGTATTT	2520
	TAACCTGTAT	ACTCTTGAAT	TCCTCTCAAA	TTCAAGCTCTG	ATCTGAGGCT	AAGACACACT	2580
	CCCCACTTCA	CTTTCTTCAA	AGCCACATTT	TTTGAGGTAT	CACTGCAGTC	ACCTCTTCTA	2640
	CCCTCATCAT	CATAGGTAAG	GTTTCAAGG	TGGCAATTGG	GGCGGAGCCC	CGGCTTCTTA	2700
25	TAGAAGCTTC	AGCAGGAGGC	AAGCGTGTTC	TCAGCACATA	TGGGAACATAT	GAGGAGCCTC	2760
	TGATCAAAAT	GGCTACAATC	TTGGAGCTGC	TTGGACGGAT	TCCTTGGCAG	CCGGGTTAGC	2820
	ATGTGTGACT	TTCAAGCTAC	TGTTCTTGAC	AATCATCTCC	AATGGAAAGC	TTTTCAGTGT	2880
	TCCCAAAGTG	AACTCTCAAA	TCCAAATGG	TTATCTTTGA	GACCATCCAT	TCTCCTCAGT	2940
	GGCTTCTCCA	GGGAATTTCT	ACAGCCAAGT	TGTGACAGTC	ACTGCATTTG	CCTGCTTCTT	3000
30	TTCCAGAAACC	AAAGTAGGAG	ATGAAACTGG	TTCTCATATC	CTAAGGTTC	TGCTTTCTCT	3060
	CTCATGCCTC	CTGAGGCTGT	TTTTGGCTGT	TTTCCCTCTG	CTGCTTTTGG	GGAAATGAGG	3120
	GAAGCCATTT	TCCAAGTGAC	TTGCAATCCA	GGCTGTTCTC	AGCGTTTTGA	GTTTAAACC	3180
	TGGGATCCTG	ACTAAGCCTT	GTAATTAAGG	GTGCTTGCT	TGCCCTCCAA	ATGTCCTTTC	3240
	TCAAAGGGGC	CAACTAACCC	GTGCAGAAC	AGCACTAAGG	TGGACAGCAG	ACAAGAGGGC	3300
35	AAGCCTCTAA	TGTACCAAGT	GCTTCTTACA	AAGACGCAAG	GTGTGCTCC	AACCACAGAT	3360
	GGGCAAAACC	TGGTGCTTTC	CTTCATCTCC	CACGAACTCA	AGGGTTTTCC	AAGTGTAGCT	3420
	AACAGTTGCC	ACATCACACA	GACCTCCAGT	TTCTGGTAAG	ACTGCTGTT	GACATCAGAC	3480
	CCAACCCATT	GAAGGCTGGA	AGGCAGCAGG	CATTTGTCTAA	GGCAGCTGAT	CCAGGCAATC	3540
	GTTCTGCTGG	CCAAGAAAGT	AAACTATTTT	GAGCATTAGA	ATGGAGGAAA	TCCGGTCAGC	3600
40	CAAGTGCAGA	GTTCAAGACT	CGCTAAGGGC	TTGTTTTTCT	TCAGCATTTA	CTTGAAGATT	3660
	AATGTAGGAT	GACAGGCTCT	CCTGGCTGTC	CTACCATCAG	CTCTGCCCTG	CAGTGTGGTC	3720
	GTCAACTTTC	GTCAAATCAA	AAACAGGCAG	GTACAGGTAG	TGGGCTCACA	ACGTTTGACC	3780
	TCGACTGGTT	TTTCTAAGTT	ATTTTGTACA	TTTTTCAGCA	GCAAAACCAA	ACTGGGTCTT	3840
	CAGCTTTATC	CCCGTTTCTT	GCAAGGGGAG	AGCCTTTATA	CAATTGGACG	CATTTTGGTT	3900
45	TTTCTCTATT	GAGAATTCAA	ATCCTCTTTT	GTATTGTTTC	TACAATAATT	TGTAACATA	3960
	TTTATTTTAA	CCTGCTTTTT	TTTTTTTTTT	TAATTTTCAG	GTCAGTTTTT	TTATACTGCA	4020
	CTTATTTGTC	AAAATAAAGA	TTCTCACAT				

Seq ID NO: 174 Protein sequence:
Protein Accession #: AAF36984

50	1	11	21	31	41	51	
	MPVQLTALR	VVGTSFLFALA	VLGGILAAYV	TGYQFIHTEK	HYLSFGLYGA	ILGLHLLIQS	60
55	LFAPLEHRRM	RRAGQALKLP	SPRRGSVALC	IAAYQEDPDY	LRKCLRSAGR	ISFPDLKVVM	120
	VVDGNRQEDA	YMLDIFHEVL	GGTEQAGFFV	WRSNFHEAGE	GETEASLQEG	MDRVRDVVRA	180
	STFSIMQKW	GGKREVMYTA	FKALGDSVDY	IQVCDSDTVL	DPACTIEMLR	VLEEDPQVGG	240
	VGGDVQILNK	YDSWISFLSS	VRYWMAFNVE	RACQSYFGCV	QCISGFLGMY	RNSLLQGFLE	300
	DWYHQKPLGS	KCSFGDDRHL	TNRVLSLGYR	TKYTARSKCL	TETPTKYLRW	LNQOTRWSKS	360
60	YFREWLXNSL	WFHKLHLMWT	YESVVTGFFP	FFLIATVIQL	FYRGRIRWNL	LFLLTLVQLVG	420
	IIKATYACFL	RGNAEMIFMS	LYSLLYMSSL	LPAKIFAIAT	INKSGWGTSG	RKTIVVNFIG	480
	LIPVSIWVAV	LLEGLAYTAY	CQDLFSETEL	AFLVSGAIFY	GCYVWALLML	YLAIIRRCG	540
	KKPEQYSLAF	AEV					

Seq ID NO: 175 DNA sequence
Nucleic Acid Accession #: NM_000691
Coding sequence: 43..1404

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	GCCGTGAAGC	GCGCCCGCGC	CGCCTTCAGC	TCGGGCAGGA	CCCGTCCGCT	GCAAGTCCGA	120
	TTCCAGCAGC	TGGAGGCGCT	GCAGCGCCTG	ATCCAGGAGC	AGGAGCAGGA	GCTGGTGGGC	180
75	GCGCTGGCCG	CAGACTCTGCA	CAAGAAATGAA	TGGAAAGCCT	ACTATGAGGA	GGTGGTGTAC	240
	GTCCTAGAGG	AGATCGAGTA	CATGATCCAG	AAGCTCCCTG	AGTGGGCCCG	GGATGAGCCC	300
	GTGGAGAAGA	CGCCCCAGAC	TCAGCAGGAC	GAGCTCTACA	TCCACTCGGA	GCCACTGGGC	360
	GTGGTCTCTG	TCAATGGCAC	CTGGAACTAC	CCCTTCAACC	TCACCATCCA	GCCCATGGTG	420
	GGCGCCATCG	CTGCAGGGAA	CGCAGTGGTC	CTCAAGCCCT	CGGAGCTGAG	TGAGAACATG	480
80	GCGAGCCTGC	TGGCTACCAT	CATCCCCCAG	TACCTGGACA	AGGATCTGTA	CCCAGTAATC	540
	AATGGGGGTG	TCCCTGAGAC	CACGGAGCTG	CTCAAGGAGA	GGTTCGACCA	TATCCTGTAC	600
	ACGGGCAGCA	CGGGGGTGGG	GAAGATCATC	ATGACGGCTG	CTGCCAAGCA	CCTGACCCCT	660
	GTACAGCTGG	AGCTGGGAGG	GAAGATGCCC	TGCTACGTGG	ACAAGAACTG	TGACCTGGAC	720
	GTGGCCTGCC	GACGCATCGC	CTGGGGGAAA	TTCAATGAACA	GTGGCCAGAC	CTGCGTGGCC	780
85	CCAGACTACA	TCCTCTGTGA	CCCCTCGATC	CAGAAACAAA	TTGTGGAGAA	GCTCAAGAAG	840
	TCATGAAAG	AGTTCTACGG	GGAAGATGCT	AAGAAATCCC	GGGACTATGG	AAGAATCATT	900
	AGTGCCCGGC	ACTTCCAGAG	GGTGATGGGC	CTGATTGAGG	GCCAGAAAGT	GGCTTATGGG	960
	GGCACCCGGG	ATGCCGCCAC	TCGCTACATA	GCCCCACCA	TCCTCACGGA	CGTGGACCCC	1020

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CAGTCCCGG	TGATGCAAGA	GGAGATCTTC	GGGCTGTGTC	TGCCCATCGT	GTGCGTGGCG	1080
AGCCTGGAGG	AGGCCATCCA	GTTCATCAAC	CAGCGTGAGA	AGCCCTGGC	CCTCTACATG	1140
TTCTCCAGCA	ACGACAAGGT	GATTAAGAAG	ATGATTGCAG	AGACATCCAG	TGGTGGGGTG	1200
GCGGCCAACG	ATGTCATCGT	CCACATCACC	TTGCACTCTC	TGCCCTTCGG	GGGCGTGGGG	1260
AACAGCGGCA	TGGGATCCGA	CCATGGCAAG	AAGAGCTTCG	AGACTTTCTC	TCACCGCGC	1320
TCTTGCTCGG	TGAGGCTCT	GATGAATGAT	GAAGCGCTGA	AGGTCAGATA	CCCCCGAGC	1380
CCGCCAAGA	TGACCCAGCA	CTGAGGAGGG	GTGCTCCGC	CTGGCCTGGC	CATACTGTGT	1440
CCCATCGGAG	TGCGGACCC	CCTCACTGGC	TCTCCTGGCC	CTGGAGAATC	GCTCCTGCAG	1500
CCCCAGCCCA	GCCCCACTCC	TCTGCTGACC	TGCTGACCTG	TGCACACCCC	ACTCCACAT	1560
GGGCCCAGGC	CTCACCATT	CAAGTCTCCA	CCCCTTTCTA	GACCAATAAA	GAGACAATA	1620
CAATTTTCTA	ACTCGG					

Seq ID NO: 176 Protein sequence:
Protein Accession #: NP_000682

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1	11	21	31	41	51	
MSKISEAVKR	ARAAPSSGR	RPLQFRFQQL	EALQRLIQEQ	EQELVGALAA	DLHKNEWNAY	60
YEEVVYVLEE	IEYMIQKLPE	WAADPEVEKT	PQTQQDELYI	HSEPLGVVLV	IGTWNYPFNL	120
TIQPMVGAIA	AGNAVVLKPS	ELSENMASLL	ATIIPQYLDK	DLYPVINGGV	PETTELLKER	180
FDHILYTGST	GVGKIIMTAA	AKHLTPVTLE	LGGKSPCYVD	KNCCLDVACR	RIANGKFMNS	240
GQTCVAPDYI	LCDPSIQNQI	VEKLKSLKE	FYGEDAKKSR	DYGRISARH	QRVMGLIEG	300
QKVAYGGTGD	AATRYIAPT	LTDVDPQSPV	MQEEIFGPVL	PIVCVRSLEE	AIQFINQREK	360
PLALYMFSSN	DKVIKIMIAE	TSSGGVAAND	VIVHITLHSL	PFGVGNSGM	GSYHGKKSFE	420
TFSHRRSCLV	RPLMNDGLK	VRYPPSPAKM	TQH			

Seq ID NO: 177 DNA sequence
Nucleic Acid Accession #: NM_001067.1
Coding sequence: 108-4703

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CTGTTTAGTC	GCTTTACAGG	TTCTTGAGCC	CCTTCAAGAC	CGTCACCATG	GAAGTGTGCA	120
CATTGCAGCC	TGTAAATGAA	AATATGCAAG	TCAACAAAAT	AAAGAAAAAT	GAAGATGCTA	180
AGAAAAGACT	GTCTGTGAA	AGAATCTATC	AAAAGAAAAC	ACAATTGGAA	CATATTTTGC	240
TCCGCCCAGA	CACCTACATT	GGTCTGTGG	AATTAGTGAC	CCAGCAAATG	TGGGTTTACG	300
ATGAAGATGT	TGGCATTAAC	TATAGGGAAG	TCACTTTTGT	TCCTGGTTTG	TACAAAATCT	360
TTGATGAGAT	TCTAGTTAAT	GCTGCGGACA	ACAAACAAAG	GGACCCAAAA	ATGTCCTGTA	420
TTAGAGTCAC	AATTGATCCG	GAAAACAATT	TAATTAGTAT	ATGGAATAAT	GGAAAAAGTA	480
TTCTCTGTGT	TGAACACAAA	GTTGAAAAGA	TGTATGTCCC	AGCTCTCATA	TTTGGACAGC	540
TCCTAACTTC	TAGTAACAT	GATGATGATG	AAAAGAAAAGT	GACAGGTGGT	CGAAATGGCT	600
ATGGAGCCAA	AATTGTGTAAC	ATATTAGTAA	CCAAATTTAC	TGTGGAACA	GCCAGTAGAG	660
AATCAAGAA	AATGTTCAAA	CAGACATGGA	TGGATAATAT	GGGAAGAGCT	GGTGAGATGG	720
AACTCAAGCC	CTTCAATGGA	GAAGATTATA	CATGTATCAC	CTTTCAGCCT	GATTGTCTA	780
AGTTTAAAA	GCAAAAGCCTG	GACAAAGATA	TTGTTGCACT	AATGGTCAGA	AGAGCATATG	840
ATATTGCTGG	ATCCACCAAA	GATGTCAAAG	TCTTTCTTAA	TGGAATAAAA	CTGCCAGTAA	900
AAGGATTTTG	TAGTTATGTT	GACATGTATT	TGAAGGACAA	GTTGGATGAA	ACTGGTAACT	960
CCTTGAAAGT	ATACATAGAA	CAGTAAACC	ACAGGTGGGA	AGTGTGTTTA	ACTATGAGTG	1020
AAAAGAGCTT	TTCAGCAAA	AGCTTTGTCA	ACAGCATTGC	TACATCCAAG	GGTGGCAGAC	1080
ATGTTGATTA	TGTAGCTGAT	CAGATTGTGA	CTAAACTTGT	TGATGTTGTG	AAGAAGAAGA	1140
ACAAGGGTGG	TGTTGCAATG	AAAGCACATC	AGGTGAAAAA	TCACATGTGG	ATTTTGTGTA	1200
ATGCCCTAAT	TGAAAGCCCA	ACCTTTGACT	CTCAGACAAA	AGAAAACATG	ACTTTACAAC	1260
CCAAGAGCTT	TGGATCAACA	TGCCAATTGA	GTGAAAAATT	TATCAAAGCT	GCCATTGGCT	1320
GTGGTATTGT	AGAAAGCATA	CTAAACTGGG	TGAAGTTTAA	GGCCCAAGTC	CAGTTAAACA	1380
AGAAAGTGTCT	AGCTGTAAAA	CATAATAGAA	TCAAGGGAAT	TCCCAAACTC	GATGATGCCA	1440
ATGATGCAGG	GGGCCGAAAC	TCCACTGAGT	GTACGCTTAT	CCTGACTGAG	GGAGATTGAG	1500
CCAAAACCTT	GGCTGTTTCA	GGCCTTGGTG	TGTTTGGGAG	AGACAAATAT	GGGGTTTTCC	1560
CTCTTAGAGG	AAAATATCTC	AATGTTGAG	AAGCTTCTCA	TAAGCAGATC	ATGGAATAATG	1620
CTGAGATTAA	CAATATCATC	AAGATTGTGG	GTCTTCAGTA	CAAGAAAAAC	TATGAAGATG	1680
AAGATTCAAT	GAAGACGCTT	CGTTATGGGA	AGATAATGAT	TATGACAGAT	CAGGACCAAG	1740
ATGGTTCCCA	CATCAAGAGC	TTGCTGATTA	ATTTTATCCA	TCACAACCTG	CCCTCTCTTC	1800
TGCGACATCG	TTTTCTGGAG	GAATTTATCA	CTCCATTGT	AAAGGTATCT	AAAAACAAGC	1860
AAGAAATGGC	ATTTTACAGC	CTTCCTGAAT	TTGAAGAGTG	GAAGAGTTCT	ACTCCAAATC	1920
ATAAAAAATG	GAAAGTCAAA	TATTACAAAG	GTTTGGGCAC	CAGCACATCA	AAGGAAGCTA	1980
AAGAATACTT	TGCAGATATG	AAAAGACATC	GTATCCAGTT	CAAATATTCT	GGTCTGAAG	2040
ATGATGCTGC	TATCAGCCTG	GCCTTTAGCA	AAAAACAGAT	AGATGATCGA	AAGGAATGGT	2100
TAACATAATT	TATGGAGGAT	AGAAGACAAC	GAAAGTTACT	TGGGCTTCCT	GAGGATTACT	2160
TGTATGGACA	AACTACCACA	TATCTGACAT	ATAATGACTT	CATCAACAAG	GAATTATCT	2220
TGTTCTCAAA	TTCTGATAAC	GAGAGATCTA	TCCCTTCTAT	GGTGGATGGT	TTGAAACCAG	2280
GTACAGAGAA	GGTTTGTGTT	ACTTGCTTCA	AACGGAATGA	CAAGCGAGAA	GTAAGGTTTG	2340
CCCAATTAGC	TGGATCAGTG	GCTGAAATGT	CTTCTTATCA	TCATGGTGAG	ATGTCATAA	2400
TGATGACCAT	TATCAATTGT	GCTCAGAAAT	TTGTGGGTAG	CAATAATCTA	AACCTCTTGC	2460
AGCCCATTTG	TCAGTTTGGT	ACCAGGCTAC	ATGGTGGCAA	GGATTCTGCT	AGTCCAGGAT	2520
ACATCTTTAC	AATGCTCAGC	TCTTTGGCTC	GATTGTTATT	TCCACCAAAA	GATGATCACA	2580
CGTTGAAGTT	TTTATATGAT	GACAAACAGC	GTGTTGAGCC	TGAATGGTAC	ATTCCTATTA	2640
TTCCCATGGT	GCTGATAAAT	GGTGCTGAAG	GAATCGGTAC	TGGGTGGTCC	TGCAAAATCC	2700
CCAACCTTGA	TGTGCGTGAA	ATTGTAAATA	ACATCAGGCG	TTTGATGGAT	GGAGAAGAAC	2760
CTTTGCCAAT	GCTTCCAAGT	TACAAGAACT	TCAAGGGTAC	TATTGAAGAA	CTGGCTCCAA	2820
ATCAATATGT	GATTAGTGCT	GAGTAGCTA	TTCTTAATTC	TACAACCATT	GAAATCTCAG	2880
AGCTTCCCGT	CAGAACATGG	ACCCAGACAT	ACAAAGAACA	AGTTCTAGAA	CCCATGTTGA	2940
ATGGCACCGA	GAGACACCT	CCTCTCATAA	CAGACTATAG	GGAATACCAT	ACAGATACCA	3000
CTGTGAAATT	TGTTGTGAAG	ATGACTGAAG	AAAACTGGC	AGAGGCAGAG	AGAGTTGGAC	3060
TACACAAAGT	CTTCAAACTC	CAAAGTAGTC	TCACATGCAA	CTCTATGGTG	CTTTTGGACC	3120
ACGTAGGCTG	TTTAAAGAAA	TATGACACGG	TGTTGGATAT	TCTAAGAGAC	TTTTTGAAC	3180
TCAGACTTAA	ATATTATGGA	TTAAGAAAAG	AATGGCTCCT	AGGAATGCTT	GGTGCTGAAT	3240
CTGCTAAACT	GAATAATCAG	GCTCGCTTTA	TCTTAGAGAA	AATAGATGGC	AAAATAATCA	3300

	TTGAAATATA	GCCTAAGAAA	GAATTAATTA	AAGTTCTGAT	TCAGAGGGGA	TATGATTCGG	3360
	ATCCTGTGAA	GGCCTGGAAA	GAAGCCCAGC	AAAAGGTTCC	AGATGAAGAA	GAAAATGAAG	3420
	AGAGTGACAA	CGAAAAGGAA	ACTGAAAAGA	GTGACTCCGT	AACAGATTCT	GGACCAACCT	3480
5	TCAACTATCT	TCTTGATATG	CCCCTTTGGT	ATTTAACCAA	GGAAAAGAAA	GATGAACCTCT	3540
	GCAGGCTAAG	AAATGAAAAA	GAACAAGAGC	TGGACACATT	AAAAAGAAAG	AGTCCATCAG	3600
	ATTTGTGGAA	AGAAGACTTG	GCTACATTTA	TTGAAGAATT	GGAGGCTGTT	GAAGCCAAGG	3660
	AAAAACAAGA	TGAACAAGTC	GGACTTCCTG	GGAAAGGGGG	GAAGGCCAAG	GGGAAAAAAA	3720
	CACAAATGGC	TGAAGTTTTC	CCTTCTCCGC	GTGGTCAAAG	AGTCATTCCA	CGAATAACCA	3780
10	TAGAAATGAA	AGCAGAGGCA	GAAAAGAAAA	ATAAAAGAAA	AATTAAGAAT	GAAAACTACTG	3840
	AAGGAAGCCC	TCAAGAAGAT	GGTGTGGAAC	TAGAAGGCCT	AAAACAAGA	TTAGAAAAGA	3900
	AACAGAAAAG	AGAACCAGGT	ACAAAGACAA	AGAAACAAAC	TACATTGGCA	TTTAAGCCAA	3960
	TCAAAAAAGG	AAAGAAAGAA	AATCCCTGGC	CTGATTGAGA	ATCAGATAGG	AGCAGTGACG	4020
	AAAGTAATTT	TGATGTCCCT	CCACGAGAAA	CAGAGCCACG	GAGAGCAGCA	ACAAAAACAA	4080
15	AATTCACAAT	GGATTGGGAT	TCAGATGAAG	ATTTCTCAGA	TTTTGATGAA	AAAAGTATG	4140
	ATGAAGATTT	TGTCCCATCA	GATGCTAGTC	CACCTAAGAC	CAAACTTCC	CCAAAACTTA	4200
	GTAACAAAGA	ACTGAAACCA	CAGAAAAGTG	TCGTGTGAGA	CCTTGAAGCT	GATGATGTTA	4260
	AGGGCAGTGT	ACCACTGTCT	TCAAGCCCTC	CTGCTACACA	TTTCCAGAT	GAAACTGAAA	4320
	TTACAAACCC	AGTTCTCTAA	AAGAAATGTA	CAGTGAAGAA	GACAGCAGCA	AAAAGTCAGT	4380
20	CTTCCACCTC	CACTACCGGT	GCCAAAAAAA	GGGCTGCCCC	AAAAGGAACT	AAAAGGGATC	4440
	CAGCTTTGAA	TCTGTGGTTC	TCTCAAAAGC	CTGATCCTGC	CAAAACCAAG	AATCGCCGCA	4500
	AAAGGAAGCC	ATCCACTTCT	GATGATTCTG	ACTCTAATTT	TGAGAAAATT	GTTTCGAAAG	4560
	CAGTCAACA	CAAGAAATCC	AAGGGGAGAG	GTGATGACTT	CCATATGGAC	TTTGACTCAG	4620
	CTGTGGCTCC	TCGGGCAAAA	TCTGTACGGG	CAAAGAAACC	TATAAAGTAC	CTGGAAGAGT	4680
25	CAGATGAAGA	TGATCTGTTT	TAAAAATGTA	GGCGATTATT	TTAAGTAATT	ATCTTACCAA	4740
	GCCCAAGACT	GGTTTTAAAG	TTACCTGAAG	CTCTTAACCT	CCTCCCCTCT	GAATTTAGTT	4800
	TGGGGAAGGT	GTTTTTTAGT	CAAGACATCA	AAGTGAAGTA	AAGCCCAAGT	GTTCTTTAGC	4860
	TTTTTATAAT	ACTGTCTAAA	TAGTGACCAT	CTCATGGGCA	TTGTTTTCTT	CTCTGCTTTG	4920
	TCTGTGTTTT	GAGTCTGCTT	TCTTTTGTCT	TAAAAACCTG	ATTTTTAAGT	TCTTCTGAAC	4980
30	TGTAGAAATA	GCTATCTGAT	CACCTCAGCG	TAAAGCAGTG	TGTTTATTAA	CCATCCACTA	5040
	AGCTAAAAC	AGAGCAGTTT	GATTTAAAG	TGCTACTCTT	CCTCCTTTTC	TACTTTCAGT	5100
	AGATATGAGA	TAGAGCATA	TTATCTGTTT	TATCTTAGTT	TTATACATA	TTTACCATCA	5160
	GATAGAACTT	GCTATCTTCT	GTACAGATAC	TCTACTACAC	TCAGCCTCTT	ATGTGCCAAG	5220
	TTTTTCTTTA	AGCAATGAGA	AATTGCTCAT	GTTCTTCATC	TTCTCAAATC	ATCAGAGGCC	5280
35	AAAGAAAAAC	ACTTTGGCTG	TGTCTATAAC	TTGACACAGT	CAATAGAATG	AAGAAAAATTA	5340
	GAGTAGTTAT	GAAATCTTGA	CAGCTTATTG	CCTGTCCCCT	CTGGCTGCCT	CTGAGTCTGA	5400
	ATCTCCCAA	GAGAGAAACC	AATTTCTAAG	AGGACTGGAT	TGCAGAAGAC	TCGGGGACAA	5460
	CATTTGATCC	AAGATCTTAA	ATGTTATATT	GATAACCATG	CTCAGCAATG	AGCTATTAGA	5520
	TTCAATTGGG	GAAATCTCCA	TAATTTCAAT	TTGTAAACTT	TGTTAAGACC	TGTTCTACAT	5580
40	GTTATATGTG	TGTGACTTGA	GTAATGTTAT	CAACGTTTTT	GTAATATTTT	ACTATGTTTT	5640
	TCTATTAGCT	AAATTCCAAC	AATTTTGTAC	TTTAATAAAA	TGTTCTAAAC	ATTGC	

Seq ID NO: 178 Protein sequence:
Protein Accession #: NP_001058.1

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	MWVYDEDVGI	NYREVTFVPG	LYKIFDEILV	NAADNKQRDP	KMSCIRVTID	PENNLISIWV	120
	NGKGIPVVEH	KVEKMYVPAL	IFGQLLTSSN	YDDDEKKVTG	GRNGYGAQLC	NIFSTKFTVE	180
50	TASREYKKMF	QQTWMDNMR	AGEMELKPFN	GEDYTCITFQ	PDLKSKFMQS	LKDIDIVALMV	240
	RRAYDIAGST	KDVKVFLNGN	KLPVKGRFSY	VDMYLKDLD	ETGNSLKVIV	EQVNHREWVC	300
	LTMSEKGFQ	ISFVNSIATS	KGGRHVVDYA	DQIVTKLVDV	VKKKNKGVA	VKAHQVKNHM	360
	WIFVNALIEV	PTFDSQTKEN	MTLQPKSFGS	TCQLSEKFIK	AAIGCGIVES	ILNWVKFKAQ	420
	VQLNKKCSAV	KHNRIKGIK	LDDANDAGGR	NSTECTLILT	EGDSAKTLAV	SGLGVVGRDK	480
55	YGVFPLRGKI	LNVREASHKQ	IMENAEINNI	IKIVGLQYKK	NYEDEDLTKT	LRYGKIMIMT	540
	DQDQDGSNIK	GLLINFIHNN	WPSLLRHRFL	EEFITPIVKV	SKNKQEMAFY	SLPEFEWKS	600
	STPNHKKWKV	KYYKGLGTST	SKEAKEYFAD	MKRHRIFQFY	SGPEDDAAIS	LAFSKKQIDD	660
	RKEWLTNFMF	DRRQRKLLGL	PEDYLYGQTT	TYLTYNDFIN	KELILFSNSD	NERSIPSMVD	720
60	GLKPGQRKVL	FTCFKRNDRK	EVKVAQLAGS	VAEMSSYHNG	EMSLMTIIN	LAQNFGVSNV	780
	LNLLQPIQGF	GTRLHGGKDS	ASPRYIFTML	SSLARLLFPP	KDHTLTKFLY	DDNQREVEPW	840
	YIPIIPMLVI	NGAEGIGTGW	SKIPNFVDVR	EIVNNIRRLM	DGEELPMLP	SYKNFKGTIE	900
	ELAPNQYVTS	GEVALNSTT	IEISELPVRT	WTQYKEQVLE	EPMLNGTEKT	PPLITDYREY	960
	HTDITVKFVV	KMTBEKLEAE	ERVGLHKVFK	LQSLTLCNSM	VLPFDHVGCLK	KYDVTLDILR	1020
65	DPFELRLKYY	GLRKEWLLGM	LGAESAKLNN	QARFILEKID	GKIIIEKNPK	KELIKVLIQR	1080
	GYSDPVPKAW	KEAQQKVPDE	EENEESDNEK	ETEKSDSVTD	SGPTFNYLLD	MPLWYLTKEK	1140
	KDELCLRLNE	KEQELDTLKR	KSPSDLWKED	LATFIEELEA	VEAKEKQDEQ	VGLPGKGGKA	1200
	KGKKTQMAEV	LPSPRGQRVI	PRITIEKMAE	AEKKNKKKIK	NENTEGSPQE	DGVELEGLKQ	1260
	RLEKKQKREP	GTKTKKQTLI	AFKPIKKGKK	RNPWPDSESD	RSSDESNDV	PPRETEPRRA	1320
70	ATKTKFTMDL	DSDEDFSDFD	EKTDDDFVP	SDASPPKTKT	SPKLSNKKEL	PQKSVVSDLE	1380
	ADDVKGVSPL	SSSPATHFPP	DEBITNPVP	KKNVTVKKTA	AKSQSSTSTT	GAKKRAAPKG	1440
	TKRDPALNSG	VSQKPDPAKT	KNRKRKPKST	SDDSDSNFEK	IVSKAVTSKK	SKGESDDPHM	1500
	DFDSAVAPRA	KSVRAKKPIK	YLEESDEDDL	F			

75 Seq ID NO: 179 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 148-7095

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	CGCGAGGGGG	CCGACAGACC	TCTGGAAATG	CGAATCCTAA	AGCGTTTCCT	CGCTTGCAAT	180
	CAGCTCCTCT	GTGTTTGGCG	CCTGGATTGG	GCTAATGGAT	ACTACAGACA	ACAGAGAAAA	240
85	TTTGTGTAAG	AGATTGGCTG	GTCCTATACA	GGAGCACTGA	ATCAAAAAAA	TTGGGGAAAG	300
	AAATATCCAA	CATGTAATAG	CCCAAAACAA	TCTCCTATCA	ATATTGATGA	AGATCTTACA	360
	CAAGTAAATG	TGAATCTTAA	GAAACTTAAA	TTTCAGGGTT	GGGATAAAAC	ATCATTGGAA	420

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Seq ID NO: 180 Protein sequence:
Protein Accession #: Eos sequence

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Seq ID NO: 181 DNA sequence
Nucleic Acid Accession #: Eos sequence

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	CAGCTTGCTG	AAAAGGATGG	CAAACTGACT	GATTATATCA	ATGCCAATTA	TGTTGATGGC	2940
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	GTCCACTGCA	GTGCTGAGC	TGGAAGAACA	GGCACATATA	TTGTGCTAGA	CAGTATGTTG	3420
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70	TGGGACCATA	ATGCCCAACT	GGTGGTTATG	ATTCTGTATG	GCCAAAACAT	GGCAGAAGAT	3960
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	CTTATGGCTG	AAGAACACAA	ATGCTATCT	AATGAGGAAA	AACTTATAAT	TCAGGACTTT	4080
	ATCTTAGAAG	CTACACAGGA	TGATTATGTA	CTTGAAGTGA	GGCACTTTCA	GTGTCTTAAA	4140
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	TGTAAATAAA	ACACTCTTCC	ATATGATATT	CAACATTTTA	CAACTGCAGT	ATTCACCTAA	4980

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Seq ID NO: 182 Protein sequence:
 Protein Accession #: Eos sequence

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Seq ID NO: 183 DNA sequence
 Nucleic Acid Accession #: EOS sequence
 Coding sequence: 148-4494

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Seq ID NO: 184 Protein sequence:
 Protein Accession #: EOS sequence

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Seq ID NO: 185 DNA sequence
 Nucleic Acid Accession #: EOS sequence
 Coding sequence: 501-4514

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Seq ID NO: 186 Protein sequence:
 Protein Accession #: EOS sequence

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35

Seq ID NO: 187 DNA sequence
 Nucleic Acid Accession #: EOS sequence
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Seq ID NO: 188 Protein sequence:
Protein Accession #: EOS sequence

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	ILPEVGTEN	LDPKAIIDGV	ESVSRFGKQA	ALDPPILLNL	LPNSTDKYYI	YNGSLTSPPC	240
	TDVDWIVTGL	DTVSISSTGL	AVFCEVLTMQ	QSGYVMLMDY	LQNNFREQQY	KFSRQVFSY	300
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 20 GATATTATCT ACAACACTG CAGAACAGCA TCATGTCATA AACGATTCTG AGCCATTAC 1320
 ACTTTTATT TAATTAAATG TATTTAATTA AATCTCAAT TTATTTAAT GTAAAGAACT 1380
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 CCAGCTCATA CAAAATAAAT GGTTCCTGAA AATGTTTAA TATTAACCTA CAAGGATATA 1500
 25 GGTTTTTCTC ATGTATCTT TGTTTCATTG GCAAGATGAA ATAATTTTTC TAGGGTAATG 1560
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Seq ID NO: 190 Protein sequence:
Protein Accession #: NP_002811

1 11 21 31 41 51
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 30 MQRRLVQQWS VAVFLLSYAV PSCGRSVEGL SRRLKRAVSE HQLLHDKGKS IQDLRRRPFL 60
 HHLIAEIHIA EIRATSEVSP NSKPSFNTKN HPVRFSGSDE GRYLTQETNK VETYEQPLK 120
 35 TPGKKKKGKP KIRKEQEKKK RRTRSAWLDS GVTGSGLEGD HLSDTSTSL ELDSE

Seq ID NO: 191 DNA sequence
Nucleic Acid Accession #: XM_059328
Coding sequence: 52..1023

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 45 GGTATCGTGG AGGCTTTTCT GGCCGGGGCT GTGACCAGCG TGTCCCTGCT GGTCAACGGT 180
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 50 GGCCCGGAAG GCTTCTCTCT TGGCAAGATG GGATTCCGGG AGGCGGTGGC GGCAGGAGAC 360
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 60 CCAGGGGAGG AGGTCCCTCT TGAGCCCACT CTGGAACCTT TCCTGGAACC CTCCTACTC 1020
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 65 TGGTGCCCTT CCATGTTGCA ATGCAAAACAC CTTCACCACT GGGGCGAGTG GGAGAGATGG 1320
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Seq ID NO: 192 Protein sequence:
Protein Accession #: XP_059328

1 11 21 31 41 51
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 70 MSRRPRLVV TADDFGYCPR RDEGIVEAFL AGAVTSVSLI VNGAATESAA ELARRHSIPT 60
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 75 RELGLRAPH ADGHQHVHVL PGVCQVFAEA LQAVGVRFTR LPLERGVGGC TWLEAPARAF 180
 ACAVERDARA AVGPFSRHGL RWTDAFVGLS TCGRHMSAHR VSGALARVLE GTLAGHTLTA 240
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Seq ID NO: 193 DNA sequence
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	GGAGAACTCG	ACCGTGTGAA	TGCCAAGATG	CCTTGGAAAC	AGCAGCCCGA	GCCGAGGGCC	300
5	TCCTCTTGA	TGCTCTCAT	CATTCTCAGC	TCAGAATCCT	GGATGAGGAG	CATCCCAAGG	360
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	ACCCAGTGGG	CAATGCTGGG	CTTTTTCCT	GTATGACTTT	TTCGTGGCTT	TCTTCTCTGG	480
	CCCGTGTGGC	CCACAAGAAG	GGGGAGCTCT	CAATGGAAGA	CGTGTGGTCT	CTGTCCAAGC	540
	ACGAGTCTTC	TGACGTGAAC	TAGAGAGACT	TGCAGAAGAC	GTGGCAAGAA	GAGCTGAATG	600
10	AAGTTGGGGC	AGACGCTGCT	TCCCTGCGAA	GGGTGTGTG	GATCTTCTGC	CGCACCAGGC	660
	TCATCTGTCT	CATCGTGTGC	CTGATGATCA	CGCAGCTGGC	TGGCTTCAGT	GGACCAGCCT	720
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	TGTTGTAGT	GCTGGGCTCT	CTCCTGACGG	AAATCGTGCG	GTCTTGGTGG	CTTGCACTGA	840
	CTTGGGCATT	GAATTACCGA	ACCGGTGTCC	GCTTGGCGGG	GGCCATCCTA	ACCATGGCAT	900
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	GCTTCTGTGG	ATCAGCTGTT	TTTATCCCTC	TTTATCCAGC	AATGATGTTT	GCATCACGGC	1140
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25	AAGCCTCAGT	GGCTGTGTAC	AGATTAAAGA	GTTTGTCTT	AATGGAAGAG	GTTCACATGA	1560
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30	CCGAAGAGGA	AGAAGCCAG	CACATCCACC	TGGGCCACCT	CGCCTTACAG	AGGACACTGC	1860
	ACAGCATCGA	TCTGGAGATC	CAAGAGGGTA	AACCTGTTGG	AATCTGCGGC	AGTGTGGGAA	1920
	TTGGAAAAAC	CTCTCTCATT	TCAGCCATTT	TAGGCCAGAT	GACGCTTCTA	GAGGGCAGCA	1980
	TTGCAATCAG	TGGAACTCTC	GCTTATGTGG	CCCAGCAGGC	CTGGATCCTC	AATGCTACTC	2040
	TGAGAGACAA	CATCTGTGTT	GGGAAGGAAT	ATGATGAAGA	AAGATACAAC	TCTGTGCTGA	2100
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35	GAGAGCGAGG	AGCCAACTCT	AGCGGTGGGC	AGCGCCAGAG	GATCAGCCCT	GCCCGGGCCT	2220
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40	CCATTTTAA	TAACTGTGTT	CTGGGAGAGA	CACCGCCAGT	TGAGATCAAT	TCAAAAAAGG	2520
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	AGGAAAAAGC	AGTAAAGCCA	GAGGAAGGGC	AGCTTGTGCA	GCTGGAAGAG	AAAGGGCAGG	2640
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45	TCCTGGTTAT	TATGGCCCTT	TATGTGCTGA	ATGTAGGCAG	CACCGCCTTC	AGCACCTGGT	2760
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	CCCTCTCCAT	CGCAGTCATG	GTGATCCTGA	AAGCCATTCT	AGGAGTTGTC	TTTGTCAAGG	2940
	GCACGCTGCG	AGCTTCTCTC	CGGCTGCATG	ACGAGCTTTT	CCGAAGGATC	CTTCGAAGCC	3000
50	CTATGAAGTT	TTTGTGACAG	ACCCCCACAG	GGAGGATTCT	CAACAGGTTT	TCCAAAGACA	3060
	TGGATGAAGT	TGACGTGCGG	GTGCGTTCC	AGGCCGAGAT	GTTTCATCCAG	AACGTTATCC	3120
	TGGTGTCTTT	CTGTGTGGGA	ATGATCGCAG	GAGTCTTCCC	GTGGTTCCTT	GTGGCAGTGG	3180
	GGCCCTTGT	CATCCTCTTT	TCAGTCTCTG	ACATTTGTCT	CAGGTCCTG	ATTGCGGAGC	3240
	TGAAGCGTCT	GGACAATATC	AGCAGTCTAC	CTTCTCTCTC	CCACATCACG	TCCAGCATA	3300
55	AGGGCCTTGC	CACCATCCAC	GCCTACAATA	AAGGGCAGGA	GTTTCTGCAC	AGATACCAGG	3360
	AGCTGTGGA	TGACAACCAA	GCTCCTTTT	TTTGTGTTAC	GTGTGCGATG	CGGTGGCTGG	3420
	CTGTGCGGCT	GGACCTCATC	AGCATGCCCC	TCATCACCAC	CACGGGGCTG	ATGATCGTTC	3480
	TTATGCACGG	GCAGATTCCC	CCAGCCTATG	CGGGTCTCGC	CATCTCTTAT	GCTGTCCAGT	3540
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	GTGATATTGG	CCCTGCGCAG	CTCCGAAGCA	AACCTCTCTAT	CATTCTCTCA	GAGCCGGTGC	3960
65	TGTTCAAGTG	CAGTGTGAGA	TCAAAATTGG	ACCCCTTCAA	CCAGTACACT	GAAGACCAGA	4020
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	GCATAGCTAG	AGCCCTGCTC	CGCCACTGTA	AGATTCTGAT	TTTAGATGAA	GCCACAGCTG	4200
70	CCATGGACAC	AGAGACAGAC	TTATTGATT	AAGAGACCAT	CCGAGAAGCA	TTTGCAGACT	4260
	GTACCATGCT	GACCATTGCC	CATCGCCTGC	ACACGGTTCT	AGGCTCCGAT	AGGATTATGG	4320
	TGCTGGGCCA	GGGACAGTGT	GTGGAGTTTG	ACACCCCATC	GGTCTCTCTG	TCCAAACGACA	4380
	GTTCCCGATT	CTATGCCATG	TTTGCTGCTG	CAGAGAACAA	GGTCTCTCTG	AAGGGCTGAC	4440
	TCCTCCCTGT	TGACGAAGAT	TCCTTTCTTT	AGAGCAATGC	CATTCCCTGC	CTGGGGCGGG	4500
75	CCCTCATGCT	CGTCTCTCTA	CGGAAACCTT	GCCTTTCTCG	ATTTTATCTT	TCGCACAGCA	4560
	GTTCCGGATT	GGCTTGTGTG	TTTCACTTTT	AGGGAGAGTC	ATATTTTGAT	TATTGTATTT	4620
	ATTCCATATT	CATGTAAACA	AAATTAGATT	TTTGTCTTTA	ATTGCACTCT	AAAAGGTTCA	4680
	GGGAACCGTT	ATTATAATG	TATCAGAGGC	CTATAATGAA	GCTTTATACG	TGTAGCTATA	4740
	TCTATATATA	ATTCTGTACA	TAGCCTATAT	TTACAGTGAA	AATGTAAGCT	GTTTATTTTA	4800
	TATTAATAAT	AGCACTGTGG	TAAATAACAGT	GCATATTCCT	TTCTATCATT	TTGTACAGT	4860
80	TTGCTGTACT	AGAGATCTCG	TTTGCTATT	AGACTGTAGG	AAGAGTAGCA	TTTCACTCTT	4920
	CTCTAGCTGG	TGGTTTCACG	GTGCCAGGTT	TTCTGGGTGT	CCAAAGGAAG	ACGTGTGGCA	4980
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	GAGACGGGTG	GGCGGCTGGA	AGCCATGTCAG	AGCGCCGTGA	GTTCTCAGGG	CTCCTGCTTT	5100
	CTGTCTGGT	GTCACTTACT	GTTTCTGTCA	GGAGAGCAGC	GGGGCGAAGC	CCAGGCCCTT	5160
85	TTTCACTCCC	TCCATCAAGA	ATGGGGATCA	CAGAGACATT	CCTCCGAGCC	GGGGAGTTTC	5220
	TTTCTGCTCT	TCTCTTCTTT	GCTGTTGTTT	CTAAACAAGA	ATCAGTCTAT	CCACAGAGAG	5280
	TCCCACTGCC	TCAGGTTCTT	ATGGCTGGCC	ACTGCACAGA	GCTCTCCAGC	TCCAAGACCT	5340

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Seq ID NO: 194 Protein sequence:
 Protein Accession #: NP_005679.1

1 11 21 31 41 51
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 ALNYRTGVRL RGAILTMAFK KILKLKNIKE KSLGELINIC SNDGQRMFEA AAVGSLLAGG 300
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Seq ID NO: 195 DNA sequence
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Seq ID NO: 196 Protein sequence:
Protein Accession #: NP_006461

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EPVKDHNWRY CPAHHSPLSA FCCPDQQCIC QDCCQEHSGH TIVSLDAARR DKEAELQCTQ 180
LDLERLKLKN ENAISRLQAN QKSVLVSVE VKAVAEMQFG ELLAAVRKAQ ANVMLFLEEK 240
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SDMETPLKAG PPRRLGVYID FPGGILSPYG VEYDTMTLVH KPACKFSEPV YAAFWLSKKE 540
NAIRIVDLGE EPEKPAPSLG VTAP

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Coding sequence: 433-1149

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GCGCCAGCGG CAGCCTCACA CGCGAGCGCC ACGCGAGGCT CCCGAAGCCA ACCCGCGAAG 180
GGAGGAGGGG AGGGAGGAG AGGCGGCGTG CAGGGAGGAG AAAAAGCATT TTCACCTTTT 240
TTGCTCCAC TCTAAGAAGT CTCCCGGGA TTTGTATAT ATTTTAAAC TTCGTCAGG 300
GCTCCCGCTT CATATTTCTT TTTCTTTCCC TCTCTGTTCC TGCACCCAAG TTCTCTCTGT 360
GTCCCGCTCG CGGGCCCGCG ACCTCGCGTC CCGGATCGCT CTGATTCCGC GACTCCTTGG 420
CCGCGCTGTC GCATGGAAG CTCTGCCAAG ATGGAGAGCG GCGGCGCGG CCAGCAGCCC 480
CAGCCGCGAG CCCAGCAGCC CTTCCTGCGG CCCGCGAGCT GTTCTTTTGC CACGGCCGCA 540
GCGCGGCGCG CCGCAGCGCG CGCAGCGGCA GCGCAGAGCG CGCAGCAGCA GCAGCAGCAG 600
CAGCAGCAGC AGCAGCAGCA GCAGGCGCGG CAGCTGAGAC GCGGCGCGA CGGCCAGCCC 660
TCAGGGGGCG GTCACAAGTC AGCGCCCAAG CAAGTCAAGC GACAGCGCTC GTCTTCGCC 720
GAACTGATGC GCTGCAAAAG CCGGCTCAAC TTCAGCGGCT TTGGCTACAG CCTGCCGCG 780
CAGCAGCGCG CGCCGCTGCG GCGCGCAAC GAGCGCGAGC GCAACCGCGT CAAGTTGGTC 840
AACCTGGGCT TTGCCACCCT TCGGGAGCAC GTCCCAACG GCGCGGCCAA CAAGAAGATG 900
AGTAAGGTGG AGACACTCGT CTCGCGGTC GAGTACATCC GCGCGCTGCA GCAGCTGCTG 960
GACGAGCATG AGCGGTGAG CGCCGCTTC CAGGCAGGCG TCCTGTGCGC CACCATCTCC 1020
CCCACTACT CCAACGACTT GAACTCCATG GCCGGCTCGC CGGTCTCATC CTACTCGTCG 1080
GACGAGGGCT CTTACGACCC GCTCAGCCCC GAGGAGCAGG AGCTTCTCGA CTTACCAAC 1140
TGTTCTGAG GGGCTCGGCC TGGTCAGGCC CTGGTGCAG TGGACTTTGG AAGCAGGGTG 1200
ATCGCACAA CTGCATCTTT AGTGCTTTCT TGTCACTGGC GTTGGGAGGG GGAGAAAAGG 1260
AAAAGAAAAA AAAAGAAGAA GAAGAAGAAA AGAGAAGAAA AAAAAAACGA AAACAGTCAA 1320
CCAAACCCAT CCGCAACTAA GCGAGGCATG CCTGAGAGAC ATGGCTTTCA GAAACCGGGA 1380
AGCGCTCAGA ACAGTATCTT TGCATCCAA TCATTACGG AGATATGAAG AGCAACTGGG 1440
ACCTGAGTCA ATGCGCAAAA TGCAGCTTGT GTGCAAAAGC AGTGGGCTCC TGGCAGAAGG 1500
GAGCAGCACA CGCGTTATAG TAACTCCCAT CACCTCTAAC ACGCACAGCT GAAAGTTCTT 1560
GCTCGGGTCC CTTACCTTCC CCGCCCTTTC TTAGAGTGCA GTTCTTAGCC CTCTAGAAAC 1620
GAGTTGGTGT CTTTC

Seq ID NO: 198 Protein sequence:
Protein Accession #: NP_004307

1 11 21 31 41 51
MESSAKMESG GAGQQPQPQP QPFLPPAAC FFATAAAAAA AAAAAAQA QQQQQQQQQ 60
QQQAPQLRP AADGQPSGGG HKSAPKQVKR QRSSPELMR KRRLLNFSGF GYSLPQQQPA 120
AVARRNERER NRVKLVNLGF ATLREHVPNG AANKKMSKVE TLRSAYEYIR ALQQLLDEHD 180
AVSAAFQAGV LSPTISPNSY NDLNSMAGSP VSSYSDEGS YDPLSPPEQE LLDFTNWF

Seq ID NO: 199 DNA sequence
Nucleic Acid Accession #: NM_007015
Coding sequence: 1-1005

1 11 21 31 41 51
ATGACAGAGA ACTCCGACAA AGTTCCCATG GCCCTGGTGG GACCTGATGA CGTGGGAATTC 60
TGACAGCCCC CGGCGTACGC TACGCTGACG GTGAAGCCCT CCAGCCCCGC GCGGCTGCTC 120
AAGGTGGGAG CCGGTGCTCT CATTTCCGGA GCTGTGCTGC TGCTCTTTGG GGCCATCGGG 180
GCCTTCTACT TCTGGAAGGG GAGCGACAGT CACATTTACA ATGTCCATTA CACCATGAGT 240
ATCAATGGGA AACTACAAGA TGGGTCAATG GAAATAGACG CTGGGAACAA CTTGGAGACC 300
TTTAAATGG GAAGTGGAGC TGAAGAAGCA ATTGCAGTTA ATGATTTCGA GAATGGCATC 360
ACAGGAATTC GTTTTGCTGG AGGAGAGAAG TGCTACATTA AAGCGCAAGT GAAGGCTCGT 420
ATTCTGAGG TGGGCGCCGT GACCAACAG AGCATCTCCT CCAAACTGGA AGGCAAGATC 480
ATGCCAGTCA AATATGAAGA AAATTCCTT ATCTGGGTGG CTGTAGATCA GCCTGTGAAG 540
GACACAGACT TCTGAGTTC TAAGGTGTTA GAACTCTGCG GTGACCTTCC TATTTCTGG 600
CTTAACCAA CCTATCCAAA AGAAATCCAG AGGGAAAGAA GAGAAGTGGT AAGAAAAATT 660
GTTCCAACTA CCACAAAAG ACCACACAGT GGACCACGGA GCAACCCAGG CGCTGGAAGA 720
CTGAATAATG AAACCAGACC CAGTGTTCAG GAGGACTCAC AAGCTTCAA TCCTGATAAT 780

CCTTATCATC AGCAGGAAGG GGAAAGCATG ACATTGCGACC CTAGACTGGA TCACGAAGGA 840
 ATCTGTTGTA TAGAATGTAG GCGGAGCTAC ACCCACTGCC AGAAGATCTG TGAACCCCTG 900
 GGGGGCTATT ACCCATGGCC TTATAATTAT CAAGGCTGCC GTTCGGCTCG CAGAGTCATC 960
 ATGCCATGTA GCTGGTGGGT GGGCCGTATC TTGGGCATGG TGTGAAATCA CTTCATATAT 1020
 CACGTGCTGT AAAATAAGAA CTAGCTGAAG AGACAACCAA AGAAGCATT AAGGCAGGTTG 1080
 ATGCTGATGG GACCATAAAA TATTTTACA CGCAGCCTGA GCGGTTATTC TTGACACTCT 1140
 TAACAGAATT TTTTAAATCG TTTTCCAGAA CTTTAGTATA TGCAAATGCA CTGAAAGGGT 1200
 AGTTCAAGTC TAAATGCCA TAACCCCGTT ATTTGTTATT TTTTATTTGC ATTGATTTGC 1260
 CATAAGTCTT CCCTGCTTG CATCTTCAA AGCTATTTCG AAATAAACAC GAAATTTTAC 1320
 AGTTTGCC

Seq ID NO: 200 Protein sequence:
 Protein Accession #: NP_008946

1 11 21 31 41 51
 MTENSDKVEI ALVGPDDVEF CSPPAYATLT VKPSSPARLL KVGAVVLISG AVLLLFGAIG 60
 AFYFWKGS DS HIYNVHYTMS INGLQDGS M EIDAGNNLET FKMGSAGEEA IAVNDFQNGI 120
 TGI RPA GGEK CYIKAQVKAR IPEVGAVTKQ SISKLEBKI MPVKYEENSL IWVAVDQPVK 180
 DNSFLSSKVL ELCDGLPIFW LKPTYPKBIQ RERREVRKI VPTTTKRPHS GPRSNPGAGR 240
 LNNETRPSVQ EDSQAFNPDN PYHQEGESM TFDPRLDHEG ICCIECRRSY THCQKICEPL 300
 GGYYPWPYNY QGCRSACRVI MPCSWWVARI LGMV

Seq ID NO: 201 DNA sequence
 Nucleic Acid Accession #: NM_000728.2
 Coding sequence: 112..495

1 11 21 31 41 51
 GTAATAAGAG CGGGGTCTCC GCGGGGAAGG CGCCACAGC AGGTGTGGTG TTCATCCCGG 60
 GTCGACCGGC CGCTCGCGCT GCCCTGAAAC TCTAGTCGCC AGAGAGCGCG CATGGGTTTC 120
 CGGAAGTTCT CCCCCTTCTT GGCTCTCAGT ATCTTGGTCC TGTACCAGGC GGGCAGCCTC 180
 CAGGCGCGGC CATTCAGGTC TGCCCTGGAG AGCAGCCAG ACCCGGCCAC ACTCAGTAAA 240
 GAGGACGCGC GCCTCCTGCT GGCTGCACTG GTGCAGGACT ATGTGCAGAT GAAGGCCAGT 300
 GAGCTGAAGC AGGAGCAGGA GACACAGGGC TCCAGCTCCG CTGCCAGAA GAGAGCCTGC 360
 AACACTGCCA CTTGTGTGAC TCATCGGCTG GCAGGCTTGC TGAGCAGATC AGGGGGCATG 420
 GTGAAGAGCA ACTTCGTGCC CACCAATGTG GGTTCCAAAG CCTTTGGCAG GCGCCGCAGG 480
 GACCTTCAAG CCTGAGCAGA TGAATGACTC CAGGAAGAAG GTGTGCTCCTA AATCCAATGA 540
 CATATCCTTA TAAGAGATTG ACTCAGAAGA CACATGTGGA GAAGGTGACA TGACAGAGGC 600
 AAGGAGGCAC AAGCCCAAGG AGTCTGTGTC TACCAGAAGC CAGAATCACA GAACAGTCTC 660
 TGGAGAAGA GAGCCCTGTC TGACACCTAG AGTTTGGACT TCCAGCTTCC AGAACTGTGA 720
 GAGAATAAAT TCTGTGTTT TAAGCCACAA AGTTTGTGGT AATTGTGTTAT GACAGCCCTA 780
 GGAACATAAT ACAATACATT TTCAATTATT TTGGGTAAAT GCCTTGGAGT GGGATTGCTG 840
 GGTATTGTTG AAGGTGTGTA TTAACTCTG TAAGAACTG CCAAATATT TTCTGAAGTG 900
 ACTGTACCAC TTGCTCTTCT TGCCAGCCAC ATATGAGAGC TCTAGTATTT CCACAAATAG 960
 GTATGTAGCA GTATCTCATT GCTGTTTTAA TTTGTATTTC CCAATGACT AATGACGTTG 1020
 AGCATCTATT TTACCATATG TTTATCACTT TTATTGAAGG GTCTGTTTAA ATCTTCTGCT 1080
 AAATTTTGTG TGCTTGTCTT GCTTTATTAG TGTGTAGTTT TTAGAGCTCT TTATATGTTG 1140
 TGGATGCAAG ATTGTTTTCA GATATATAGT TTGGAACCTT CCTTCCCTG AATCTGCGGA 1200
 TTGCTTTTTT ATTTTCTTAG CAGTGTCTCT CACAGAGAAA AAGTTGTAAT TTGAATAAGA 1260
 TCCAATTCAT CTTTTTTTTT CTTTATGTA TTGTGCTTTT AGTTCATGTC TAAGAACTCT 1320
 TTGCCTAACT AAGGTCCCAA GGTCACAATA ACCTTATTCT ATACTTTCTT GTAAAAAGTTT 1380
 TATAGTTTTA TATTTTATAT GTAGATTAGT GATCTATTTT GAGTTAATTT TTGTATAAGG 1440
 TGAGAGGTGT AGGTTGAAAT TCATACCTGT GAATATAGAT ACCCAATTGT TTCAGTGCCA 1500
 TTTGTTAAAA AGACTGTTAT TTACCATTTT AATTGCCCTT GCACCTTTGT CAAAAAGCAA 1560
 CTGATCATAT TTGTGTGGGT ATATTCTGCG GTTCTCAATT CTGTCTCATT GATTGATTG 1620
 ACCATTCTTT TGCCAATGTC ATACTGCCCT GATTAGTGTA GTGTTAAAGT GAATCTCAAA 1680
 ACCAGATAAT GTGGGTCTAC CAACATTGTT CATTCTTGT CAAAAAGATT TTAGTACAT 1740
 CTAAAAATATT TTCTACATCT TTTATACATT TTAGAATCAG TGTGTTACTA TCTACAAAAT 1800
 TTCTGATGAG ATTTTAATG GATTTGTGTT AAATCAGTGG GTTAATTTTG GGAGAATTAG 1860
 CATATTAATA ATATTAAGT GTTCAATTCA TGAACACAAT ACATGTTTTC ACTTATTAG 1920
 GTTTTCTCTG TTTTTTTTTT TTTAACAGTG TTCTCAGTTT TCAACAGAAA TATTCTACAC 1980
 ATATCTTGTT AGATTTTAA CTATTTTATT TTTTGTGCT AATGTAAATG GTACTTAAAC 2040
 ATTTTGTGTT TTAATTGTTT ATTGCTAGTA GATAGAAATA CAATATTTAA AATATTAGGA 2100
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA

Seq ID NO: 202 Protein sequence:
 Protein Accession #: NP_000719.1

1 11 21 31 41 51
 MGFRKFSFPL ALSILVLYQA GSLQAAPFRS ALESSPDPAT LSKEDARLLL AALVQDYVQM 60
 KASELKQEQE TQSSSSAAQK RACNTATCVT HRLAGLLSRS GGMVKSNEVP TNVGSKAFGR 120
 RRRDLQA

Seq ID NO: 203 DNA sequence
 Nucleic Acid Accession #: NM_001741
 Coding sequence: 71..496

1 11 21 31 41 51
 CTCTGGCTGG ACGCCGCGGC CGCGCTGCC ACCGCTCTG ATCCAAGCCA CCTCCGCGCA 60
 GAGAGGTGTC ATGGGCTTCC AAAAGTTCTC CCCCTTCTG GCTCTCAGCA TCTTGGTCTC 120
 GTTGCAAGCA GGCAGCCTCC ATGCAGCACC ATTCAGTCT GCCCTGGAGA GCAGCCAGC 180
 AGACCCGCCC ACGCTCAGTG AGGACGAAGC GCGCCTCCTG CTGGCTGCAC TGGTGCAGGA 240
 CTATGTGCAG ATGAAGGCCA GTGAGCTGGA GCAGGAGCAA GAGAGAGAGG GCTCCAGCCT 300

GGACAGCCCC AGATCTAAGC GGTGCGGTAA TCTGAGTACT TGCATGCTGG GCACATACAC 360
 GCAGGACTTC AACAAAGTTTC ACACGTTCCC CCAAAGTGA ATTGGGGTTG GAGCACCTGG 420
 AAAGAAAAGG GATATGTCCA GCGACTTGGA GAGAGACCAT CGCCCTCATG TTAGCATGCC 480
 CCAGAAATGC AACTAAATC TCCTCTTCC TCCCTAATT CCCTTCTTGC ATCCTTCTTA 540
 TAACTTGATG CATGTGGTTT GGTTCCTCTC TGGTGGCTCT TTGGGCTGGT ATTGGTGGCT 600
 TTCTTGTGG CAGAGGATGT CTCAACTTC AGATGGGAGG AAAGAGAGCA GGACTCACAG 660
 GTTGAAGAG AATCAGCTGG GAAAATACCA GAAATGAGG GCCGCTTTGA GTCCCCCAGA 720
 GATGTCATCA GAGCTCTCT GTCTGCTTC TGAATGTGCT GATCATTGA GGAATAAAAT 780
 TATTTTCCC C

Seq ID NO: 204 Protein sequence:
 Protein Accession #: NP_001732

1 11 21 31 41 51
 | | | | |
 MGQKFPSPFL ALSILVLLQA GSLHAAPFRS ALESSPADPA TLSEDEARLL LAALVQDYVQ 60
 MKASELEQEQ EREGSSLDSP RSKRCGNLST CMLGTYTQDF NKFHTFPQTA IGVGAPGKKR 120
 DMSSDLERDH RPHVSM PQNA N

Seq ID NO: 205 DNA sequence
 Nucleic Acid Accession #: NM_005361
 Coding sequence: 1-945

1 11 21 31 41 51
 | | | | |
 ATGCTCTTGG AGCAGAGGAG TCAGCACTGC AAGCCTGAAG AAGCCTTGA GGCCCGAGGA 60
 GAGGCGCTGG GCCTGGTGGG TGCAGAGGCT CCTGCTACTG AGGAGCAGCA GACCGCTTCT 120
 TCCTCTTCTA CTCTAGTGA AGTTACCTTG GGGGAGGTGC CTGCTGCCGA CTCACCGAGT 180
 CCTCCCCACA GTCTCAGGG AGCCTCCAGC TTCTCGACTA CCATCAACTA CACTCTTTGG 240
 AGACAATCCG ATGAGGGCTC CAGCAACCAA GAAGAGGAGG GGCCAAGAAT GTTCCCGAC 300
 CTGGAGTCCG AGTTCCAAAG AGCAATCAGT AGGAAGATGG TTGAGTTGGT TCATTTTCTG 360
 CTCTCAAGT ATCGAGCCAG GGAGCCGGTC ACAAGGCAG AAATGCTGGA GAGTGTCTCT 420
 AGAAATTGCC AGGACTTCTT TCCCCTGATC TTCAGCAAAG CCTCCGAGTA CTTCAGCTG 480
 GTCTTTGGCA TCGAGGTGGT GGAAAGTGGT CCCATCAGCC ACTTGTACAT CCTTGTCAAC 540
 TGCTGGGGCC TCTCTACGA TGGCTGTCTG GGCAGCAATC AGGTCTATGCC CAAGACAGGC 600
 CTCTCTGATA TCGTCTGTGC CATAATCGCA ATAGAGGGCG ACTGTGCCCC TGAGGAGAAA 660
 ATCTGGGAGG AGCTGAGTAT GTTGGAGGTG TTTGAGGGGA GGGAGGACAG TGTCTTCGCA 720
 CATCCAGGCA AGCTGCTCAT GCAAGATCTG GTGCAGGAAA ACTACCTGGA GTACCCGCGAG 780
 GTGCCCGGCA GTGATCTCTG ATGCTACGAG TTCCTGTGGG GTCCAAGGGC CCTCATTGAA 840
 ACCAGCTATG TGAAGTCTCT GCACCATACA CTAAAGATCG GTGGAGAACC TCACATTTC 900
 TACCACCCC TGCATGAACG GGCTTTGAGA GAGGGAGAAG AGTGA

Seq ID NO: 206 Protein sequence:
 Protein Accession #: NP_005352

1 11 21 31 41 51
 | | | | |
 MPLEQRSQHC KPEEGLEARG EALGLVGAQA PATEEQQTAS SSSTLVEVTL GEVPAADSPS 60
 PPHSPQGASS PSTTINYTLW RQSDGSSNQ EEEGRPMFPD LESEFQAIS RKMVELVHFL 120
 LLKYRAREPV TKAEMLESLV RNCQDFFPVI FSKASEYLQL VFGIEVVEVV PISHLYILVT 180
 CLGLSYDGLL GDNQVMPKTG LLIIVLAIIA IEGDCAPEEK IWEELSMLEV FEGREDSVFA 240
 HPRKLLMQDL VQENYLEYRQ VPGSDPACYE FLWGPRLALIE TSYVKVLHHT LKIGGEPHIS 300
 YPPLHERALR EGEE

Seq ID NO: 207 DNA sequence
 Nucleic Acid Accession #: NM_021115
 Coding sequence: 743-2893

1 11 21 31 41 51
 | | | | |
 AAAGGAAGGG AGGAGGGGAG AAAGGAGAAG TTGGTTTAGA GGCCAGCCGG ACGAGCTTTG 60
 GGACACGCCC TTAGGAGGGC CACCCTCAGA GTCTGACAGC AGGTGAAGGT CCTAAATCTC 120
 CCCAACTAA CTGGTGTCTT TTCTCTCTTT CCAAGATGCT CTTCGCGAGG GAGATGCTAG 180
 CCCTTTGGGT CCTTACCTCC TGCCCTCAGG AGCCCGGAG AGAGGCAGTC CTGGCAAAGA 240
 GCACCTGAA GAGAGAGTGG TAACAGCGCC CCCAGTTCC TCACAGTCGG CGGAAGTGCT 300
 GGGCGAGCTG GTGCTGGATG GGACCGCACC CTCTGCACAT CACGACATCC CAGCCCTGTC 360
 ACCGCTGCTT CCAGAGGAGG CCGGCCCAA GCACGCTTG CCCCCAAGA AGAAACTGCC 420
 TTCGCTCAAG CAGGTGAAC CTGCCAGGAA GCAGCTGAGG CCCAAGGCC CCTCCGCGAG 480
 CACTGTCCAA AGGCGAGGT CCCAGCCAGC GTCCAGGGC CTAGATCTCC TCTCTCTCTC 540
 CACGGAGAAG CTGGGCCACC CGGGGACCC GGACCCCATC GTGGCCTCCG AGGAGGCATC 600
 AGAAGTGCCC CTTTGGCTGG ACCGAAAGGA GAGTGCCTG CCTACAACAC CCGCACCCCT 660
 GCAAATCTCC CCCTTCACTT CGCAGCCCTA TGTGGCCAC AACTTCCCC AGAGGCCAGA 720
 ACCCGGGGAG CACTGGCCCT ACATGGCCCA GGAGGCCCCC CAGGAGGACA CAGGCCCAT 780
 GGCCTGATG GACAAAGGTG AGAATGAGCT GACTGGGTCA GCCTCAGAGG AGAGCCAGGA 840
 GACCACTACC TCCACCATTA TCACCAACAC GGTTCATACC ACCGAGCAGG CACCAGCTCT 900
 GTGCACTGTG AGCTTCTCCA ATCCTGAGGG GTACATTGAC TCCAGCGACT ACCCACTGCT 960
 GCCCTCAAC AACTTCTCG AGTGACATA CAACGTGACA GTCTACACTG GCTATGGGGT 1020
 GGAGCTCCAG GTGAAGAGT TGAACCTGTC CGATGGGGAA CTGCTCTCCA TCCGCGGGGT 1080
 GGACGGCCCT ACCCTGACCG TCTGGCCAA CCAGACACTC CTGGTGAGG GGCAGGTAAT 1140
 CCGAAGCCCC ACCAACACCA TCTCGTCTA CTTCCGAGC TTCCAGGACG ACGGCCTTGG 1200
 GACCTTCCAG CTTCACTACC AGGCCCTTCAT GCTGAGCTGC AACTTTCCC GCCGCGCTGA 1260
 CTCGCGGGAT GTCACTGCTA TGGACCTGCA CTCAGGTGGG GTGGCCCACT TTCACTGCCA 1320
 CCTGGGCTAT GAGCTCCAGG GCGCTAAGAT GCTGACATGC ATCAATGCCT CCAAGCCGCA 1380
 CTGGAGCAGC CAGGAGCCCA TCTGCTCAGC TCCTTGTGGA GGGGCAGTGC ACAATGCCAC 1440
 CATCGGCGGC GTCTCTCCC CAAGTTACCC TGAACACCA AATGGGAGC AATTCTGCAT 1500
 CTGGACGATT GAAGCTCCAG AGGGCCAGAA GCTGCACCTG CACTTTGAGA GGCTGTGCT 1560

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GCATGACAAG GACAGGATGA CGGTTCCACAG CGGGCAGACC AACAGTCAG CTCCTCTCTA 1620
CGACTCCCTT CAAACCGAGA GTGTCCCTTT TGAGGGCCTG CTGAGCGAAG GCAACACCAT 1680
CCGCATCGAG TTCACGTCCG ACCAGGCCCG GCGCGCCTCC ACCTTCAACA TCCGATTGTA 1740
AGCGTTTGAG AAAGGCCACT GCTATGAGCC CTACATCCAG AATGGGAAT TCACTACATC 1800
CGACCCGACC TATAACATTG GCACTATAGT GGAGTTCACC TGCGACCCCG GCCACTCCCT 1860
GGAGCAGGGC CCGGCCATCA TCGAATGCAT CAATGTGCGG GACCCATACT GGAATGACAC 1920
AGAGCCCTG TGACAGAGCA TGTGTGGTGG GGAGCTCTCT GCTGTGGCTG GGGTGGTATT 1980
GTCCCCAAAC TGGCCCGAGC CTACGTGGA AGGTGAAGAT TGTATCTGGA AGATCCACGT 2040
GGGAGAAGAG AAACGATCT TCTTAGATAT CCAGTTCCTG AATCTGAGCA ACAGTGACAT 2100
CTTGACCATC TACGATGGCG ACGAGGTCAT GCCCCACATC TTGGGGCAGT ACCTTGGGAA 2160
CAGTGGCCCC CAGAAACTGT ACTCCTCCAC GCCAGACTTA ACCATCCAGT TCCATTGGGA 2220
CCCTGCTGGC CTCATCTTTG GAAAGGCCCA GGGATTATC ATGAACTACA TAGAGGTATC 2280
AAGGAATGAC TCCTGCTCGG ATTTACCCGA GATCCAGAAT GGCTGGAAAA CCACCTCTCA 2340
CAGGAGTTG GTGCGGGGAG CCAGAAATCAC CTACCAAGT GACCCCGGCT ATGACATCGT 2400
GGGGAGTGAC ACCCTCACCT GCCAGTGGGA CCTCAGCTGG AGCAGCGACC CCCCATTTTG 2460
TGAGAAAATT ATGTACTGCA CCGACCCCGG AGAGGTGGAT CACTCGACCC GCTTAATTTC 2520
GGATCCTGTG CTGCTGGTGG GGACCAACCAT CCAATACACC TGCAACCCCG GTTTTGTGCT 2580
TGAAGGGAGT TCTCTTCTGA CTGTCTACAG CCGTGAACA GGGACTCCCA TCTGGACGTC 2640
TCGCCTGCCC CACTGCGTTT CAGAAGCGGC AGCAGAGACG TCGCTGGAAG GGGGGAACAT 2700
GGCCTGGGCT ATCTTCATCC CGGTCTCAT CATCTCCTTA CTGCTGGGAG GAGCCTACAT 2760
TTACATCACA AGATGTGCT ACTATTCCAA CCTCCGCTG CCTCTGATGT ACTCCACCC 2820
CTACAGCCAG ATCAGCTGG AAACCGAGTT TGACAACCCC ATTTACGAGA CAGGGGGAAC 2880
CCAAAAGGTT TAGGGTTTCA TTTAAAAAGA GGTACCCCTT AAAAAGGGGC TTGTGAATC 2940
AACCCCAATT TCCCCGAGAC ATTTATCCAA AGGCCCTGGG GGCCTTGATT TAAACCCCA 3000
AAAGGCGGCT GTTTTTTGGT TAAACTTTT AACAAAGGCT TACGGGTTT TTCCCGGAT 3060
TTTATAAATT TTTAAAGTG

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Seq ID NO: 208 Protein sequence:
Protein Accession #: NP_066938

30
35
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45

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1 11 21 31 41 51
| | | | |
MAQEAPQEDT SPMALMDKGE NELTGSASEE SQETTTSTII TTTVITTEQA PALCSVSFSN 60
PEGYIDSSDY PLLPLNNFLE CTYNVTVYTG YGVELQVKS V NLSDGELLSI RGVGDGPTLV 120
LANQTLLVEG QVIRSPNTI SVYFRFTQDD GLGTFQLHYQ AFMLSCNFPR RPDSDGDTV 180
DLHSGGVAHF HCHLGYELQG AKMLTCLINAS KPHWSSQEP I CSAPCGGAVH NATIGRVLSP 240
SYPTNTNGSQ FCIWTIEAPE GQKLHLHFER LLLHDKORMT VHSQGTNKSA LLYDSLQTES 300
VPFEGLLSEG NTIRIEFTSD QARAASTFNI RFEAFKGHG YEPYIQNGNF TTSDPYTNIG 360
TIVEFTCDPG HSLTEQPAII ECINVRDPYV NDTEPLCRM CCGELSAVAG VVLSFNWPEP 420
YVEGEDCIWK IHVGEERKIF LDIQFLNLSN SDILTIYDGD EVMPHILQY LGNSGPGKLY 480
SSTPDLTIQF HSDPAGLIFG KGQGFIMNYI EVSRNDSGSD LPEIQNGWKT TSHTELVRGA 540
RITYQCDPGY DIVGSDTLTC QWDLWSWSDP PFCEKIMYCT DPGEVDHSTR LISDPVLLVG 600
TTIQTNCNPG FVLEGGSLLT CYSRETGTPI WTSRLPHCVS EAAAETSLEG GNMALAIPIP 660
VLIISLLGG AYIYITRCRY YSNLRLPLMY SHPYSQITVE TEFDNPIYET GGTQKV

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Seq ID NO: 209 DNA sequence
Nucleic Acid Accession #: NM_001327.1
Coding sequence: 89-631

50
55
60
65

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1 11 21 31 41 51
| | | | |
AGCAGGGGGC GCTGTGTGTA CCGAGAATAC GAGAATACCT CGTGGGCCCT GACCTTCTCT 60
CTGAGAGCCG GGCAGAGGCT CCGAGGCCAT GCAGGCCGAA GGCAGGGGCA CAGGGGGTCT 120
CAGCGGCGAT GCTGATGGCC CAGGAGGCCC TGGCATTCCT GATGGCCAG GGGCAATGC 180
TGGCGGCCCA GGAGAGGCGG GTGCCACGGG CGGCAGAGGT CCGCGGGCG CAGGGGCAGC 240
AAGGGCTCG GGCAGGGGAG GAGGCGCCCC GCGGGGTCG CATGGCGCG CCGCTTCAGG 300
GCTGAATGGA TGCTGCAGAT GCGGGGCCAG GGGGCCGAG AGCCGCTGC TTGAGTTCTA 360
CCTCGCCATG CCTTTCGCGA CACCCATGGA AGCAGAGCTG GCCCGCAGGA GCCTGGCCCA 420
GGATGCCCCA CCGCTTCCCG TGCCAGGGGT GCTTCTGAAG GAGTTCAGTG TGTCCGCAA 480
CATACTGACT ATCCGACTGA CTGCTGCAGA CCACGCCCAA CTGCAGCTCT CCATCAGCTC 540
CTGTCTCCAG CAGCTTTCCT TGTGATGTG GATCAGCGAG TGCTTCTGC CCGTGTTTT 600
GGCTCAGCCT CCGTCAGGGC AGAGCGGCTA AGCCAGCCT GCGCGCCCTT CCTAGGTCAT 660
GCCTCCTCCC CTAGGGAATG GTCCAGCAC GAGTGCCAG TTCATTGTGG GGCCTGATT 720
GTTTGTGCTG GGAGGAGGAC GGCTTACATG TTTGTTCTG TAGAAAAATA AACTGAGCTA

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Seq ID NO: 210 Protein sequence:
Protein Accession #: NP_001318.1

70
75

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1 11 21 31 41 51
| | | | |
MQAEGRTGG STGDADPGG PGIPDPGGN AGGPGEAGT GGRGPRGAGA ARASGPGGGA 60
PRGPHGGAAS GLNGCCRCGA RGPESRLLEF YLAMPFATPM EAEALARRSLA QDAPPLVPVG 120
VLLKEFTVSG NLTIRLTAA DHRQLQLSIS SCLQQLSLLM WITQCFLPVF LAQPPSQRR

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Seq ID NO: 211 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 52-459

80
85

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1 11 21 31 41 51
| | | | |
CCTCGTGGGC CCGACCTTC TCTCTGAGAG CCGGGCAGAG GCTCCGGAGC CATGCAGGCC 60
GAAGGCCAGG GCACAGGGGG TCGACGGGC GATGCTGATG GCCCAGGAGG CCCTGGCATT 120
CCTGATGGCC CAGGGGGCAA TGCTGGCGGC CCAGGAGAGG CGGGTGCCAC GGGCGGCAGA 180
GGTCCCCGGG GCGCAGGGGC AGCAAGGGCC TCGGGGCCGA GAGGAGGCGC CCCCGGGGGT 240
CCGCATGGCG GTGCCCTTC TGCGCAGGAT GGAAGGTGCC CCTGCGGGC CAGGAGGCCG 300

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GACAGCGGCC TGCTTCAGTT CCGACTGACT GCTGCAGACC ACCGCCAACT GCAGCTCTCC 360
 ATCAGCTCCT GTCTCCAGCA GCTTTCCTG TTGATGTGGA TCACGCAGTG CTTTCTGCCC 420
 GTGTTTTTGG CTCAGGCTCG CTCAGGGCAG AGGCGCTAAG CCCAGCCTGG CGCCCCCTTC 480
 TAGGTCATGC CTCCTCCCTT AGGGAATGGT CCCAGCACGA GTGGCCAGTT CATTTGTGGG 540
 GCCTGATTGT TTGTCGCTGG AGGAGGACGG CTTACATGTT TGTTCCTGTA GAAAAATAAG 600
 CTGAGCTA

Seq ID NO: 212 Protein sequence:
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 | | | | |
 MQAEGQGTGG STGDADGPGG PGIPDGPGGN AGGPGEAGAT GGRGPRGAGA ARASGPRGGA 60
 PRGPHGGAAS AQDGRCPGCA RRPDSRLQLF RLTAADHRQL QLSISSCLQQ LSLLMWITQC 120
 FLPVFLAQAP SGQRR

Seq ID NO: 213 DNA sequence
 Nucleic Acid Accession #: NM_000555
 Coding sequence: 416..1498

1 11 21 31 41 51
 | | | | |
 CTTATTTTTT ATGAATGTGC GATAGCTGCA CCAGCTTGCT GGGGAAAGGG TTTGATGAAT 60
 AGCACAAAGA CACTGGCTGT TCCTGGAGG CTGTCCCTTT AAAGGAGAAT CTTAGTTTAT 120
 TCTGGGGGGA GGGGATGCAC ACATTAGAGT AGGAAAGAGG GCTTGAATA AAATGAAAC 180
 ACTCCCCCTT CATAGTCATT GTACTGAAAT GCAAAGACTG CTTCTAAGC TGGAGATGCT 240
 AACCTTGGGT AGCTCCTTCT GTTCTCTTCA AGGGGAATTT TGTCAAGCTA TGGATTCATT 300
 TACAACGTGT AGTCATGTGG GCATGTGTGA GGAAACAGAT GCCAGTTTAA ATGTATTAG 360
 CCGGAAGTTC CAATTTGATA GGAGCCACTG TCAGTCTCTG AGGTTCACCC AAAATATGGA 420
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 GATGAATGGG TTGCCTAGCC CCACTCACAG CGCCCACTGT AGCTTCTACC GAACAGAAC 540
 CTTGCAGGCA CTGAGTAATG AGAAGAAAGC CAAGAAGGTA CGTTTCTACC GCAATGGGGA 600
 CCCTACTTTC AAGGGGATTG TGTACGCTGT GTCCCTGAC CGTTTTCGCA GCTTTGACGC 660
 TTTGCTGGCT ACCCTGACGC GATCTCTGTC TGACAAATC AACCTGCTC AGGGAGTGCG 720
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 GGAAGCTAT GTCTGTCTCT CAGACAACTT CTTTAAAGAG GTGGAGTACA CCAAGAAATG 840
 CAATCCCAAC TGGTCTGTCA ACGTAAACAT ATCTGCCAAT ATGAAAGCCC CCCAGTCTT 900
 GGCTAGCAGC AACAGTGCAC AGGCCAGGGA GAACAAGGAC TTTGTGCGCC CCAAGCTGGT 960
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 CAGACCCAC TCCTTTGAGC AAGTCTCTAC TGATATCACA GAAGCCATCA AACTGGAGAC 1080
 CGGGGTTGTC AAAAATCTCT ACACCTGGA TGGAAACAG GTAACCTGTC TCCATGATTT 1140
 CTTTGGTGAT GATGATGTGT TTATTGCTGT TGGTCTGAA AAATTTGCTC ATGCTCAGGA 1200
 TGATTTTCT CTGGATGAAA ATGAATGCCG AGTCATGAAG GGAAACCCAT CAGCCACAGC 1260
 TGGCCCAAG GCATCCCAAC CACCTCAGAA GACTTCAGCC AAGAGCCCTG GTCCTATGCG 1320
 CCGAAGCAAG TCTCCAGCTG ACTCAGCAAA CGGAACCTCC AGCAGCCAGC TCTCTACCCC 1380
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 GGACCTGTAC CTGCTCTGTG CTTGGATGTA CTCGGACTCG CTTGGTGATT CCATGTAAAG 1500
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 TCTGCTCAAG TGTCACACAG GGCTATTGGT GCTTCAAGT TTTTATTTTG TTTGTGTTGT 1620
 TATTTTGAAA AACACATTGT AATATGTTGG GTTTATTTTC CTGTGATTTC TCTCTGGGC 1680
 CACTGATCCA CAGTTACCAA TTATGAGAGA TAGATTGATA ACCATCCTTT GGGGCAGCAT 1740
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 TAAATTTGCC CCGCTTCAAT TTGCCCAAC AGTTTTCCTT TTGTAGAGGG GTGTTTAAAT 1860
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 ACAACACAAA GTGCCCTTT TCTCTGATC TCAAGATGG TGGAGGACCC TGAAGGACA 1980
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 TGCTTAGGAT CCTGGTGCTG GGTTAGCTAA GAGAAATGAG AGAATTGGAA AATACTGCAG 2160
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 CATGTCTGTA TTTCAAGAGC AAACCTCTCA GGCTCCTTTT TTATAAACTG GTGATTTTTC 2520
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 CATTAATAAT TTCAATGTGG ACCAGACAT CTAATTATAT TTTAAATGAA ATGTTACAGC 2760
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 CTTTCACTTG TCTTTAATC TAGAAAGGAT TTCTCTTAC TAAGGACTGA TCATTGAAA 2880
 TAGTTTTCAG TCTTTTGAGA TACAGGTTTA TAACACTGCT TTTTTCCTCC TGTAAACATA 2940
 GCCCATAAAT GCAAAACCAA CTAATTTTAA TTGAAGGTCT TGCTTGCCAN TCCTGTGTTG 3000
 GCTTTNACCA AATATAAAAA TTCCCTTATT CCTTGGTAAT GGTGCAATN TTTGGAAGG 3060
 CACAGCATCC AAACCAAGCT GCTGTTTGGC TACTGAAATGG CTGTGAGTTG TCTCTCAGT 3120
 CTAAATGGAA TGAGCTTGCT GTGTGTGTGT GTGGTGGTGG TGGGAGGGGG TGGTGCAATG 3180
 GTGTGTGTGT GTGTGCATCT GCAGCTGCTT CAAAATTAAAG AAATACTACA AGACACCCCT 3240
 GTAATGGATT GGTGGCAACT GGTGGCACT GCTGATGTGC ACTGTGTAGG GGGGAACCCA 3300
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 ACATTTTCGG TTCAAGAAAA GTGAGATGAT GGTAGTACTG GTTCTGGTG AAATTGAAAA 3420
 ACCCAAAATG ATGAGGACTC CTTTTCCTTT TTTTGTAAAC CCATTCAAAA 3480
 CCATTAATAA GCCCAATTTA CTAANCCCTT ATTTCTTTCT AGAAGCTCAG GGTITNCTTA 3540
 GTGCCCTCCA NAACATTTTG TAGTTAATTG GGAAGAAAGT ATACTTGGAT TAGGGGGTGT 3600
 GGGCATAAAG AATGGTGGGA GGCCTGATT TAAATTCAG GCCAGAACCC CCAATGACTC 3660
 CACCCATAGT NTCACTTTAG GTCTCATTTA GTCCATCACC TTTATTTTAA GTTGAGGAAG 3720
 TGGAGGCTGG TAAAGAGCAG GACCAGAGGA AGAATCCAGA TTTCTTATG CTTGGGCTC 3780
 ACCTAGCTC TINTGATATT TCTTGTATTG CGGTATATGT ACTACTAGAA AATACCAAT 3840
 GGATATATTT TCTTTAGGAT AACCTTTGAA CCAACAAATNT TCAATAACAA TAGTACATCT 3900

272

CAGACCCCTT TCATCTCCTG TGCCGTGAAC ACCCTCTCTC CCCCACCCCC TCCGCAATTC 9180
 AATGAGGGCT TTCTGGGTC AGAGGACTTC AAGGTGTCT AGAGAAGTTT GCCATGTGTG 9240
 TAAGGTGCTG TGAACGTGTA GTGCTGAAGA TTCGAGCAT TCAATACCAG GCAGCCAAAG 9300
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 TGTACATTTG CAAGATGTGT GTAATGTCAT TTTCCAAAA TAAATTTGA TTTCAAT

Seq ID NO: 214 Protein sequence:
 Protein Accession #: NP_000546

1 11 21 31 41 51
 MELDFGHFDE RDKTSRNMGR SRMNGLPSP T HSAHCSFYRT RTLOALSNEK KAKKVRFYRN 60
 GDRYFKGIVY AVSSDRFRSF DALLADLTR LSDNINLPQG VRYIYTTIDGS RKIGSMDELE 120
 EGESYVCSSD NFFKKVEYTK NVNPNWSVNV KTSANMKAPQ SLASSNSAQA RENKDFVRPK 180
 LVTIIRSGVK PRKAVRVLLN KKTAFSFEQV LTDITEAIKL ETGVVKKLYT LDGKQVTCLEH 240
 DFFGDDVFI ACPPEKFRYA QDDFSLDENE CRVMKGNPSA TAGPKASPTP QKTSKSPGP 300
 MRRSKSPADS AMGTSSSQLS TPKSKQSPIS TPTSPGSLRK HKDLYLPLSL DDSDSLGDMS

Seq ID NO: 215 DNA sequence
 Nucleic Acid Accession #: NM_130467
 Coding sequence: 312..644

1 11 21 31 41 51
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 CTTTCCAACA TCTTCGTCTT TTCTCACTGA CCGAGACTCA GCCGGTAGGT CTGCAGAGTG 120
 TCCTTCCTGG TAATTAGTGT GTGAGTGAAT GTGTGGAGGA GCCAGCGGGC TTAGGACAGG 180
 TCTCTGGCA CAGTCCGTGG CTTTGAGGGA AAAGGGCCTC GCGGTGGTCC TCCGCTTCC 240
 CCCAGGTCGT GATGCAGGCG CCATGGGCGG GTAATCGTGG CTGGGCTGGA ACGAGGGAGG 300
 AAGTGAGAGA TATGAGTGAG CATGTAACAA GATCCCAATC CTCAGAAAGA GGAAATGACC 360
 AAGAGTCTTC CCAGCCAGT GGACCTGTGA TTGTCCAGCA GCCCACTGAG GAAAAACGTC 420
 AAGAAGAGGA ACCACCAACT GATAATCAGG GTATTGCACC TAGTGGGGAG ATCAAAAATG 480
 AAGGAGCACC TGCTGTTCAA GGGACTGATG TGAAGCTTT TCAACAGGAA CTGGCTCTGC 540
 TTAAGATAGA GGATGCAGT GGAGATGGTC CTGATGTCAG GGAGGGGACT CTGCCACTT 600
 TTGATCCAC TAAAGTGCTG GAAGCAGGTG AAGGGCAACT ATAGGTTTAA ACCAAGACAA 660
 ATGAAGACTG AAACCAAGAA TATTGTTCTT ATGCTGGAAA TTTGACTGCT AACATTCTCT 720
 TAATAAAGTT TTACAGTTT CTGCAAAAAA AAAAAAAAAA AAA

Seq ID NO: 216 Protein sequence:
 Protein Accession #: NP_569734

1 11 21 31 41 51
 MSEHVTRSQS SERGNDQESS QPVGPFVIVQ PTEEKQEEE PPTDNQGIAP SGEIKNEGAP 60
 AVQGTDFEAF QQELALLKIE DAPGDPDVR EGTLPFTDPT KVLEAGEGQL

Seq ID NO: 217 DNA sequence
 Nucleic Acid Accession #: NM_001476.1
 Coding sequence: 82..435

1 11 21 31 41 51
 GCCAGGGAGC TGTGAGGCAG TGCTGTGTGG TTCCTGCCGT CCGGACTCTT TTCCTCTAC 60
 TGAGATTCAT CTGTGTGAAA TATGAGTTGG CGAGGAAGAT CGACCTATTA TTGGCCTAGA 120
 CCAAGGCGCT ATGTACAGCC TCCTGAAGTG ATTGGGCTTA TGCGGCCCGA GCAGTTCAGT 180
 GATGAAGTGG AACCAGCAAC ACCTGAAGAA GGGGAACAG CAAGTCAACG TCAGGATCCT 240
 GCAGCTGCTC AGGAGGGAGA GGATGAGGGA GCATCTGCAG GTCAAGGGCC GAAGCCTGAA 300
 GCTGATAGCC AGGAACAGGG TCACCCACAG ACTGGGTGTG AGTGTGAAGA TGGTCTGAT 360
 GGGCAGGAGG TGGACCCGCC AATCCAGAG GAGGTGAAAA CGCCTGAAGA AGGTGAAAAG 420
 CAATCACAGT GTTAAAGAA GACACGTTGA AATGATGCAG GCTGCTCCTA TGTGGAAAT 480
 TTGTTCAATTA AATTTCTCCC AATAAAGCTT TACAGCCTTC TGCAAAA

Seq ID NO: 218 Protein sequence:
 Protein Accession #: NP_001467.1

1 11 21 31 41 51
 MSWRGRSTY WPRPRRYVQP PEVIGPMRPE QFSDEVEPAT PEEGEPATQR QDPAAAQEGE 60
 DEGASAGQGP KPEADSQEQG HPQTGCECED GPDGQEVDP NPEEVKTPBE GEKQSQC

Seq ID NO: 219 DNA sequence
 Nucleic Acid Accession #: NM_001476
 Coding sequence: 90-3671

1 11 21 31 41 51
 ACAGCGGAGC GCAGAGTGAG AACCACCAAC CGAGGCGCGG GGCAGCGACC CTGCAGCGG 60
 AGACAGAGAC TGAGCGGCCC GGCACCGCCA TGCCTGCGCT CTGGCTGGGC TGCTGCCTCT 120
 GCTTCTCGCT CCTCTGCCC GCAGCCCGGG CCACCTCCAG GAGGGAAGTC TGTGATTGCA 180
 ATGGGAAGTC CAGGCAGTGT ATCTTTGATC GGGAACTTCA CAGACAACT GGTAATGGAT 240
 TCCGCTCGCT CAAGTGAAT GACAACACTG ATGGCATTCA CTGCGAGAAG TGCAAGAATG 300
 GCTTTTACCG GCACAGAGAA AGGGACCGCT GTTGCCTG CAATTGTAAC TCCAAAGGTT 360

5 CTCTTAGTGC TCGATGTGAC AACTCTGGAC GGTGCAGCTG TAAACCAGGT GTGACAGGAG 420
 CCGATGCGCA CCGATGTCTG CCAGGCTTCC ACATGCTCAC GGATGCGGGG TGCACCCAAG 480
 ACCAGAGACT GCTAGACTCC AAGTGTGACT GTGACCCAGC TGGCATCGCA GGGCCCTGTG 540
 ACGCGGGCCG CTGTGTCTGC AAGCCAGCTG TTACTGGAGA ACGCTGTGAT AGGTGTGAT 600
 CAGGTTACTA TAATCTGGAT GGGGGGAACC CTGAGGGCTG TACCCAGTGT TTCTGTCTATG 660
 GGCATTACAG CAGCTGCCGC AGCTCTGCAG AATACAGTGT CCATAAGATC ACCTCTACCT 720
 TTCATCAAGA TGTGTATGGC TGGAAAGCTG TCCAACGAAA TGGGTCTCCT GCAAAGCTCC 780
 AATGGTCACA GCGCCATCAA GATGTGTTTA GCTCAGCCCA ACGACTAGAC CCTGTCTATT 840
 10 TTGTGGCTCC TGCCAAATTT CTGGGAATC AACAGGTGAG CTATGGGCAA AGCCTGTCTC 900
 TTGACTACCG TGTGGACAGA GGAGGAGAC ACCCATCTGC CCATGATGTG ATTCTGGAAG 960
 GTGCTGGTCT ACGGATCACA GCTCCCTTGA TGCCACTTGG CAAGACACTG CCTTGTGGGG 1020
 TCACCAAGAC TTACACATTC AGGTTAAATG AGCATCCAAG CAATAATTGG AGCCCCCAGC 1080
 TGAGTTACTT TGAGTATCGA AGGTTACTGC GGAATCTCAC AGCCCTCCGC ATCCGAGCTA 1140
 15 CATATGGAGA ATACAGTACT GGGTACATTG ACAAATGTGAC CCTGATTCCA GCCCGCCTG 1200
 TCTCTGGAGC CCCAGCACCC TGGGTTGAAC AGTGTATATG TCCTGTTGGG TACAAGGGGC 1260
 AATTCTGCCA GGATTGTGCT TCTGGCTACA AGAGAGATTG AGCGAGACTG GGGCCTTTTG 1320
 GACCTGTAT TCTTGTAACT TGTCAAGGGG GAGGGGCTG TGATCCAGAC ACAGGAGATT 1380
 GTTATTACAG GGATGAGAACT CCTGACATTG AGTGTGCTGA CTGCCCAATT GGTTCCTACA 1440
 20 ACGATCCGCA CGACCCCGC AGCTGCAAGC CATGTCCCTG TCATAAGGGG TTCAGCTGCT 1500
 CAGTGATGCC GGAGATCGAG GAGGTGGTGT GCAATAACTG CCCTCCCGGG GTCAACGGTG 1560
 CCCGCTGTGA GCTCTGTGCT GATGGCTACT TTGGGGACCC CTTTGGTGAA CATGGCCAG 1620
 TGAGGCCTTG TCAGCCCTGT CAATGCAACA ACAATGTGGA CCCAGTGCC TCTGGGAATT 1680
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 25 ACCAGTGCAA AGCAGGCTAC TTCGGGGACC CATTGGCTCC CAACCCAGCA GACAAGTGTG 1800
 GAGCTTGCAA CTGTAAACCC ATGGGCTCAG AGCCTGTAGG ATGTGCAAGT GATGGCACCT 1860
 GTGTTTGCAA GCCAGGATT TGGTGGCCCA ACTGTGAGCA TGGAGCATTC AGCTGTCCAG 1920
 CTTGCTATAA TCAAGTGAAG ATTCAAGTGG ATCAGTTTAT GCAGCAGCTT CAGAGAATGG 1980
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 30 GCAGGATGCA CAGGCTGAG CAGGCCCTTC AGGACATTCT GAGAGATGCC CAGATTTTCA 2100
 AAGGTGCTAG CAGATCCCTT GGTCTCCAGT TGGCCAAGGT GAGGAGCCAA GAGAACAGCT 2160
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 AGTACCAGAA CCGAGTCCGG GATACTCACA GGCTCATCAC TCAGATGCAG CTGAGCTCGG 2280
 CAGAAAGTGA AGCTTCTCTG GGAACAATA ACATTCTCTG CTCAGACCAC TACGTGGGGC 2340
 35 CAAATGGCTT TAAAGTCTG GCTCAGGAG CCACAAGATT AGCAGAAAGC CAGCTTGAGT 2400
 CAGCCAGTAA CATGGAAGG CTGACAAGGG AAATCTGAGGA CTATTCCAAA CAAGCCCTCT 2460
 CACTGGTGGC CAAGGCCCTG CATGAAGGAG TCGGAAGCGG AAGCGGTAGC CCGGACGGTG 2520
 CTGTGGTGCA AGGGCTTGTG GAAAATTTGG AGAAAACCAA GTCCCTGGCC CAGCAGTTGA 2580
 40 CAAGGGAGGC CACTCAAGCG GAAATTGAAG CAGATAGGTC TTATCAGCAC AGTCTCCGCG 2640
 TCCTGGATTG AGTGTCTCGG CTTCAAGGAG TCAGTGATCA GTCTTTTCA GTGGAAGAAG 2700
 CAAAGAGGAT CAAACAAAAG GCGGATTCAC TCTCAACGCT GGTAAACCAG CATATGGATG 2760
 AGTTCAAGCG TACACAAAAG AATCTGGGAA ACTGGAAAGA AGAAGCACAG CAGCTCTTAC 2820
 AGAATGGAAG AAGTGGGAGA GAGAAATCAG ATCAGCTGCT TTCCCGTGCC AATCTTGCTA 2880
 45 AAGCAGAGC ACAAGAAGCA CTGAGTATGG GCAATGCCAC TTTTATGAA GTTGAGAGCA 2940
 TCCTTAAAAA CTTAGAGAG TTTGACCTGC AGGTGGACAA CAGAAAAGCA GAAGCTGAAG 3000
 AAGCCATGAA GAGACTCTCC TACATCAGCC AGAAGGTTTC AGATGCCAGT GACAAGACCC 3060
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 AAGCCAAATG GACAGCAGAT GGAGCCTTGG CCAATGGAAA GGGACTGGCC TCTCTGAAGA 3240
 50 TGAGATGAG GGAAGTGGAA GGAGAGCTGG AAAGGAAGGA GCTGGAGTTT GACACGAATA 3300
 TGGATGAGT ACAGATGGTG ATTACAGAAG CCCAGAAGGT TGATACCAGA GCCAAGAACG 3360
 CTGGGGTTAC AATCCAAGAC AACTCAACA CATTAGACGG CCTCTGCTAT CTGATGGACC 3420
 AGCCTCTCAG TGTAGATGAA GAGGGGCTGG TCTTACTGGA GCAGAACTT TCCCGAGCCA 3480
 55 AGACCCAGAT CAACAGCAG CTGCGGCCCA TGATGTGAGA GCTGGAAGAG AGGGCAGCTC 3540
 AGCAGAGGGG CCACCTCCAT TTGCTGGAGA CAAGCATAGA TGGGATTCTG CTTGATGTGA 3600
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 AGCAACAGT AAGCTGCCAT AAATTTTCT CAACTGAGGT TCTTGGGATA CAGATCTCAG 3720
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 TATGCTCAGG TCACTGACC TGACCCCAT CTGATGCCA TGGCCAGGTG GTTGTCTTAT 3840
 60 TGACCATAC CTTTCTCTTC CTGATGCTGG GCAATGAGGC AGATAGCACT GGGTGTGAGA 3900
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 65 ACTATTGCTT CATATTGCTT TCTGCAAGCT TCTTGCTGAT CAGAGTTCTT CCTACTTACA 4200
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 70 ATTTTATTA AAGCATTTCC TACCAGCAA GCAATGTTG GGAAGTATT TACTTTTTCG 4440
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 CACACTTCAG CTGGGTCACA TCCATCCCTC CATTCATCCT TCCATCCATC TTTCCATCCA 4680
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 75 GTGGACAGT GGTGACATG TCTTGCCCT CATAGAGTTG ATTGTCTAGT GAGGAAGACA 4800
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 CATTCAGCTG GTCACCTGTG GCCTTTCTAC AACTGATTGC AACAGACTGT TGAGTTATGA 5040
 80 TAACACCACT GGAATTTGCT GGAGGAACCA GAGGCACTTC CACCTTGGCT GGGGAAGACTA 5100
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 CAATTGTTAG ATGCC

Seq ID NO: 220 Protein sequence:
 Protein Accession #: NP_005553

1 11 21 31 41 51
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	MPALWLGCC	CFSLLLPAAR	ATSRREVCDC	NGKSRQCIPD	RELHRQTGNG	FRCLNCNDNT	60
	DGIHCEKCKN	GFYRHRERDR	CLPCNCNSKG	SLSARCDNSG	RCSCCKPGVTG	ARCDRCCLPGF	120
	HMLTDAGCTQ	DQRLLDKCD	CDPAGIAGPC	DAGRVCVKPA	VTGERCDRCR	SGYYNLDGGN	180
5	PEGCTQCFCY	GHSASCRSSA	EYSVHKITST	FHQDVGWKA	VQRNGSPAKL	QWSQRHQDVF	240
	SSAQRLLDPVY	FVAPAKPLGN	QVVSYGQSL	FDYRVDRGGR	HPSAHDVILE	GAGLRITAPL	300
	MPLGKTLPCG	LTKYTYFRLN	EHPNNWSPQ	LSYFEYRRL	RNLTLALRIR	TYGEYSTGYI	360
	DNVTLSARP	VSGAPAPWE	QCICPVGYKG	QFCQDCASGY	KRDSARLPGF	GTCIPCNQCG	420
	GGACDPDTGD	CYSGDENPDI	ECADCPIGFY	NDPHDPRSCK	PCPCHNGPSC	SVMPEETREVV	480
10	CNNCPGVTG	ARCELCADGY	FGDPFGEHGP	VRPCQPCQCN	NNVDPSASGN	CDRLTGRCLK	540
	CIHNTAGIYC	DQCKAGYFGD	PLAPNPADKC	RACNCPMGS	EPVGCERSDGT	CVCKPGFGGP	600
	NCEHGAFCSP	ACYNQVKIQM	DQFMQQLQRM	EALISKAQGG	DGVVPDTELE	GRMQQAEOAL	660
	QDILRDAQIS	EGASRSGLGL	LAKVRSQENS	YQSRLLDLKM	TVERVRALGS	QYQNRVRDTH	720
	RLITQMQLSL	AESEASLGNT	NIPASDHYVG	PNGFKSLAQE	ATRLAESHVE	SASNMEQLTR	780
15	ETEDYSKQAL	SLVRKALHEG	VSGSGSPDGG	AVVQGLVEKL	EKTKSLAQOL	TREATQAEIE	840
	ADRSYQHSLL	LLDSVSRLQG	VSDQSQVEE	AKRIKQKADS	LSTLVTRHMD	EFKRTQKNLG	900
	NWKEEAQQLL	QNGKSGREKS	DQLLSRANLA	KSRQAQALSM	GNATFYEVES	ILKNLREFFDL	960
	QVDNRKAEAE	EAMKRLSYIS	QKVSDASDKT	QQAERALGSA	AADAQRAKNG	AGEALBISSE	1020
	IEQEIGSLNL	EANVTADGAL	AMEKGLASLK	SEMREVEGEL	ERKELEFDTN	MDAVQMVITE	1080
20	AQKVDTRAKN	AGVTIQTDLN	TLDGLLHLM	QPLSVDEEGL	VLEQLKLSRA	KTQINSQLRP	1140
	MMSELEERAR	QQRGHLHLE	TSIDGILADV	KNLENIRDNL	PPGCTNTQAL	EQQ	

Seq ID NO: 221 DNA sequence
Nucleic Acid Accession #: NM_016529
Coding sequence: 13-1854

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30	ACATTATGCC	ATCTGGGAATA	CTTTGCCACG	GAAGGCTTGC	GGACTCTCTG	TGTGGCTTAT	180
	GCTGATCTCT	CTGAGAAATGA	GTATGAGGAG	TGGCTGAAAG	TCTATCAGGA	AGCCAGCACC	240
	ATATTGAAGG	ACAGAGCTCA	ACGGTTGGAA	GAGTGTACG	AGATCATTGA	GAAGAATTG	300
	CTGCTACTTG	GAGCCACAGC	CATAGAAGAT	CGCCTTCAAG	CAGGAGTTCC	AGAAACCATC	360
	GCAACACTGT	TGAAGGCAGA	AATTAAATA	TGGGTGTTGA	CAGGAGACAA	ACAAGAACT	420
35	GCGATTAATA	TAGGGTATTC	CTGCCGATTG	GTATCGCAGA	ATATGGCCCT	TATCCTATTG	480
	AAGGAGGACT	CTTTGGATGC	CACAAGGGCA	GCCATTACTC	AGCACTGCAC	TGACCTTGGG	540
	AATTGTCTGG	GCAAGGAAAA	TGACGTGGCC	CTCATCATCG	ATGGCCACAC	CCTGAAGTAC	600
	GCGCTCTCCT	TCGAAGTCCG	GAGGAGTTTC	CTGGATTGG	CACTCTCGTG	CAAAGCGGTC	660
	ATATGCTGCA	GAGTGTCTCC	TCTGCAGAAG	TCTGAGATAG	TGGATGTGGT	GAAGAAAGCG	720
40	GTGAAGGCCA	TCACCCCTCG	CATCGGAGAC	GGCGCCACG	ATGTCGGGAT	GATCCAGACA	780
	GCCCACGTGG	GTGTGGGAAT	CAGTGGGAAT	GAAGGCATGC	AGGCCACCAA	CAACTCGGAT	840
	TACGCCATCG	CACAGTTTTC	CTACTTAGAG	AAGCTTCTGT	TGGTTCATGG	AGCCTGGAGC	900
	TACAACCGGG	TGACCAAGTG	CATCTTGTAC	TGCTTCTATA	AGAACGTGGT	CCTGTATATT	960
45	ATTGAGCTTT	GGTTCGCTT	TGTTAATGGA	TTTTCTGGGC	AGATTTTATT	TGAACGTTGG	1020
	TGCATCGGCC	TGATCAATGT	GATTTTCACC	GCTTTGCCGC	CCTTCACTCT	GGGAATCTTT	1080
	GAGAGGTCTT	GCACTCAGGA	GAGCATGCTC	AGGTTTCCCC	AGCTCTACAA	AATCACCAG	1140
	AATGGCGAAG	GCTTCAACAC	AAAGGTTTTC	TGGGGTCACT	GCATCAACGC	CTTGGTCCAC	1200
	TCCCTCATCC	TCTTCTGGTT	TCCCATGAAA	GCTCTGGAGC	ATGATCTGT	GTTTGACAGT	1260
50	GGTCATGCTA	CCGACTATT	ATTGTTTGA	AATATGTGTT	ACACATATGT	TGTTGTACT	1320
	GTTTGTCTGA	AAGCTGGTTT	GGAGACCACA	GCTTGGACTA	AATTCAGTCA	TCTGGCTGTC	1380
	TGGGGAAGCA	TGCTGACCTG	GCTGGTGT	TTTGGCATCT	ACTCGACCAT	CTGGCCACCC	1440
	ATTTCCATTG	CTCCAGTAT	GAGAGGACAG	GCAACTATGG	TCCTGAGCTC	CGCACACTTC	1500
	TGGTTGGGAT	TATTTCTGGT	TCCTACTGCC	TGTTTGATTG	AAGATGTGGC	ATGGAGAGCA	1560
	GCCCAAGCACA	CCTGCAAAAA	GACATTGCTG	GAGGAGGTGC	AGGAGCTGGA	AACCAAGTCT	1620
55	CGAGTCTCTG	GAAAGCGGT	GCTGCGGGAT	AGCAATGGAA	AGAGGCTGAA	CGAGCGCGAC	1680
	CGCTGATCA	AGAGGCTGGG	CCGGAAGACG	CCCCCGACGC	TGTTCCGGGG	CAGCTCCCTG	1740
	CAGCAGGGCG	TCCCGCATGG	GTATGCTTTT	TCTCAAGAA	AACACGGAGC	TGTTAGTCAG	1800
	GAAGAAGTCA	TCCGTGCTTA	TGACACCACC	AAAAAGAAAT	CCAGGAAGAA	ATAAGACATG	1860
	AATTTTCTCT	ACTGATCTTA	GGAAAGAGAT	TCAGTTTGTT	GCACCCAGTG	TTAACACATC	1920
60	TTTGTGACAG	AAGACTGGCG	TCCAAGGCCA	AAACACCAGG	AAACACATTT	CTGTGGCCTT	1980
	AGTTAAGCAG	TTTGTGATTT	ACATATTCCC	TCGCAAACT	GGAGTGCAGA	CCACAGGGGA	2040
	AGCTATCTTT	GCCCTCCCAA	CTCGTCTGCA	GTGCTTAGCC	TAAGTTTGT	TTATGTCGTT	2100
	ATGAAGCATT	CAACTGTGCT	CTGTAGGTC	TCAAATTAAT	AACATTATGT	TTACCAATA	2160
65	AGAAAAAA	AAAAAA					

Seq ID NO: 222 Protein sequence:
Protein Accession #: NP_057613

70	1	11	21	31	41	51	
	MSVIVRTPSG	RLRLYCKGAD	NVIFERLSKD	SKYMEETLCH	LEYFATEGLR	TLCVAYADLS	60
	ENYEWEWLKV	YQEAETILKD	RAQRLEECYE	IEKNLLLLG	ATAIEDRLQA	GVPETIATLL	120
	KAEIKIWLVT	GDKQETAINI	GYSCRLVSQN	MALILLKEDS	LDATRAAITQ	HCTDLGNLLG	180
75	KENDVALIID	GHTLKYALSF	EVRRSFLDLA	LSCKAVICCR	VSPLOKSEIV	DVVKRVRKAI	240
	TLAIGDGDAN	VGMIQTAVHG	VGISGNEGMQ	ATNNSDYAIA	QFSYLEKLLL	VHGAWSYNRV	300
	TKCILYCFYK	NVLYLYIELW	FAFVNGFSQ	ILFERWCIGL	YNYVFTALPP	FTLGIFERSC	360
	TQESMLRFPQ	LYKITONGEG	FNTKVFWGHC	INALVHSLIL	FWFPMKALEH	DTVFDSGHAT	420
	DYLFVGNIVY	TYVVVTVCLK	AGLETTAWTK	FSHLAVWGS	LTWLVFVFIY	STIWPITPIA	480
	PDMRGQATMV	LSSAHFWLGL	FLVPTACLE	DVAWRAAKHT	CKKTLLEEVQ	ELETKSRVLG	540
80	KAVLRDSNGK	RLNERDLRIK	RLGRKTPPTL	FRGSSLQGGV	PHGYAFSQEE	HGAVSQEEVI	600
	RAYDTTKKKS	RKK					

Seq ID NO: 223 DNA sequence
Nucleic Acid Accession #: BC017001
Coding sequence: 1-394

85	1	11	21	31	41	51	

5
10
15
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25
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35
40
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AACGCTGGGC	AGGGCCGCGC	CGGGTCGGGG	GGCGCCCGAG	GGGCCCGGGC	CGAGCGGCGG	60
CGCGCAGGGC	GGCAGCATCC	ACTCGGGCCG	CATCGCCGCG	GTGCACAACG	TGCCCGCTGAG	120
CGTGCTCATC	CGGCCGCTGC	CGTCCGTGTT	GGACCCCGCC	AAGGTGCAGA	GCCTCGTGGA	180
CACGATCCGG	GAGGACCCAG	ACAGCGTGCC	CCCCATCGAT	GTCCCTCTGGA	TCAAAGGGGC	240
CCAGGGAGGT	GACTACTTCT	ACTCCTTTGG	GGGCTGCCAC	CGCTACGCGG	CCTACCAGCA	300
ACTGCAGCGA	GAGACCATCC	CCGCCAAGCT	TGTCCAGTCC	ACTCTCTCAG	ACCTAAGGGT	360
GTACCTGGGA	GCATCCACAC	CAGACTTGCA	GTAGCAGCCT	CCTTGGCACC	TGCTGCCACC	420
TTCAAGAGCC	CAGAAGACAC	ACCTGGCCTC	CAGCAGGCTG	GGCCATGCAG	AAGGGATAGC	480
AGGGGTGCGT	TCTCTTTGCA	CCTGGCGAGA	GGTCTGACT	CTGGGCACCC	CTCTCACCGG	540
CTACAAGGCC	TTGGACTCAG	TGTACAGTGT	GGGAGCCCCA	GTTCACACCT	CTGTGACAAT	600
AGGATCATGG	CCTTACCCTT	GAAGCATTAC	CGAGAAGGAG	AACAGAGATG	GGCTTGAAGA	660
GCCACGTGCT	GCCGGCTCCA	AATTCCCAAG	GACAAGGATC	CCTCTGCATT	TTGTCTATG	720
TAACTCTTTA	TATGGACTAC	ATTGAGCTGC	AAGGAAAGGA	AAACCTTGAT	TGCAGTGGTT	780
TAAACAAACA	GAAGATTGTT	TTTCCACATA	GCATGGATTG	TGGAGATGGG	TGGCTAATGG	840
TATTGGTTCA	ACAACTCCAC	GGAGGTAGGG	GTCACTCTTT	GGATCCTTTT	GCCTTAATCT	900
CAGTGCTCGT	TACTTCATGG	TCCCAAGATG	GCTGCTGTAT	CCCCAAGAT	CATGCTCGG	960
TTCAAGGAAG	GAGGGGTGGA	GGAAGAGGAA	GGGCCAAACT	AGCTGGACCC	GTCACTTCT	1020
ATCAGAAATG	AAAACCTCGT	CAGAAGTCTG	TTTCTGCTC	TCCTCCCTCTG	CATATCTTCA	1080
CTTAGATGCC	CTTGGCCCGA	GCCAGCTACC	ATTGCACCTC	TAGCTGCAAA	CAAAAGCTAAG	1140
ACAGCAGGGA	ACAGAATTGT	CATGGCTGAA	TAGACCAATC	GTGTTCCATC	TACTGAGACT	1200
GGCACACTGC	CTCCTGCAAT	AAAACCTGGG	TCCCATTACC	AAGAGAGAAA	TGCAGAATTG	1260
TGTACCAATT	AGCTTTTGCT	GTGTAAACAA	CCATCCCCAA	ACTTGGCAGC	TAGAAACAAA	1320
CCCTGTATTT	TCCCAACAAT	CTATGGGTTG	GCAATTGTTG	CTGGGCTCAA	CAGGGCAGTT	1380
CTGCTGCTCA	CACCTGGGAT	CCCTCATGGA	GCTAAGGTCA	GCTGTTACCT	CAGCTGGGCC	1440
TGGATGGTCT	AGGATAGCCT	TACTCACTTG	CCTGGCAGGT	GACAGGCTGT	TGGCTGGAAT	1500
TGCTTGGTTC	TCCTCCATGT	GGCCTCTCCA	GCAGGCTAGC	TCAGGCTTAT	TCACATGATG	1560
GCCTCAGGAT	TCCAAAGAGA	GTGAGAGTAG	AAGCTGAAAG	ACTTCTTGAG	TTCTTGGCCT	1620
GGAACTGGGA	CTGAGCTGAG	GTCACTTCTG	CTAAGTCTTT	TTGGTCAGAG	CAAAATCACA	1680
GGCTTTACCC	AGATTCAAGG	GATGAGAAAC	AGACTACATG	TCTTGATGAG	GGGAACCACA	1740
AAGAGCTTGT	GGCCATTTT	CACCTATCAC	AAATAATTTT	GGATGGGTAT	TTATTTGGAT	1800
AAAGGTATTT	CCCTTTTCCC	CTGTCTCTC	TGTCTCATGG	GGCCTCACTC	TGCCAAGTTG	1860
GAAGGCACTA	AGACATTGTC	CTGGCCCTCA	GGGTCTAGGG	GAAGAGGTGT	TGGGGCAGGA	1920
AGTGAGTCTC	TCCATGGGCT	GGACCCACTG	TAGTAGGAGT	GCCTCCTTGT	CTGCACTGCT	1980
GGTATGGGCT	TAGGCCAGGT	AGGACATTCC	AGAGGGGCTT	CTGAAAACCA	AGAGTCCCTG	2040
GGGAAAGGGA	ACAGAGTAAG	GCAGGCCCTG	TTCTCACTGC	CCTCTAAGGG	AACCTTGGTCA	2100
CTCGGCACCT	TTAAGCCCTCA	GTTTCTCCAG	TTCAATAATA	AGGACAAGAG	CTTTTCCCAT	2160
GCATTCTCTT	TCCCGGGGAA	AGTTGACTGA	GGTGACCAGT	AATAGAAATTG	AAAAGGGAGA	2220
GTGTCTTCAG	TGCAATGTGG	CATCCTGGAT	TGGGTCTTGG	AACAAAACA	GGACATTAGT	2280
GGGAAAATTG	GAAATCTGAA	AAAAGTCTGA	ATTTTAGTTA	ATATACCAAT	TTCACTCTCT	2340
TGGTTTGGAC	AGACTCTTTG	TACTATCTCT	GCAACTTCTC	TGTAATCTA	GTATCATTCC	2400
GGGTATACAG	GAATCTCTTG	TACTATCTCT	GCAACTTCTC	TGTAATCTA	GTATCATTCC	2460
AAAATAAAAG	TTTATTATAT	TTAAAAAATA	AAAAAATAAA	AA		

Seq ID NO: 224 Protein sequence:
Protein Accession #: AAH17001.1

50

1	11	21	31	41	51	
TLGRAGAGRG	APEGPGPSGG	AQGGSIHSGR	IAAVHNVPLS	VLIRPLPSVL	DPAKVQSLVD	60
TIREDPDSVP	PIDVLWIKGA	QGGDYFYSFG	GCHRYAAYQQ	LQRETIPAKL	VQSTLSDLRV	120
YLGASTPDLQ						

55
Seq ID NO: 225 DNA sequence
Nucleic Acid Accession #: NM_021048
Coding sequence: 1..1110

60
65
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75
80

1	11	21	31	41	51	
ATGCCTCGAG	CTCCAAAGCG	TCAGCGCTGC	ATGCCTGAAG	AAGATCTTCA	ATCCCAAAGT	60
GAGACACAGG	GCCTCGAGGG	TGCACAGGCT	CCCCTGGCTG	TGGAGGAGGA	TGCTTCATCA	120
TCCACTTCCA	CCAGCTCCTC	TTTCCATCC	TCTTTCCCT	CCTCCTCTC	TTCTCCTCC	180
TCCTCTGCT	ATCCTCTAAT	ACCAAGCACC	CCAGAGGAGG	TTTCTGCTGA	TGATGAGACA	240
CCAAATCCTC	CCCAGAGTGC	TCAGATAGCC	TGCTCCTCCC	CCTCGGTCTG	TGCTTCCCTT	300
CCATTAGATC	AATCTGATGA	GGGCTCCAGC	AGCCAAAAGG	AGGAGAGTCC	AAGCACCCTA	360
CAGGTCTCTG	CAGACAGTGA	GTCTTTACCC	AGAAGTGAGA	TAGATGAAAA	GGTGACTGAT	420
TTGGTGCACT	TTCTGCTCTT	CAAGTATCAA	ATGAAGGAGC	CGATCACAAA	GGCAGAAATA	480
CTGGAGAGTG	TCATAAAAAA	TTATGAAGAC	CACCTCCCTT	TGTTGTTTAG	TGAAGCCTCC	540
GAGTGCAATG	TGCTGGTCTT	TGGCATTGAT	GTAAGGAAG	TGGATCCAC	TGGCCACTCC	600
TTTGTCTTGG	TCACCTCCCT	GGGCTCACC	TATGATGGGA	TGCTGAGTGA	TGTCCAGAGC	660
ATGCCCAAGA	CTGGCATTCT	CATACCTATC	CTAAGCATAA	TCTTCATAGA	GGGCTACTGC	720
ACCCTCTGAG	AGGTCTCTG	GGAAGCACTG	AATATGATGG	GGCTGTATGA	TGGGATGGAG	780
CACCTCATTT	ATGGGGAGCC	CAGGAAGCTG	CTACCCCAAG	ATTGGGTGCA	GGAAAACATC	840
CTGGAGTACC	GGCAGGTGCC	TGGCAGTGAT	CCTGCACGGT	ATGAGTTTCT	GTGGGTGCCA	900
AGGGCTCATG	GTGAAATTAG	GAAGATGAGT	CTCCTGAAAT	TTTTGGCCAA	GGTAAATGGG	960
AGTGATCCAA	GATCCTTCCC	ACTGTGGTAT	GAGGAGGCTT	TGAAAGATGA	GGAAAGAGAG	1020
GCCCAGGACA	GAATTGCCAC	CACAGATGAT	ACTACTGCCA	TGGCCAGTGC	AAGTTCTAGC	1080
GCTACAGGTA	GCTTCTCCTA	CCCTGAATAA				

Seq ID NO: 226 Protein sequence:
Protein Accession #: NP_066386

85

1	11	21	31	41	51	
MPRAPKRQRC	MPEEDLQSQS	ETQGLEGAQA	PLAVEEDASS	STSTSSSFPS	SFPSSSSSSS	60

SSCYPLIPST PEEVSADDET PNPPQSAQIA CSSPSVVASL PLDQSDGESS SQKEESPSTL 120
 QVLPDSSESLP RSEIDKVD TD LVQFLLFKYQ MKEPITKAEI LESVIKNYED HFPLLPSEAS 180
 ECLMLVFGID VKEVDPTGHS FVLVTSGLT YDGM LSDVQS MPKTGILILI LSIIFIEGYC 240
 TPBEVIWEAL NMMGLYDGM HLIYGEPRKL LTQDWDVQENY LEYRQVPGSD PARYEFLWGP 300
 RAHAERIKMS LLKPLAKVNG SDPRSFLPWY EEALKDEBER AQDRIATD TD TTAMASASSS 360
 ATGSFSYPE

Seq ID NO: 227 DNA sequence
 Nucleic Acid Accession #: NM_005025.1
 Coding sequence: 82-1314

1 11 21 31 41 51
 | | | | |
 GCGGAGCACA GTCCGCCGAG CACAAGCTCC AGCATCCCGT CAGGGGTGTC AGGTGTGTGG 60
 GAGGCTTGAA ACTGTACAA TATGGCTTTC CTGGACTCT TCTCTTGCT GGTCTGCAA 120
 AGTATGGCTA CAGGGGCCAC TTCCCTGAG GAAGCCATG CTGACTGTGC AGTGAATATG 180
 TATAATCGTC TTAGAGCCAC TGGTGAAGAT GAAAATATTC TCTTCTCTCC ATTGAGTATT 240
 GCTCTTGCAA TGGGAATGAT GGAACCTGGG GCCCAAGGAT CTACCCAGAA AGAAATCCGC 300
 CACTCAATGG GATATGACAG CCTAAAAAAT GGTGAAGAAT TTTCTTTCTT GAAGGAGTTT 360
 TCAAACATGG TAACTGCTAA AGAGAGCCAA TATGTGATGA AAATTGCCAA TTCCTTGTTT 420
 GTGCAAAATG GATTTTCATG CAATGAGGAG TTTTTCGAAA TGATGAAAAA ATATTTTAAT 480
 GCAGCAGTAA ATCATGTGGA CTTAGTCAA AATGTAGCCG TGGCCAACTA CATCAATAAG 540
 TGGGTGGAGA ATAACACAAA CAATCTGGTG AAAGATTGGG TATCCCAAG GGATTTTGAT 600
 GCTGCCACTT ATCTGCCCTT CATTAATGCT GTCTATTTC AAGGGAACTG GAAGTCGCGA 660
 TTTAGGCTG AAAATACTAG AACCTTTTCT TTTACTAAAG ATGATGAAAG TGAAGTCCAA 720
 ATTCCAATGA TGTATCAGCA AGGAGAATTT TATTATGGGG AATTTAGTGA TGGCTCCAAT 780
 GAAGCTGGTG GTATCTACCA AGTCTTAGAA ATACCATATG AAGGAGATGA AATAAGCATG 840
 ATGCTGGTGC TGTCCAGACA GGAAGTTTCT CTGTCTACTC TGGAGCCATT AGTCAAAGCA 900
 CAGCTGGTGG AAGAATGGGC AAACCTCTGT AAGAAGCAAA AAGTAGAAGT ATACCTGCCC 960
 AGGTTACAG TGAACAGGA AATTGATTAA AAAGATGTTT TGAAGGCTCT TGAATAAAT 1020
 GAAATTTTCA TCAAAGATGC AAATTTGACA GGCCTCTCTG ATAATAAGGA GATTTTCTT 1080
 TCCAAGCAAA TTCACAAGTC CTTCTAGAG GTTAATGAAG AAGGCTCAGA AGCTGCTGCT 1140
 GTCTCAGGAA TGATTCAAT TAGTAGGATG GCTGTGCTGT ATCTCAAGT TATTGTGAC 1200
 CATCCATTTT TCTTTCTTAT CAGAAACAGG AGAAGCTGTA CAATCTATT CATGGGACGA 1260
 GTCATGCATC CTGAACAAT GAACACAAGT GGACATGATT TCGAAGAACT TTAAGTTACT 1320
 TTATTGGAAT AACAAGGAAA ACAGTAACTA AGCACATTAT GTTTGCAACT GGTATATATT 1380
 TAGGATTGT GTTTTACAGT ATATCTTAAG ATAATATTTA AAATAGTTCC AGATAAAAA 1440
 AATATATGTA AATTATAAGT AACTGTGCAA GGAATGTTAT CAGTATTAAAG CTAATGGTCC 1500
 TGTATGTCA TTGTGTTTGT GTGCTGTTGT TTAATAATAA AGTACCTATT GAACATGTG

Seq ID NO: 228 Protein sequence:
 Protein Accession #: NP_005016.1

1 11 21 31 41 51
 | | | | |
 MAFLGLPSLL VLQSMATGAT FPPEAIADLS VMYNNRLRAT GEDENILFSP LSIALAMGMM 60
 ELGAQGSTQK EIRHSMGYDS LKNGEEFSFL KEFSNMVTAK ESQVVMKIAN SLFVQNGFHV 120
 NEEFLQMKMK YNAAVNVHVD FSQNVAVANY INKVVNNNTN NLVKDLVSPR DFDAATYLLAL 180
 INAVYFKGNW KSQFRPENTR TFSFTKDDDES EVQIPMMYQQ GEFYYGEFSD GSNEAGGIYQ 240
 VLEIPYEGDE ISMMLVLSRQ EVPLATLEPL VKAQLVEEWA NSVKKQKVEV YLPRFTVEQE 300
 IDLKDVLKAL GITEIFIKA NLTLGLSDNKE IFLSKAIHKS FLEVNEEGSE AAASVGMIAI 360
 SRMAVLYPQV IVDHPFFFLI RNRRTGTILF MGRVMHPETM NTSGHDFEEL

Seq ID NO: 229 DNA sequence
 Nucleic Acid Accession #: NM_003695
 Coding sequence: 12-398

1 11 21 31 41 51
 | | | | |
 CGACATCAGA GATGAGGACA GCATTGCTGC TCCTTGCAAG CCTGGCTGTG GCTACAGGGC 60
 CAGCCCTTAC CTGCGCTGC CACGTGTGCA CCAGCTCCAG CAACTGCAAG CATCTGTGTG 120
 TCTGCCCGGC CAGCTCTCGC TTCTGCAAGA CCACGAACAC AGTGGAGCCT CTGAGGGGGA 180
 ATCTGGTGAA GAAGGACTGT GCGGAGTCGT GCACACCCAG CTACACCCCTG CAAGGCCAGG 240
 TCAGCAGCGG CACCAGCTCC ACCCAGTGCT GCCAGGAGGA CCTGTGCAAT GAGAAGCTGC 300
 ACAACGCTGC ACCCACCCGC ACCGCCCTCG CCCACAGTGC CCTCAGCCTG GGGCTGGCCC 360
 TGAGCCTCCT GGCGTCATC TTAGCCCCCA GCCTGTGACC TTCCCCCAG GGAAGGCCCC 420
 TCATGCCTTT CCTTCCCTTT CTCTGGGGAT TCCACACCTC TCTTCCCCAG CCGGCAACGG 480
 GGGTGCCAGG AGCCCCAGGC TGAGGGCTTC CCCGAAAGTC TGGGACCAGG TCCAGGTGGG 540
 CATGGAATGC TGATGACTTG GAGCAGGCC CACAGACCCC ACAGAGGATG AAGCCACCCC 600
 ACAGAGGATG CAGCCCCCAG CTGCATGGAA GGTGGAGGAC AGAAGCCCTG TGGATCCCCG 660
 GATTTCACAC TCTTCTGTGT TTGTTGCCGT TTATTTGTGA CTCAATCTC TACATGGAGA 720
 TAAATGATT AAAC

Seq ID NO: 230 Protein sequence:
 Protein Accession #: NP_003686

1 11 21 31 41 51
 | | | | |
 MRTALLLLAA LAVATGPALT LRCHVCTSSS NCKHSVVCPA SSRFCKTTNT VEPLRGNLVK 60
 KDCAESCTPS YTLQGQVSSG TSSTQCCQED LCNEKLHNAA PTRTALAHS LSLGLALSLL 120
 AVILAPSL

Seq ID NO: 231 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 126-752

	1	11	21	31	41	51	
	CCGGGCGAGGT	GGCTCATGCT	CGGGAGCGTG	GTTGAGCGGC	TGGCGCGGTT	GTCTTGAGGC	60
5	AGGGGCGCAG	GAATTCCTGAT	GTGAAACTAA	CAGTCTGTGA	GCCCTGGAAC	CTCCACTCAG	120
	AGAAGATGAA	GGATATCGAC	ATAGGAAAAG	AGTATATCAT	CCCCAGTCTCT	GGGTATAGAA	180
	GTGTGAGGGA	GAGAACCAGC	ACTTCTGGGA	CGCACAGAGA	CCGTGAAGAT	TCCAAGTTCA	240
	GGAGAACTCG	ACCGTTGGAA	TGCCAAGATG	CCTTGGAAAC	AGCAGCCCGA	GCCGAGGGCC	300
	TCTCTCTTGA	TGCCTCCATG	CATTCTCAGC	TCAGAATCCT	GGATGAGGAG	CATCCCAAGG	360
10	GAAAGTACCA	TCATGGCTTG	AGTGCTCTGA	AGCCCATCCG	GACTACTTCC	AAACACCAGC	420
	ACCCAGTGGG	CAATGCTGGG	CTTTTTCCT	GTATGACTTT	TTCGTGGCTT	TCTTCTCTGG	480
	CCCGTGTGGC	CCACAAGAAG	GGGGAGCTCT	CAATGGAAGA	CGTGTGGTCT	CTGTCCAAGC	540
	ACGAGTCTTC	TGACGTGAAC	TGCAGAAGAC	TAGAGAGACT	GTGGCAAGAA	GAGCTGAATG	600
	AAGTTGGGCG	AGACGCTGCT	TCCCTGCGAA	GGGTTGTGTG	GATCTTCTGC	CGCACCAGGC	660
15	TCATCCTGTC	CATCGTGTGC	CTGATGATCA	CGCAGCTGGC	TGGCTTCAGT	GGACCAAATT	720
	TTCAAGATGG	CTGTATTCTG	CGGTGAGAAT	GAGAGAGTCA	AGCTGGGCAG	AATCTCTCGC	780
	CAAGAGTTCA	GGCTTCTTTG	GGAGACTGCT	CCATCAGTGC	CGAGGTGTGT	GGGAACAGGC	840
	TTCACTGCAC	CGCCATCTTA	CTGAGTTGCT	TCACGTGAGG	AAAAGGGGGC	TTTGGCCCTG	900
	TGACTCAGTT	CCAGTATTTG	GATTGATATC	TGGAAAAGAA	GCCAACTCTC	TTGCTAGTAA	960
20	ACCAAGCAAC	CGAGCTGATA	CAGTGGTGAC	CCAAGCAATG	GATATAAACC	TAAAAATCTG	1020
	AGGGAGGGGA	GAGGTGGAAT	ACAGTAGTTC	TTGGAATCTG	AAGTCTCCTA	TTTGATCAGG	1080
	TTATTTCTGT	GGACTTGGCA	AAAATCTGAT	TGGTGGGGAT	CTCCTAGGAC	CTAGTGGACA	1140
	TCTGGTATTA	ATTAACTCTC	AGGAAAAACA	AGAAATTAAC	CCAGAGAGAG	TCTGGGTTTT	1200
	GGAATTCAGC	GTAGTACCTT	CCAGACCGTG	GTGTCTGGCC	TCCATTTTTC	TCTGTCTATC	1260
	AGCTCTGACT	TACAGCTGCA	GTCACTTTTG	CTATAAGGCA	CCTGGGTAGA	AGGGTGGATG	1320
25	GGCTTCACT	CAATTTTCTT	CTTCTTTTAG	GGTGGGGGAT	TGGTTTGGCT	TTCTTTTGTG	1380
	GTGGTTTTTT	GTTTTATTTT	TGTCAAGATT	GATTTTTTGA	TGCAAGGACT	TGAAAAGACC	1440
	CAGAAGGATG	CCACCAAGTT	TTCTTTGAGG	CCTAGGATTT	TTTATTCTGT	CCCCAGCAGA	1500
	GGTAATTCCT	CACAACCTTAG	TGCACCAGTA	GCACCAGCCA	TTTGTAGCAG	AGTACCTCTT	1560
	TGGGGAGGCT	TTGTTTGTGT	TTTGTTTTTA	ATTCTCTTTC	CTTAGCAGCA	AGGTCTTTTT	1620
30	TCCTAGAGAA	TCTACTCCGT	TGCAGAACTA	TTGCAACCTC	AGGAGCCCTC	ACTGATTGAG	1680
	TGCTGTGAGC	CTGATATACT	ACTTTGGACT	CTGGAAACAG	ATATGGGTTT	TATTCTCTAT	1740
	TTCTACTGTG	TGTCGTTAAA	CAACCGTCGG	AGACCAGATG	ACCTGTTAGA	TGGCTAGTCC	1800
	TGTATAACTC	GACTCTGTAT	GTTTCAATGT	ATGTTACTGC	AATGCTTCAC	CTGCTGTACA	1860
35	GTGTTGTGTA	GATGCTCTTT	GAAGATGGTA	CTTTTATATT	T		

Seq ID NO: 232 Protein sequence:
Protein Accession #: Eos sequence

	1	11	21	31	41	51	
40	MKDIDIGKEY	IIPSPGYRSV	RERTSTSGTH	RDREDSKFR	TRPLECQDAL	ETAARAEGLS	60
	LDASMHSQLR	ILDEEHPKKG	YHGLSALKP	IRTSKHQHP	VDNAGLFSCM	TFSWLSLLAR	120
	VAHKKGELSM	EDVWSLSKHE	SSDVNCRRL	ELWQEBELNE	GPDAASLRV	WVIFCRTRLI	180
45	LSIVCLMITQ	LAGFSGPNFQ	DGCILRSE				

Seq ID NO: 233 DNA sequence
Nucleic Acid Accession #: CAT cluster

	1	11	21	31	41	51	
50	TTTAAATGGT	GCTCATATAT	ACTGTATTTT	TGTTGTTTTA	GTTTACTTCA	TTGAGAGTGT	60
	CACAACATGA	ATCACATAAT	CATGATTTT	TTTTTTTACT	TTTACTCCCC	AAATTATTTCA	120
	TGTTTCTTAG	ATCGTAGTCA	TTGAGAAGTC	CCAATAACTC	TAACTTTTTC	AGTTATAACG	180
	TAGTAAACTT	CTCTTTCATC	TTTGTGTTAG	CTCTGTAGTC	TAACTCTGGA	TTTAAATTTT	240
55	TTTGTTTCCA	AAGTCACAAT	TGAATTATTC	TTAGATACCT	TAAAGCACTG	AATTCAGTTC	300
	TGTTTGACTG	AAAGCAAAAC	AACGTGACAG	TTTATTTTCA	AACACTAACT	TCTTGATATT	360
	TTGTTATGGT	ATATCTTTTT	ATTAAATATT	TATTTTGACT	AAGCTTTCAT	AAAATATTTG	420
	AAGCTATTTT	AATCATCAAG	TATGGAAAAC	AAATTACTAT	TGCATTTTCC	TATATATGCA	480
60	TATATTATGG	ATTAAACCAGA	ATTGTATCAT	TTTTGGCCTA	ATGCTCGGAT	ATAAAAGATA	540
	ATTAGCCTAC	TATAGTATTA	ATAAATTTT	CAGTTGGTTT	GGGCAAAATT	AAACCTGAAA	600
	AATAGGTTAA	AAAGTAGTTA	CAAATTAAC	TTACTAATTT	ATACCTGATT	TTTTTCTTTC	660
	AATTAAGGTA	CATTTTAAAT	GAGCTTTATA	ATACCTTAAA	AAGTTGGTTC	TAATTTAAAA	720
	TATGAAAGCT	CTGGCTATCA	TCTGGGATA	GTAATTTCTA	ATTATATAGT	ATTTCAAAAC	780
	TATATATTTT	TTAGTTCCTT	TGAGATAACT	AATTTCTAAT	TATATATGTT	TCAAAAACCA	840
65	TATCCTGTAT	TTTTTTTAA	AATTGTTTTA	TAAATAGGTC	ATAAGATACA	AGGTCTGCAT	900
	TAGAAGACCC	ACTCTTACTA	GGTCCCTCAA	GGATCTGCCA	TAGATTTTTC	TTTTTTTTTT	960
	TTTTTTTTCG	GTAGTTTAAA	GCAAGCACTG	ATACCAAGTG	GAGTTGGTCT	TGATCTAGGA	1020
	GATTCTGTGA	AGCATCCAAA	AACAATGCCT	AATTTTCAGT	CTTAGGTTAT	GGCTTGTGAC	1080
70	TCCAGATAAA	AGATGGAGAA	TACCTCATGT	ACTGTGACTT	GAAATGAAT	TCTTAAATTT	1140
	CTTAGGCTCT	CTCCATGTAT	CTTTCTTAAG	GAAAAGTTTC	TGAGTGTGAT	CTCTCTTTTC	1200
	CCATAGTATC	AAGTGGAGGG	TAGTTTCAGAA	AAGTTAATAG	GAAATCTTTT	GTGACAGCAG	1260
	ACTATAATAG	AAGTTTGAGT	AATATTTTAA	TAAATTTATA	TAATTCAAAT	GATAAAAATG	1320
	TATCAATGTT	ATCCAATGAT	TTTTATTAAA	AAATTACCTT	ATTATTAGAA	CTGTGCCTAT	1380
75	TACATAAAAA	GTGCTCATGT	ATTTGAATTT	TAAATAATTT	ATTTAAATCA	AGACCACCAT	1440
	AAGTCATTAA	TAAATTAATA	ATTGTTTAAA	ATCAGTGGTT	TTCACCCCTC	ACTTCATATT	1500
	AGAACTATCT	GAGGACTTTT	AATATGGAAT	CCACCTCATA	ACAATTAAGT	CTAAATTTCT	1560
	GGAAGATGGA	GCCATGCTTG	TTTTTCCAAA	AGCTCTTTGA	GTGATTCTAA	TTTGTAGTCA	1620
	GAGTTGAAGA	CCACTGCTCT	AAATTAGTGC	AGGAAAATGC	TTTTATTTC	CCCATGTTAA	1680
80	CTTTTAAAC	TAGTAATGTA	CCCAGTTAAG	TTTTGTAGGT	TAAATTTCCA	CTAAAGAAC	1740
	TATTCCTTCTA	ATAACTAGCA	TTTATTACAT	GAAATTTAAG	AGTTTAAAGT	CCATCAAACT	1800
	AGCCCTTGTG	TAAAGATTAT	ATTTCTTCTC	TATAACTTCA	AAATAGATAT	TTCAATCAAA	1860
	CTGTTCAAGT	GAGAAAACAT	AATGGATTTT	TTTTTTTTTC	CTCTGGAGCT	CTCTGTTTCA	1920
	TGAGATGGAG	GAGGTGGGCA	CATTTAAGGT	CAGTTCACTA	ACCTATGGTT	CAGAGTTCTG	1980
	ATCATATGGA	AGTTTGGAAA	AGAGAGCTTA	TCACAGGTTT	GTATGCTGGT	GAATGGATAG	2040
85	TTTTAATCT	CACGTCTCTA	AAAGAGAATC	AGCTCTCCAG	CAGTTCTAGA	AAAGCTTTGA	2100
	CAATCCCCAA	GGGGCAGTGT	TACCTTACTC	CTTCACTGCT	TCTTAGAAGG	TAGAATTAAG	2160
	TTTCTGGAAT	TGCACCTACA	TGTTTTCTTA	TTAACATTCA	GAAATGGGAA	TATTAATTTT	2220

TCCAGTGAAGT AGTTTTCTGA AATTGGTAAC TTGGAGAGTA AAATAACGTA TTTTGCTTTT 2280
 CAATTTTGTG TTTGTTTACT TTTATGTAAG AATTGTATAT GTGAATTACA CAGTTCTAAT 2340
 AAAACCTCAT GCCTTTTCAT TACATCTAAT TTGAACCTCTC AACTTCAGTG CCAGAAGTGC 2400
 TTTAAAGATG CTTTAAATGA AAGTATTAAG AAAATATATA GATTGTATG TCAGTTTATA 2460
 CTTTCAGAAAT CCATATATTT GTCATATTTA TTTTITTAGA AACCTCCTAA TTGGATAACT 2520
 AGATGGTATT TAAATGAAT GCCCAAAAT ATCTGTATACC TTGTCCAAA AGTTTATCTG 2580
 TTGGAAGCCG CCAGCCATTC ATGTAGAGAG TTTATAAGAA AATAATTTAA AATTGTATGC 2640
 ATTTTATATT ACTATGGTAT CTGTGTACCA TATTTCTAAG TATTCATTAT TAAATTGGTA 2700
 CTTCTTAAAA CCATAACCTG GCTTGCCCTT TAGTGTATAA CACAAAATCC AACATTGTAT 2760
 ATAGAGATTG TTCTTTTATG AAGAAGAGCT GACGTAATTT ATTACCAGTG CATCTGCACA 2820
 AAGACATTAA CATAAGTCTC TGAGCAGTGA TACATTTTCA AACATGAAGA GTGACAACCA 2880
 CCACATTAAA CAACCCAGCGC AACACTCAGA CTGTGGCACTT TCCTACGAAT CCATCCTATA 2940
 TGTGCCTGGT ATGCGCTCTG GCATAACTTA CACGAATCGT CCTCCCTACT TGTCTACGCT 3000
 CCTTCATCAA GCACTTGCCA ACACATTACAC CTCTAACTTG TACAACCTTA CCAACTCACC 3060
 ACAACATCTG CAACTCTACC CTATCAACTG CCAACCTAAA GACCCCCAAC ACAACACAAC 3120
 CCCCAACAC AAAACCACTA AATCATAACC ACCACACACG CCACACACCA CACACCCACC 3180
 CACACAACCA ACACACACG ACCAAACACC CCACCACAAA CAAGCTAACA ACCACAAACA 3240
 GACACACAT CACATACACT CACTACCCCC CCATACCTCC ACCCACC

Seq ID NO: 234 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 27-281

1 11 21 31 41 51
 AGCAGGAGGA GAGCTGGCGG GAAGACATGC ACCCCTTGAA GACCCAGAGA GAGGCCGTCT 60
 GTCTACCGCG TAGCAGTTAC ATCAGACTGA GACACTTCCT GTTTACAGGA GACTATAAAA 120
 TTCTGCCCC GTGCTCATTT GGGGCTGACG CCATTTTAGG CCTCAGCCCA TCTGCACCCA 180
 GGCCTCACT GAAACAGTGT GTTGCTCCAC ACCGCCTGT TTTGCTTGT GCGCGCTCT 240
 CAGGGTCCG ACCAATCCAA GAGCCTTGCA GAAAGCATT ACGTGCTTT CTCTTTGGCA 300
 GAGTTTTCT TTGCTCTGAT CTTGGAGACA TCCCTCTGCC TAGTGGAAAC ATAAGGAATA 360
 CAGAAAGAA AGAAGGAGAT AGACCAACGT GAGATTCTCC TTCATGCACT CAAGAGAAAG 420
 ATGTTGCAGG AAGAGCTAGT CTTTCAGGCT GGGCTGGTGA CTTGAGAAAG AATGTCCAGC 480
 TTTTCTTCT CACTTGGCAT ATCAAGAGCC AGGCGTGGAA GACTAAAACA GGAAATGTTT 540
 ATAAAACTG TTCAGCGGTT CGCCAACAAG AAGTGGTAAA GTAGCAAAAA TGGGGATGGA 600
 GATGCCAGGA GGAAGATGCG CAGGGGTAAA GTGGGAAAT GGAACCTGA AGCCAGGAGG 660
 TCAAGCCAGG CCAACAGGTG TTTCTTTTTT CATCACAGAA CTAATAAGTG GTGCTGAGGA 720
 CTAAACCCG GGAAGGCCCA CTCTAGAACC CATGCTGGTC ATCCATATCC CCAAGGCCCT 780
 GGTCAAGACA CAGCTAAGCA GATGGCTTGG GTCATCAGGA CGTCCATTAC ATCCAAGGA 840
 AGACAGCCTG TGACGTTTCA AAAGCAAAAG TCCCTACCA GCCAGTGAAG CTACCTGATT 900
 TCTCAGTATC TTACGCCAGG TGACACGATC TACCCTCAA ACTTAAAAAA AAAAGGGAAA 960
 CATAACACA TAACAGCAGC AGCAATAATT AAAGATGAGA TGAGAACAA TAAGAAAAAA 1020
 GGAAAGGTCT CCTGTGACTG TTTTATTTTT AGGGAACAG AGAGGAAGAA GAATGATTTT 1080
 TCTTTGATG ACTCTATATC CAACTCTGAG GTTTGATTAA AGAAATGACC TTGAACCACA 1140
 GCAAGAAAA ATAAAGACA ATTTCCAGTA AGTATGCCAG TTGGAATTAA TGATTTACTT 1200
 TTTATTTTAA AACTGAATTC AGCAGAGATT TACATGCATT ACGATGATTA ACATCTGAAA 1260
 TTTGACCTG AAATAATCTT TACATTGTAA ATTCTTAATG ATCAAAACAA GGTCTCAGT 1320
 GATTAAAAA TATTAGTAAT TAATTATTAA AGGAGAATAA TTGCAATAC AACATTCTTA 1380
 AAATCTCAAG GCTTTTAAAG CATTGTGACA AATGACTGGA CATTTTTTAA ATTTGAAAAA 1440
 AAAAAAAGC CTTGAGCTCG ATTCTCATTT TCATTGTGAG TGCAACAAAC AAAAAGGTAT 1500
 GCACCTCTCT TCTCATTTTC CACTGTCTCG CAAGCTAGAA ATTCTCACGA CTACCTTTGA 1560
 TCCCATCAA GCCAAAGAAA GAAAGAAAAA TTGTTCTGTA CAGATATATG ACATTAATAA 1620
 ATAAATCCC

Seq ID NO: 235 Protein sequence:
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 MHPLKTQREA VCLPRSSYIR LRHFLFTGDY KIPAPCSFGA DAILGLSPSA PRRSLKQCVA 60
 PHRLVLLVGA LSGFRPIQEP CRKH

Seq ID NO: 236 DNA sequence
 Nucleic Acid Accession #: NM_002075
 Coding sequence: 406..1428

1 11 21 31 41 51
 CCACAATAGG GGCAGACCTG TCCATCCTTC TCTGTGGGTC CCCTGTACCT TTCTCCCCCA 60
 ACAGGATCAG ACCCAGAGGC AGCTGGTTGG GGTGTGCGA GAAGAAGGAT TATCCAGATC 120
 AGTCCTTTCT AATCTCAGCT CCTGCCTGTA CCTCCCATTA CTCACCAAAC CCTCTTCCCC 180
 ACCACCTTGA GCTGAGGAGC ACAGTTTGAG GCCCCCCCAA CCCCCCGCGG GTCGGGGCCA 240
 GGCAGGCCA GTCCAGCTTC TCTGGCAGCA GAGCCTGGGC AGGTGACGGG CGGGCGCGGG 300
 CGTCGCAGCT GAGGGAGTAA GGAGGCTCCC AGGAACCGGA GCTGGAACCC CGGCCGAGGT 360
 CCAGCCAGAG CCCAAGAGCC AGAGTGACCC CTCGACCTGT CAGCCATGGG GGAGATGGAG 420
 CAACTGCGTC AGGAAGCGGA GCAGCTCAAG AAGCAGATTG CAGATGCCAG GAAAGCCTGT 480
 GCTGACGTTA CTCTGGCAGA GCTGGTGTCT GGCCTAGAGG TGGTGGGACG AGTCCAGATG 540
 CGGACGCGGC GGACGTTAAG GGGACACCTG GCCAAGATTT ACGCCATGCA CTGGGCCACT 600
 GATTCTAAGC TGCTGGTAAAG TGCCTCGCAA GATGGGAAGC TGATCGTGTG GGACAGCTAC 660
 ACCACCAACA AGGTGCAGCG CATCCCACTG CGCTCCTCCT GGGTCATGAC CTGTGCCTAT 720
 GCCCCATCAG GGAACCTTGT GGCATGTGGG GGGCTGGACA ACATGTGTTT CATCTACAAC 780
 CTCAATCCC GTGAGGGCAA TGTCAAGGTC AGCCGGGAGC TTTCTGCTCA CACAGGTTAT 840
 CTCTCCTGCT GCCGCTTCTT GGATGACAAC AATATTGTGA CCAGCTCGGG GGACACCACG 900
 TGTGCCTTGT GGGACATTGA GACTGGGCAG CAGAAGACTG TATTTGTGGG ACACACGGGT 960
 GACTGCATGA GCTGGCTGTG GTCTCCTGAC TTCAATCTCT TCATTTGCGG GGCCTGTGAT 1020
 GCCAGTGCCA AGCTCTGGGA TGTGCGAGAG GGGACCTGCC GTCAGACTTT CACTGCGCAC 1080

GAGTCGGACA TCAACGCCAT CTGTTTCTTC CCAATGGAG AGGCCATCTG CACGGGCTCG 1140
 GATGACGCTT CCTGCCGCTT GTTTGACCTG CGGGCAGACC AGGAGCTGAT CTGCTTCTCC 1200
 CACGAGAGCA TCATCTGGGG CATCACGTCC GTGGCCTTCT CCCTCACTGG CCGCTACTA 1260
 TTCGTGGCT ACAGCACTT CAACTGCAAT GTCTGGGACT CCATGAAGTC TGAGCGTGTG 1320
 GGCACTCCTT CTGGCCACGA TAACAGGGTG AGCTGCCTGG GAGTCACAGC TGACGGGATG 1380
 GCTGTGGCCA CAGGTTCTTG GGACAGCTTC CTCAAATCT GGAACCTGAGG AGGCTGGAGA 1440
 AAGGGAAGTG GAAGGCAGTG AACACACTCA GCAGCCCCCT GCCCGACCCC ATCTCATTCA 1500
 GGTGTTCTCT TCTATATTCC GGGTGCCATT CCCACTAAGC TTTCTCCTTT GAGGGCAGTG 1560
 GGGAGCATGG GACTGTGCTT TTGGGAGGCA GCATCAGGGA CACAGGGGCA AAGAACTGCC 1620
 CCATCTCTCT CCATGGCCTT CCTTCCCCAC AGTCCTCACA GCCTCTCCCT TAATGAGCAA 1680
 GGACAACTCG CCCCTCCCCA GCCCTTTGCA GGGCCAGCAG ACTTGAGTCT GAGGGCCAG 1740
 GCCCTAGGAT TCCTCCCCCA GAGCCACTAC CTTGTGCCAG GCCTGGGTGG TATAGGGCGT 1800
 TTGGCCCTGT GACTATGCTT CTGGCACCAC TAGGGTCTTG GCCCTCTTCT TATTTCATGT 1860
 TTCTCCTTTT TCTACCTTTT TTTCTCTCCT AAGACACCTG CAATAAAGTG TAGCACCTTG 1920
 GT

Seq ID NO: 237 Protein sequence:
 Protein Accession #: NP_002066

1 11 21 31 41 51
 | | | | | |
 MGEMEQLRQE AEQLKKQIAD ARKACADVTL AELVSGLEV GRVQMRTRRT LRGLHLAKIYA 60
 MHWATDSKLL VSASQDGKLI VWDSTYTNKV HAIPLRSSWV MTCAYAPSGN FVACGGLDNM 120
 CSIYNLKSRE GNVKVSRELS AHTGYLSCCR FLDDNNIVTS SGDITCALWD IETGQKTVF 180
 VGHTGDCMSL AVSPDFNLFI SGACDASAKL WDVREGTCRQ TFTGHESDIN AICFFPNGEA 240
 ICTGSDDASC RLFDLRADQE LICFSHESII CGITSVAFSL SGRLLFAGYD DFNCNVWDSM 300
 KSERVGLISG HDNRVSLGLV TADGMAVATG SWDSFLKIWN

Seq ID NO: 238 DNA sequence
 Nucleic Acid Accession #: CAT cluster

1 11 21 31 41 51
 | | | | | |
 TCCCAATGTG TNGAACCTAC CATAAATTCT TTTCTTACNG GACAACTCTA TNCTAANCAA 60
 TACCAATTGC TTTTAAGGCA GATAATCCTC CAAGTTTCTT AATGATATCT GAAACTATTA 120
 ACTGATTCTG TGAATTATGA AATCTGAAAA GGAATTGGAA GTTGCTAAAA ATCTATCATT 180
 TGCATTGACC AGTGTGAGC ACAGTGGAAAT GAGAATGCGT GCCCTGACAC CAAAGAAAAA 240
 TAAGTGACTG GAAAGCTGAA GAATCACCGG CTTCACTGAC ATGGAACCCA GTGATTGTAT 300
 TTTTGACGAG TATCGGGTGA CTTTGAGGTG GTCAAGAAAC CACACTTTAA GAACAATGTC 360
 CAAAAAGGGG AAAAAAAGA GCAACCAAAAG AAAAAAATC CATAAAATG CACAGAAGAA 420
 AAGAAAGAAA AATAAAATAC ACAAATATGGA CGATGGAGAA AAACAGTTAC ATTTCTTTAT 480
 GGATCAAGAA GTTTGTGTAC ACATAATCTC ATTTTGAGAT ATATACTAT TTTTGTCTTT 540
 CAGAAGTGAA TCAAAATATT TCAAAATGCT GTCTTATGAA ACTACAATAT TCTCACAGAT 600
 TAGAAAAATT TTTCTGTAAA AGTCAGATAG TAAATATTTT AGGTTTGGCA GTGTCTTTTG 660
 CAACTACTCA ACTTTCCTAC TGTAGCACAA GAGTAGCTGT GGTACTGTGC AAATAAATTG 720
 CTTGTGTTC AATAAGCTT CATTTACAAA AACATGCCAT GGGCCATATT TGGCCTGTAC 780
 ACTGTTGTTT GCCAAGTCCT AATATAGTTG CTTAGCAAGT ATTGTGAGCT ATTTGAGGAA 840
 GACATGAAAG TTCAATTGGT TGCTAAAAAG TATGTAGAAA TTCAAAGGAA AATTAAATT 900
 TAGGCTAAGT TATAATACAC TGTTTTAAAC ATTGTAAAT GTAAGAGAAA TTTACAAATA 960
 AAAATCCCAA ATAAAA

Seq ID NO: 239 DNA sequence
 Nucleic Acid Accession #: NM_001786.1
 Coding sequence: 130-1023

1 11 21 31 41 51
 | | | | | |
 GGGGGGGGGG GGCACCTGGC TTCAAAGCTG GCTCTTGGAA ATTGAGCGGA GAGCGACGCG 60
 GTTGTGTAG CTGCCGCTGC GGCGCGCGG GAATAATAAG CCGGGATCTA CCATACCCAT 120
 TGACTAACTA TGGAAAGATTA TACCAAATA GAGAAAAATG GAGAAGGTAC CTATGGAGTT 180
 GTGTATAAGG GTAGACACAA AACTACAGGT CAAGTGGTAG CCATGAAAAA AATCAGACTA 240
 GAAAGTGAAG AGGAAGGGGT TCCTAGTACT GCAATTCGGG AAATTTCTCT ATTAAGGAA 300
 CTTGCTATC CAAATATAGT CAGTCTTCAG GATGTGCTTA TGCAGGATTC CAGGTATAT 360
 CTCATCTTTG AGTTTCTTTC CATGGATCTG AAGAAATACT TGGATTCTAT CCTCTCTGGT 420
 CAGTACATGG ATTCTTCACT TGTAAAGAGT TATTTATACC AAATCTTACA GGGGATTGTG 480
 TTTTGTCACT CTAGAAGAGT TCTTCACAGA GACTTAAAC CTCAAATCT CTTGATTGAT 540
 GACAAAGGAA CAATTAACCT GGCTGATTTT GGCTTGCCA GAGCTTTTGG AATACCTATC 600
 AGAGTATATA CACATGAGGT ACTTAACACT TGGTACAGAT CTCCAGAAGT ATTGCTGGGG 660
 TCAGCTCGTT ACTCAACTCC AGTTGACATT TGGAGTATAG GCACCATATT TGCTGAACCTA 720
 GCAACTAAGA AACCACTTTT CCATGGGGAT TCAGAAATG ATCAACTCT CAGGATTTTC 780
 AGAGCTTTGG GCACCTCCAA TAATGAAGTG TGGCCAGAAG TGGAAATCTT ACAGGACTAT 840
 AAGAATACAT TTCCCAATG GAAACCAGGA AGCCTAGCAT CCCATGTCAA AAACCTGGAT 900
 GAAAATGGCT TGGATTGTCT CTCGAAAATG TTAATCTATG ATCCAGCCAA ACGAATTTCT 960
 GGCAAAATGG CACTGAATCA TCATATTTT AATGATTGG ACAATCAGAT TAAGAAAGATG 1020
 TAGCTTTCTG ACAAAAAGTT TCCATATGTT ATGTCAACAG ATAGTTGTGT TTTTATGTGT 1080
 AACTCTTGTC TATTTTGTGC TTATATATAT TTCTTTGTTA TCAAACCTCA GCTGTACTTC 1140
 GTCCTCTAAT TTCAAAAAA TAACCTAAAA ATGTAATAT TCTATATGAA TTTAAATATA 1200
 ATCTGTAAAA TGTGAAAAA AAAAAA AAAA

Seq ID NO: 240 Protein sequence:
 Protein Accession #: NP_001777.1

1 11 21 31 41 51
 | | | | | |
 MEDYTKIEKI GEGTYGVVYK GRHKTTGQVV AMKKIRLESE EEGVPSTAIR EISLLKELRH 60
 PNIVSLQDVL MQDSRLYLIF EFLSMDLKKY LDSIPPGQYM DSSLVKSYLY QILQGIVFCH 120

SRRVLHRLDK PQNLLIDDKG TIKLADFLGA RAFGIPIRVY THEVVTWLWYR SPEVLLGSAR 180
 YSTPVDIWSI GTIFAEALATK KPLFHGDSEI DQLFRIFRAL GTPNNEVWPE VESLQDYKNT 240
 FPKWKPGSLA SHVKNLDENG LDLLSKMLIY DPAKRISGKM ALNHPYFNDL DNQIKKM

Seq ID NO: 241 DNA sequence

Nucleic Acid Accession #: NM_033379.1

Coding sequence: 132-854

1 11 21 31 41 51
 CGCCCGCGCG CGGGCTCAAC TTTGTAGAGC GAGGGGCCAA CTGGCAGAG CGCGCGGCCA 60
 GCTTTGCAGA GAGCGCCCTC CAGGGACTAT GCGTGCAGG ACACGGGATC TACCCATACC 120
 ATTGACTAAC TATGGAAGAT TATACCAAAA TAGAGAAAA TGGAGAAGT ACCTATGGAG 180
 TTTGTATATA GGTAGACAC AAAACTACAG GTCAAGTGGT AGCCATGAAA AAAATCAGAC 240
 TAGAAAGTGA AGAGGAAGGG GTTCTAGTA CTGCAATTCG GGAATTTCT CTATTAAAGG 300
 AACTTCGTCA TCCAAATATA GTCACTCTC AGGATGTGCT TATGCAGGAT TCCAGGTTAT 360
 ATCTCATCTT TGAGTTTCTT TCCATGGATC TGAAGAAATA CTGGATTCT ATCCCTCCTG 420
 GTCAGTACAT GGATTCCTCA CTGTGTAAGG TAGTAACACT CTGGTACAGA TCTCCAGAAG 480
 TATTGCTGGG TCCAGCTCGT TACTCAACT CAGTTGACAT TTGGAGTATA GGCACCATAT 540
 TTGCTGAAGT AGCAACTAAG AAACCACTTT TCCATGGGGA TTCAGAAAT GATCAACTCT 600
 TCAGGATTTT CAGAGCTTTG GGCACCTCCA ATAATGAAGT GTGGCCAGAA GTGGAATCTT 660
 TACAGGACTA TAAGAAATACA TTTCCTCAAT GGAACACAGG AAGCCTAGCA TCCCATGTCA 720
 AAAACTTGA TGAATATGGC TTGGATTGCT TCTCGAAAAT GTTAATCTAT GATCCAGCCA 780
 AACGAATTTT TGCCAAATAG GCACTGAATC ATCCATATTT TAATGATTG GACAATCAGA 840
 TTAAGAAGAT GTAGCTTTCT GACAAAAGT TTCCATATGT TATGTCAACA GATAGTTGTG 900
 TTTTATATGT TAACCTCTGT CTATTTTGT CTATATATA TTTCTTTGTT ATCAAACCTC 960
 AGCTGTACTT CGTCTCTAA TTTCAAAAAT ATAACCTAAA AATGTAAATA TTCTATATGA 1020
 ATTTAAATAT AATTCTGTAA ATGTGAAAAA AAAAAA

Seq ID NO: 242 Protein sequence:

Protein Accession #: NP_203698.1

1 11 21 31 41 51
 MEDYTKIEKI GEGTYGVVYK GRHKTTGQVV AMKKIRLESE EEGVPSTAIR EISLLKELRH 60
 PNIVSLQDVL MQDSRLYLIF EFLSMDLKKY LDSIPPQYIM DSSLVKVVTL WYRSPVLLG 120
 SARYSTPVDI WSGITFAEL ATKPLFHGD SEIDQLFRIF RALGTPNNEV WPEVESLQDY 180
 KNTFPKWKPG SLASHVKNLD ENGLDLLSKM LIYDPAKRIS GKMLNHPYP NDLDNQIKKM

Seq ID NO: 243 DNA sequence

Nucleic Acid Accession #: AF101051.1

Coding sequence: 221-856

1 11 21 31 41 51
 GAGCAACCTC AGCTTCTAGT ATCCAGACTC CAGCGCGGCC CGGGCGCGCG ACCCCAACCC 60
 CGACCCAGAG CTTCTCCAGC GCGCGCGCAG CGAGCAGGGC TCCCGCGCTT AACTTCTCTC 120
 GCGGGGCCCA GCCACCTTCG GAGATCCGGG TTGCCACCT GCAAACTCTC CGCCTTCTGC 180
 ACCTGCCACC CTTGAGCCAG CGCGGGCGCC CGAGCGAGTC ATGGCCAAAC CGGGGCTGCA 240
 GCTGTGGGCT TTCATTCTCG CTTTCTGGG ATGGATCGGC GCCATCGTCA GCACTGCCCT 300
 GCCCCAGTGG AGGATTACTT CCTATGCCGG CGACAACATC GTGACCGCCC AGGCCATGTA 360
 CGAGGGGCTG TGGATGTCTT GCGTGTGCGA GAGCACCAGG CAGATCCAGT GCAAAGTCTT 420
 TGACTCTCTG CTGAATCTGA GCAGCACATT GCAAGCAACC CGTGCCTTGA TGGTGGTTGG 480
 CATCTCTCTG GAGTGTATAG CAATCTTTGT GGCACCGGTT GGCATGAAGT GTATGAAGTG 540
 CTTGGAAGAC GATGAGGTGC AGAAGATGAG GATGGCTGTC ATTGGGGGTG CGATATTTCT 600
 TCTTGCAGGT CTGGCTATTT TAGTTGCCAC AGCATGGTAT GGCAATAGAA TCGTTCAAGA 660
 ATTTCTATGAC CCTATGACCC CAGTCAATGC CAGGTACGAA TTGTGTCAGG CTCTCTTCC 720
 TGGCTGGGCT CTTGCTTCTC TCTGCCCTCT GGGAGGTGCC CTACTTTGCT GTTCTCTGCC 780
 CCGAAAAACA ACCTCTTACC CAACACCAAG GCCCTATCCA AAACCTGCAC CTTCCAGCGG 840
 GAAAGACTAC GTGTGACACA GAGGCAAAAG GAGAAAATCA TGTGAAACA AACCGAAAA 900
 GGACATTGAG ATACTATTAG TAACATTAGG ACCTTAGAAT TTTGGGTATT GTAATCTGAA 960
 GTATGGTATT ACAAACAACA CAAACAACA AAAAACCCAT GTGTTAAAT ACTCAGTGCT 1020
 AAACATGGCT TAATCTTATT TTATCTTCTT TCCTCAATAT AGGAGGGAAG ATTTTACCAT 1080
 TTGTATTACT GCTTCCCATC GAGTAATCAT ACTCAATGG GGAAGGGGT GCTCCTTAAA 1140
 TATATATAGA TATGTATATA TACATGTTTT TCTATTAAAA ATAGACAGTA AAATACTATT 1200
 CTCATTATGT TGATACTAGC ATACTTAAAA TATCTCTAAA ATAGGTAAT GTATTTAATT 1260
 CCATATTGAT GAAGATGTTT ATTGGTATAT TTCTTTTTC GTCCCTATAT ACATATGTAA 1320
 CAGTCAAATA TCATTACTC TTCTTCATTA GCTTTGGGTG CCTTTGCCAC AAGACCTAGC 1380
 CTAATTTACC AAGGATGAAT TCTTTCAATT CTTCATGCGT GCCCTTTTCA TATACTTATT 1440
 TTATTTTTTA CCATAATCTT ATAGCACTTG CATCGTTATT AAGCCCTTAT TTGTTTGTG 1500
 TTTTATTGGT CTCTATCTCC TGAATCTAAC ACATTCATA GCCTACATT TAGTTTCTAA 1560
 AGCCAAGAAG AATTATTATC AAATCAGAAC TTTGGAGGCA AATCTTTCTG CATGACCAAA 1620
 GTGATAAATT CTTGTTGACC TTCCACACA ATCCCTGTAC TCTGACCAT AGCACTCTTG 1680
 TTTGCTTTGA AAATATTGT CCAATTGAGT AGCTGCATGC TGTTCCTCCA GGTGTGTAA 1740
 CACAACCTTA TTGATTGAAT TTTAAGCTA CTATTTCATA GTTTTATATC CCCCTAACT 1800
 ACCCTTTTGT TCCCATCTC TTAATTGTAT TGTTTTCCCA AGTGTAATTA TCATGCGTTT 1860
 TATATCTTCC TAATAAGGTG TGGTCTGTTT GTCTGAACAA AGTGCTAGAC TTTCTGGAGT 1920
 GATAATCTGG TGACAAATAT TCTCTCTGTA GCTGTAAAGCA AGTCACTTAA TCTTCTACC 1980
 TCTTTTTTCT ATCTGCCAAA TTGAGATAAT GATACTTAAC CAGTTAGAAG AGGTAGTGTG 2040
 AATATTAATT AGTTTATATT ACTCTCATT TTTGAACATG AACTATGCCT ATGTAGTGTG 2100
 TTTATTTGCT CAGCTGGCTG AGACACTGAA GAAGTCACTG AAAAAACCT ACACACGTAC 2160
 CTTCAATGTA TTCCTGCTT TCTCTCTCT ACCAGTCTAT TTCCACTGAA CAAAACCTAC 2220
 ACACATACCT TCATGTGGTT CAGTGCCCTC CTCTCTCTAC CAGTCTATT CCACTGAACA 2280
 AAACCTAGCG ACATACCTTC ATGTGGCTCA GTGCCCTTCT CTCTCTACCA GTCTATTTC 2340
 ATCTTTTCAG CTGTGCTGTA CATGTTTGTG CTCTGTCCA TTTTAAACAC TGCTCTTACC 2400
 TTTCCAGTCT GTACAGAATG CTATTTCACT TGAGCAAGAT GATGTATGGA AAGGGTGTG 2460

GCACTGGTGT CTGGAGACCT GGATTGAGT CTTGGTGCTA TCAATCACCG TCTGTGTTTG 2520
 AGCAAGGCAT TTGGCTGCTG TAAGCTTATT GCTTCATCTG TAAGCGGTGG TTTGTAATTC 2580
 CTGATCTTCC CACCTCAGAG TGATGTTGTG GGGATCCAGT GAGATAGAAT ACATGTAAGT 2640
 GTGGTTTTGT AATTGGAATA GTGCTATACT AAGGGAAGA ATTGAGGAAT TAACTGCATA 2700
 CGTTTTGGTG TTGCTTTTCA AATGTTTGAA AATAAAAAAA TGTTAAGAAA TGGGTTTCTT 2760
 GCCTTAACCA GCTCTCTAAG TGATGAGACA GTGAAGTAAA ATTGAGTGCA CTAAACGAAT 2820
 AAGATTCTGA GGAAGTCTTA TCTTCTGCAG TGAGTATGGC CCAATGCTTT CTGTGGCTAA 2880
 ACAGATGTAA TGGGAAGAAA TAAAGCCTA CGTGTGGTA AATCCAACAG CAAGGGAGAT 2940
 TTTTGAATCA TAATACTCA TAAGGTGCTA TCTGTTCACT GATGCCCTCA GAGCTCTTGC 3000
 TGTTAGCTGG CAGCTGAGCG TGCTAGGATA GTTAGTTTGG AAATGGTACT TCATAATAAA 3060
 CTACACAAGG AAAGTCAGCC ACCGTGCTCT ATGAGGAATT GGACCTAATA AATTTTAGTG 3120
 TGCCTTCCAA ACCTGAGAAT ATATGCTTTT GGAAGTAAA ATTTAAATGG CTTTGGCCAC 3180
 ATACATAGAT CTTTCATGAT TGAGAGTGA ATTCCATGTG GATATCAGTT ACCAAACATT 3240
 ACAAAAAAAT TTTATGGCCC AAAATGACCA ACGAAATTGT TACAATAGAA TTTATCCAAT 3300
 TTTGATCTTT TTATATTCTT CTACCACACC TGGAAACAGA CCAATAGACA TTTTGGGGTT 3360
 TTATAATGGG AATTTGTATA AAGCATTACT CTTTTTCAAT AAATTGTTTT TTAATTTAAA 3420
 AAAAGGAAAA AAAAAAATAA AAA

Seq ID NO: 244 Protein sequence:
 Protein Accession #: AAD16433.1

1 11 21 31 41 51
 | | | | |
 25 MANAGLQLLG FILAFLGWIG AIVSTALPQW RIYSYAGDNI VTAQAMYEGE WMSCVQSQTG 60
 QIQCKVFDLS LNLSSLTQAT RALMVVGILL GVIAIFVATV GMCKMKLED DEVQKMRMAV 120
 IGGAIFFLAG LAIVLATAWY GNRIVQEFYD PMTPVNARYE FGQALFTGWA AASLCLLGGA 180
 LLCCSCPRTK TSYTPRPYP KPAPSSGKDY V

Seq ID NO: 245 DNA sequence
 Nucleic Acid Accession #: CAT cluster

1 11 21 31 41 51
 | | | | |
 35 TTTTITTTTT TTTTITTTTT TTTTCAAGG AGAGCACAAG GAACITTTAT AATGACTTTC 60
 TTAATGGTGA AATGCTGTTT ACCAAGTGAC CCAGAGGCAG CGTGGTTTAG TGGTTTCAAC 120
 AGCATGGTCC CGAGAGTCTG ACAAACCTCA GTTCAAATCC TTCTTTTGTG TTCACCTAGT 180
 TTTTCTTCTT GAGATTCTAG TTCTTCATCG TTAACAATGA GGATATTAAAT ATGTTTCACA 240
 CAGTTGTGAT GAAGAATGCA TATATTAGAA TGCCTGTAGT CTCAGTACT CAGGAGGCTA 300
 40 AGGTGGGGAG GTCGCTCAAG CCCAGGAATT CAAAGCTGCA ATGCATTATG ATTACAGCTG 360
 TTAATAGCCA CTGCACTTCA GCCTGGGCAA TGTAGTAAGA TCCCATCTCT GGCTCGGAGG 420
 GTCCTACGCC CACGGAGTCT CGCTGATTGC TAGCACAGCA GTCTGAGATC AAACCTGCA

Seq ID NO: 246 DNA sequence
 Nucleic Acid Accession #: XM_058553.2
 Coding sequence: 897-1400

1 11 21 31 41 51
 | | | | |
 50 AATTTTCAGA AGTTTCGTAT GGGGATGGTT TTATATAAAT TCAGGTTTTT CCCACAATAA 60
 TAAATGTATT TAGTCTCAGT GCTCAATAGA AGAGATTCTT AATAGAAAAG GATTCAAAC 120
 GTGAAACCAT TTCTCTTTTA ATGTTTCACA TTCCTGTTAC AGATTGTGTC TCTTGTGACT 180
 CTGTTATCCA TAATATGGAG AGTCTTGAG TCCTAACATT GAGAGGTTTT CCCTTAGTGC 240
 55 ATAGAGGGAA TGAGTATTAA TTGGAGAAGC TTAAAGTATT GCCACTTTAG CACTGAAGAT 300
 TGGGATGAGA GGAGGTGAAA CCTCACTAGA AAAAGGGACA ATGTTAGTGT GGCCCTTCCT 360
 GATCATGTTT AAGAAAAGTC ATGAAAATGG TGAAGTAGTG TTTCCAAGCA TATTGGAAGG 420
 GTTGAGTGTA TACTGTCTGT CAAAGACTTC CAGCATTTC AGGTCTTAGA GAGGAACAAG 480
 ACTGGTAACC TGCTATCTG TATTTTAAAG AACCAGGAG GAAAGCTTTA TAATAGAACA 540
 60 TTAITTCGTG GTTATGTAT AAGGGGTTTT TTGTTTTTTT AAAGACAGGA TCTCACTCCA 600
 TTGTCCAGGC CAAGTGCAAT GGCACGAACC TCATAGCTCC TGGACTTAAG TGATCTGCCT 660
 GCCTTTGCCT CCGTAGTAGG TGGGACTACA GGCATGAGCC CCCATGCCCT GCTAAGTTTG 720
 TTTTITTTGT TTGTTTGTG TTTGTTTTTG GGGGGGTTG TTTTGTTTTT TGTAGAGACG 780
 TAGTCTTGCT TTGTTGCCAG GCTAGTCTCA AACTCCTGGC TTCAAGTGAT CCTCTGCCT 840
 CAGCTCCCA GAGTGCTAGG ATTACAGCAC TTGATTTCAG CTCTCTCATT TCCAACATGG 900
 65 AAGAACTTA CACCGACTCC CTGGACCCTG AGAAGCTATT GCAATGCCCC TATGACAAAA 960
 ACCATCAAAT CAGGGCTTGC AGGTTTCCTT ATCATCTTAT CAAGTGCAGA AAGATCATC 1020
 CTGATGTTGC AAGCAAAATG GCTACTTGTC CCTTCAATGC TCGCCACCAG GTTCTCTGAG 1080
 CTGAAATTAG TCATCATATC TCAAGCTGTG ATGACAGAAG TTGTATTGAG CAAGATGTTG 1140
 70 TCAACCAAAC CAGGAGCCTT AGACAAGAGA CTCTGGCTGA GAGCACTTGG CAGTGCCCTC 1200
 CTGCGATGA AGACTGGGAT AAAGATTGTT GGGAGCAGAC CAGCACCCTA TTTGTCTGGG 1260
 GCACAACTCA CTACTCTGAC AACCAACAGCC CTGCGAGCAA CATAGTTACA GAACATAAGA 1320
 ATAACCTGGC TTCAGGCATG CGAGTCCCA AATCTCTGCC GTATGTTCTG CCATGGAAAA 1380
 ACAATGGAAA TGCACAGTAA CTGAATACCT ATCTCATCAA ATGCCAGACC CTAGAAGACT 1440
 75 GTTGCTTCTT TCTTACTCAG TGGGTTCTCA TTTTCTCTCT AATCTAATTA TAGAATGGTA 1500
 AACTCCCTGT GACTTTCCAA ACTGACAAGC ACACCTTTTT CTCCCCCTCT TGAATCCTCA 1560
 TTTAATGCAA GAACCTCAT ACTCAGAAGC TTCAAATAA ACCTTTGATA CAGATTG

Seq ID NO: 247 Protein sequence:
 Protein Accession #: XP_058553.1

1 11 21 31 41 51
 | | | | |
 85 MEETYDLSLD PEKLLQCPYD KNHQIRACRF PYHLIKCRKN HPDVASKLAT CFPNARHQVP 60
 RAEISHHIS CDDRSCIEQD VVNQTRSLRQ ETLEASTWQC PPCEDEDWDK LWEQTSTPFV 120
 WGTTHYSNN SPASNIVTEH KNNLASGMRV PKSLPYVLPW KNNGNAQ

Seq ID NO: 248 DNA sequence
Nucleic Acid Accession #: NM_003392
Coding sequence: 758..1855

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1	11	21	31	41	51	
TTAAGGAAAT	CCGGGCTGCT	CTTCCCCATC	TGGAAGTGGC	TTTCCCCACA	TCGGCTCGTA	60
AACGTATTAT	GAACATACG	ATGTTAATTC	GGAGCTGCAT	TTCCGACGTG	GGCACTCTCG	120
CGCGCTGGTC	CCCGGGCCCT	CGCCCCCCAC	CCCCTGCCCT	TCCCTCCCGC	GTCTGTCCCC	180
CATCTCCAC	CCCCCGCGCT	GGCCACCCCG	CCTCCTTGGC	AGCCTCTGGC	GGCAGCGCGC	240
TCCACTCGCC	TCCCGTGCTC	CTCTCGCCCA	TGGAATTAAT	TCTGGCTCCA	CTTGTTGCTC	300
GGCCCAAGTT	GGGAGAGGA	CGAGGGTGG	CCGAGCGGG	TTCTGAGTG	AATTACCCAG	360
GAGGAGCTGA	GCACAGCACC	AACAGAGAG	GGGTGAGGG	GTGCGGACT	CGAGCGAGCA	420
GGAAGGAGGC	AGCGCTGGC	ACCAGGGCTT	TGACTCAACA	GAATTGAGAC	ACGTTTGTAA	480
TCGCTGGCGT	GCCCGCGCA	CAGGATCCCA	GCGAAAATCA	GATTTCTGG	TGAGTTGCG	540
TGGTGGATT	AATTTGGA	AAGAACTGC	CTATATCTTG	CCATCAAAA	ACTCACGGAG	600
GAGAAGCGCA	GTCATCAAC	AGTAACTTA	AGAGACCCCC	GATGCTCCCC	TGGTTTAACT	660
TGTATGCTTG	AAAATTATCT	GAGAGGGAAT	AAACATCTTT	TCCTTCTTCC	CTCTCCAGAA	720
GTCCATTGGA	ATATTAGCC	CAGGAGTTGC	TTTGGGATG	GCTGGAAGTG	CAATGTCTTC	780
CAAGTTCTTC	CTAGTGGCTT	TGGCCATATT	TTTCTCTTTC	GCCGAGGTG	TAATTGAAGC	840
CAATCTTGG	TGGTCGCTAG	GTATGAATAA	CCCTGTTTCA	ATGTCAGAAG	TATATATTAT	900
AGGAGCACAG	CCCTCTGCA	GCCAACTGGC	AGGACTTTCT	CAAGGACAGA	AGAAACTGTG	960
CCACTTGTAT	CAGGACCACA	TGCAGTACAT	CGGAGAAGGC	GCGAAGACAG	GCATCAAGA	1020
ATGCCAGTAT	CAATTCGAC	ATCGACGGTG	GAATGTCAGC	ACTGTGGATA	ACACCTCTGT	1080
TTTTGGCAGG	GTGATGCAGA	TAGGCAGCCG	CGAGACGGCC	TTACATACG	CCGTGAGCGC	1140
AGCAGGGGTG	GTGAACGCCA	TGAGCGGGC	GTGCGCGGAG	GGCGAGCTGT	CCACCTGCGG	1200
CTGCAGCGCG	GCCGCGCGCC	CCAAGGACCT	GCCGCGGGAC	TGGCTCTGGG	GCGGCTGCGG	1260
CGACAACATC	GACTATGGCT	ACCCTTTTGC	CAAGGAGTTC	GTGGACGCCC	GCGAGCGGGA	1320
GCGCATCCAC	GCCAAGGGCT	CCTACGAGAG	TGCTCGCATC	CTCATGAACC	TGCACAAACA	1380
CGAGGCCGGC	CGCAGGACGG	TGTACAACCT	GGCTGATGTG	GCTTCAAGT	GCCATGGGGT	1440
GTCCGGCTCA	TGTAGCCTGA	AGACATGCTG	GCTGCAGCTG	GCAGACTTCC	GCAAGGTGGG	1500
TGATGCCCTG	AAGGAGAAGT	ACGACAGCGC	GGCGGCCATG	CGGCTCAACA	GCCGGGGCAA	1560
GTGTGTACAG	GTCACAGCC	GCTTCAATC	GCCCACCACA	CAAGACCTGG	TCTACATCGA	1620
CCCCAGCCCT	GACTACTGCG	TGCGCAATGA	GAGCACCGGC	TGCTGGGCA	CGCAGGGCGG	1680
CCTGTGCAAC	AAGACGTGCG	AGGCGATGGA	TGGCTGCGAG	CTCATGTGCT	GCGGCCGTGG	1740
GTACGACCAG	TTCAAGACCG	TGCAGACGGA	GCGCTGCCAC	TGCAAGTTC	ACTGGTGCTG	1800
CTACGTCAAG	TGCAAGAAGT	GCAAGGAGAT	CGTGGACCG	TTTGTGTGCA	AGTAGTGGGT	1860
GCCACCCAGC	ACTCAGCCCC	GCTCCAGGA	CCGCTTATT	TATAGAAAGT	ACAGTGATTC	1920
TGGTTTTTGG	TTTTTAGAAA	TATTTTTTAT	TTTTCCCCAA	GAATTGCAAC	CGGAACCAAT	1980
TTTTTCTCTG	TTACCATCTA	AGAACTCTGT	GGTTTATTAT	TAATATTATA	ATTATTATT	2040
GGCAATAATG	GGGTGGGAA	CCAGGAAAA	TATTTATTTT	GTGGATCTTT	GAAAGGTAA	2100
TACAAGACTT	CTTTTGGATA	GTATAGAATG	AAGGGGAAAA	TAACACATAC	CCTAAGTTAG	2160
CTGTGTGGGA	CTGTGTACAC	ATCCAGAAAG	TAAAGAAATA	CATTTTCTTT	TTCTCAATA	2220
TGCCATCATA	TGGATGGGT	AGGTTCCAGT	TGAAAGAGGG	TGGTAGAAAT	CTATTACAA	2280
TTAGCTTCT	ATGACAAAA	TGAGTTGTAA	ATTCTCTGGT	GCAAGATAAA	AGGTCTTGGG	2340
AAAAACAAAC	AAAAACAAAC	AAACCTCCCT	TCCCAGCAG	GGCTGCTAGC	TGCTTTCTG	2400
CATTTTCAAA	ATGATAATTT	ACAATGGAAG	GACAAGAATG	TCATATTCTC	AAGGAAAAAA	2460
GGTATATCAT	ATGTCTCAT	CTCCTCAAT	ATTCCATTG	CAGACAGACC	GTCAATTCT	2520
AATAGCTCAT	GAAATTTGGG	CAGCAGGAG	GAAAGTCCCC	AGAAATTAAA	AAATTTAAAA	2580
CTCTTATGTC	AAGATGTTGA	TTTGAAGCTG	TTATAAGAAT	TGGATTCCA	GATTTGTAAA	2640
AAGACCCCCA	ATGATTCTTG	ACACTAGATT	TTTTGTTTGG	GGAGGTTGGC	TGAACATAA	2700
ATGAAATATC	CTGATTCTTC	TTAGGGATAC	TTGGTTAGTA	AATTATAATA	GTAGAAATAA	2760
TACATGAATC	CCATTACAG	GTTTCTCAGC	CCAAGCAACA	AGGTAATTGC	GTGCCATTCA	2820
GCACTGCACC	AGACGAGACA	ACCTATTGTA	GGAAAAACAG	TGAAATCCAC	CTTCTCTTC	2880
ACACTGAGCC	CTCTCTGATT	CCTCCGTGTT	GTGATGTGAT	GCTGGCCAGC	TTTCCAAACG	2940
GCAGCTCCAC	TGGGTCCCTT	TTGGTTGTAG	GACAGGAAAT	GAAACATTAG	GAGCTCTGCT	3000
TGGAAACAG	TTCACTACTT	AGGGATTTT	GTTTCTCTAA	ACTTTTATTT	TGAGGAGCAG	3060
TAGTTTTCTA	TGTTTTAATG	ACAGAACTTG	GCTAATGGAA	TTACAGAGG	TGTTGCAGCG	3120
TATCACTGTT	ATGATCCTGT	GTTTAGATTA	TCCACTCATG	CTTCTCTTAT	TGACTGCGAG	3180
GTGTACCTTA	AACTGTCTCC	CAGTGACTT	GAACAGTTGC	ATTTATAAGG	GGGAAATGT	3240
GGTTTAAATG	TGCCGTGATAT	CTCAAAGTCT	TTGTACATA	ACATATATAT	ATATATACAT	3300
ATATATAAAT	ATAAATATAA	ATATATCTCA	TTGCAGCCAG	TGATTTAGAT	TTACAGCTTA	3360
CTCTGGGGTT	ATCTCTCTGT	CTAGAGCATT	GTTGTCTTTC	ACTGCAGTCC	AGTTGGGATT	3420
ATTCCAAAAG	TTTTTTGAGT	CTTGAGCTTG	GGCTGTGGCC	CCGCTGTGAT	CATACCTTGA	3480
GCAAGACGAA	GCAACCTCGT	TTCTGAGGAA	GAAGCTTGAG	TTCTGACTCA	CTGAAATGCG	3540
TGTTGGGTTG	AAGATATCTT	TTTTTCTTTT	CTGCCTCACC	CCTTTGTCTC	CAACCTCCAT	3600
TTCTGTTTCA	TTGTGGGAGA	GGGCATTACT	TGTTGCTTAT	AGACATGGAC	GTAAAGAGAT	3660
ATTCAAACT	CAGAAGCATC	AGCAATGTTT	CTCTTTTCTT	AGTTCACTCT	GCAGAAATGGA	3720
AACCCATGCC	TATTAGAAAT	GACAGTACTT	ATTAATTGAG	TCCCTAAGGA	ATATTGAGCC	3780
CACATACATG	ATAGCTTTT	TTTTTTTTTT	TTTTTTTTTA	TAAGGACACC	TCTTTCCAAA	3840
CAGGCCATCA	AATATGTTCT	TATCTCAGAC	TTACGTTGTT	TTAAAAGTTT	GGAAAGATAC	3900
ACACTTTTTC	ATACCCCTCC	TTAGGAGGTT	GGGCTTTCAT	ATCACCTCAG	CCAAGTGTGG	3960
CTCTTAATTT	ATTGCAATAA	GATATCCACA	TCAGCCAACT	GTGGCTCTTT	AATTTATTGC	4020
ATAATGATAT	TCACATCCCC	TCAGTTGCAG	TGAATTGTGA	GCAAAAGATC	TTGAAAGCAA	4080
AAAGCACTAA	TAGTTTAAAA	ATGTCACTTT	TTTGGTTTTT	ATTATACAAA	AACCATGAAG	4140
TACTTTTTTT	ATTGCTTAAA	TCGATTGTTT	CCTTTTGTAG	GACTCATGTT	TATGAAGAGA	4200
GTTGAGTTTA	ACAATCCTAG	CTTTTAAAAG	AAACTATTTA	ATGTAAATA	TTCTACATGT	4260
CATTTCAGATA	TTATGTATAT	CTTCTAGCCT	TTATTCTGTA	CTTTTAATGT	ACATATTTCT	4320
GTCTGCGTG	ATTTGTATAT	TTCACTGGTT	TAAAAACAA	ACATCGAAG	GCTTATTTCA	4380
AATGGAAGAT	AGAATATAAA	ATAAAACGTT	ACTTGTAATA	AAAAAAA		

Seq ID NO: 249 Protein sequence:
Protein Accession #: NP_003383

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1 11 21 31 41 51
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MAGSAMSSKF FLVALAIFFS FAQVVEANS WWSLGMNPV QMSEVYIGA QPLCSQLAGL 60
 SQGQKLCCLL YQDHMQYIGE GAKTGIXECQ YQFRHRRWNC STVDNTSVFG RVMQIGSRET 120
 AFTYAVSAAG VVNAMSACR EGELSTCGCS RAARPKDLPR DNLWGGCGDN IDYGYRFAKE 180
 FVDARERERI HAKGSYESAR ILMMLHNEA GRRTVYNLAD VACKCHGVSG SCSLKTCWLQ 240
 LADFRKVGDA LKEKYDSAAA MRLNSRGKLV QVNSRFNSPT TDQLVYIDPS PDYCVRNEST 300
 GSLGTQGRLC NKTSEGMDGC ELMCCGRGYD QFKTVQTERC HCKFWWCYV KCKKCTEIVD 360
 QFVCK

Seq ID NO: 250 DNA sequence
 Nucleic Acid Accession #: NM_014058
 Coding sequence: 56..1324

1 11 21 31 41 51
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 15 TGACTTGGAT GTAGACCTCG ACCTTCACAG GACTCTTCAT TGCTGGTTGG CAATGATGTA 60
 TCGGCCAGAT GTGGTGAGGG CTAGGAAAAG AGTTTGTGTTG GAACCTCGGG TTATCGGCCT 120
 CGTCATCTTC ATATCCCTGA TTGTCTGGC AGTGTGCATT GGACTCAGTG TTCATTATGT 180
 GAGATATAAT CAAAGAAGA CCTACAATTA CTATAGCACA TTGTCATTTA CAACAGACAA 240
 ACTATATGCT GAGTTTGGCA GAGAGGCTTC TAACAATTTT ACAGAAATGA GCCAGAGACT 300
 20 TGAATCAATG GTGAAAATAG CATTTTATAA ATCTCCATTA AGGGAAGAAT TTGTCAAGTC 360
 TCAGGTTATC AAGTTCAGTC AACAGAAGCA TGGAGTGTG GCTCATATGC TGTGTGATTG 420
 TAGATTTTAC TCTACTGAGG ATCCTGAAAC TGTAGATAAA ATTGTTCAAC TTGTTTACA 480
 TGAAGAAGCTG TAGAGCTCTG TAGAACCCCT TAAAGTAGAT CCTCACTCAG TTAATAATTA 540
 AAAAAATCAAC AAGACAGAAA CAGACAGCTA TCTAAACCAT TGCTCGGGAA CACGAAGAAG 600
 25 TAAAACTCTA GGTGAGAGTC TCAGGATCGT TGGTGGGACA GAAGTAGAAG AGGGTGAATG 660
 GCCCTGGCAG CAGATCTCTG TAGGGGATGG GAGTCATCGC TGTGGAGCAA CCTTAATTA 720
 TGCCACATGG CTTGTGAGTG CTGCTCACTG TTTTACAACA TATAAGAACC CTGCCAGATG 780
 GACTGCTTCC TTTGGAGTAA CAATAAAACC TTGAAAATG AAACGGGGTC TCCGGAGAAT 840
 AATTGTCATG GTGAAAATAG AACACCCATC ACATGACTAT GATATTCTC TTGCAGAGCT 900
 30 TTCTAGCCCT GTTCCCTACA CAAATGCAGT ACATAGAGTT TGTCTCCCTG ATGCATCCTA 960
 TGAGTTTCAA CCAGGTGATG TGATGTTTGT GACAGGATTT GGAGCACTGA AAAATGATGG 1020
 TTACAGTCAA AATCATCTTC GACAGCACA GGTGACTCTC ATAGACGCTA CAACTTGCAA 1080
 TGAACCTCAA GCTTACAATG ACGCCATAAC TCCTAGAATG TTATGTGCTG GCTCCTTAGA 1140
 AGGAAAAACA GATCATGCC AGGGTGACTC TGGAGGACCA CTGGTTAGTT CAGATGCTAG 1200
 35 AGATATCTGG TACCTTGTCTG GAATAGTAGG CTGGGGAGAT GAATGTGCGA AACCAACAA 1260
 GCCTGGTGT TATACTAGAG TTACGGCCTT GCGGGACTGG ATTACTTCAA AAACCTGGTAT 1320
 CTAAGAGAGA AAAGCCTCAT GGAACAGATA ACATTTTTTT TTGTTTTTTG GGTGTGGAGG 1380
 CCATTTTTAG AGATACAGAA TTGAGAGAAG CTTCGAAAAC AGCTAGATTG GACTGATCTC 1440
 40 AATAAACTGT TTGCTTGATG CAAAAAATA A

Seq ID NO: 251 Protein sequence:
 Protein Accession #: NP_054777

1 11 21 31 41 51
 | | | | |
 45 MYRPDVVRAR KRVCEPWWI GLVIFISLIV LAVCIGLTVH YVRYNQKITY NYSTLSFTT 60
 DKLYAEFGRE ASNNTFEMSQ RLESMVKNFA YKSPLREEFV KQVVKFSQQ KHGVLAHMLL 120
 50 ICRPHSTEDP ETVDKIVQLV LHEKLQDAVG PPKVDPHSVK IKKINKTETD SYLNHCCGTR 180
 RSKTLGQSLR IVGTGTEVEG EWPQASLQW DGSHRGATL INATWLVSAA HCFPTYKNPA 240
 RWTASFGVTI KPSKMKRGLR RIIVHEKYKH PSHDYDISLA ELSSPVPYTN AVHRVCLPDA 300
 SYEFQPGDVM FVTGFGALKN DGYSQNHRLQ AQVTLIDATT CNEPQAYNDA ITPRMLCAGS 360
 LEGKTDACQG DSGGPLVSSD ARDWYLAGI VSWGDECAKP NKPGVYTRVT ALRDWITSKT 420
 55 GI

Seq ID NO: 252 DNA sequence
 Nucleic Acid Accession #: NM_003504.2
 Coding sequence: 71-1771

1 11 21 31 41 51
 | | | | |
 60 GGCACGAGGC CTCGTGCCGC CGGGCTCTTG GTACCTCAGC GCGAGCGCCA GCGCTCCGGC 60
 CGCCGTGGCT ATGTTCTGTG CCGATTTCOG CAAAGAGTTC TACGAGGTGG TCCAGAGCCA 120
 65 GAGGGTCTCT CTCTCTGTGG CCTCGGACGT GGATGCTCTG TGTGCGTGCA AGATCCTTCA 180
 GGCCTTGTTC CAGTGTGACC ACGTGCAATA TACGCTGGTT CCAGTTTCTG GGTGGCAAGA 240
 ACTTGAAACT GCATTCTTGT AGCATAAAGA ACAGTTTCAT TATTTTATTC TCATAAACTG 300
 TGGAGCTAAT GTAGACCTAT TGGATATTCT TCAACCTGAT GAAGACACTA TATTCTTTGT 360
 GTGTGACACC CATAGGCCAG TCAATGTCGT CAATGTATAC AACGATACCC AGATCAAATT 420
 70 ACTCATTAAA CAAGATGATG ACCTTGAAGT TCCGCGCTAT GAAGACATCT TCAGGGATGA 480
 AGAGGAGGAT GAAGAGCATT CAGGAAATGA CAGTGATGGG TCAGAGCCTT CTGAGAAGCG 540
 CACACGGTTA GAAGAGGACA TAGTGGAGCA AACCATGCGG AGGAGGCAGC GCGGAGAGTG 600
 GGAGGCCCGG AGAAGAGACA TCCTCTTTGA CTACGAGCAG TATGAATATC ATGGGACATC 660
 GTCAGCCATG GTGATGTTTG AGCTGGCTTG GATGCTGTCC AAGGACCTGA ATGACATGCT 720
 GTGGTGGGCC ATCGTTGAGC TAACAGACCA GTGGGTGCAA GACAAGATCA CTCAAATGAA 780
 75 ATACGTGACT GATGTTGGTG TCCTGCAGCG CCACGTTTCC CGCCACAACC ACCGGAACGA 840
 GGATGAGGAG AACACACTCT CCGTGGACTG CACACGGATC TCCTTTGAGT ATGACCTCCG 900
 CTTGGTGCTC TACCAGCACT GGTCCCTCCA TGACAGCCTG TGCAACACCA GCTATACCGC 960
 AGCCAGGTTT AAGCTGTGGT CTGTGCATGG ACAGAAGCGG CTCCAGGAGT TCCTTGCGAG 1020
 CATGGGTCTT CCCCTGAAGC AGGTGAAGCA GAAGTTCCAG GCCATGGACA TCTCCTTGAA 1080
 80 GGAGAAATTG CCGGAAGTGA TTGAAGAGTC TGCAAAATAA TTTGGGATGA AGGACATGCG 1140
 CGTGCAACT TTCAGCATTC ATTTTGGGTT CAAGCACAAG TTCTGGCCA GCGACGTGGT 1200
 CTTTGCCACC ATGTCTTTGA TGGAGAGCCC CGAGAAGGAT GGCTCAGGGA CAGATCACTT 1260
 CATCCAGGCT CTGCAGAGCC TCTCCAGGAG TAACCTGGAC AAGCTGTACC ATGGCCTGGA 1320
 85 ACTCGCCAAG AAGCAGCTGC GAGCCACCCA GCAGACCAAT GCCAGCTGCC TTGCAACCAA 1380
 CCTCGTCATC TCCAGGGGGC CTTTCTGTGA CTGCTCTCTC ATGGAGGGGA CTCCAGATGT 1440
 CATGCTGTTT TCTAGGCCGG CATCCCTAAG CTTGCTCAGC AAACACCTGC TCAAGTCTCT 1500
 TGTGTGTTCC ACAAAGAACC GCGCTGCAA ACTGCTGCCC CTGGTGATGG CTGCCCCCT 1560

GAGCATGGAG CATGGCACAG TGACCGTGGT GGGCATCCCC CCAGAGACCG ACAGCTCGGA 1620
 CAGGAAGAAC TTTTITGGGA GGGCGTTTGA GAAGGCAGCG GAAAGCACCA GCTCCCGGAT 1680
 GCTGCACAA CATTITGACC TCTCAGTAAT TGAGCTGAAA GCTGAGGATC GGAGCAAGTT 1740
 TCTGGACGCA CTTATTTCCC TCCTGTCTTA GGAATTGAT TCTTCCAGAA TGACCTTCTT 1800
 ATTTATGTAA CTGGCTTTCA TTTAGATTGT AAGTTATGGA CATGATTGTA GATGTAGAAG 1860
 CCATTTTITA TTAATAAAAA TGCTTATTTT AGGCTCCGTC CCAAAAAAAA AAAAAAAA 1920
 AAAAAAAA AA

Seq ID NO: 253 Protein sequence:
 Protein Accession #: NP_003495.1

1 11 21 31 41 51
 MFVSDFRKEF YEVVQSQRVL LFVASDVAL CACKILQALF QCDHVQYTLV PVSGWQELET 60
 AFLEHKEQFH YFILINCGAN VDLDLILQPD EDTIFFVCDT HRPVNVVNVY NDTQIKLLIK 120
 QDDLEVPAY EDIFRDEED EHSNGSDG SEPSEKTRRL EEEIVEQTM RRRQREWEAR 180
 RRDLFDYEQ YEYHGTSSAM VMFELAWMLS KDLDMLWWA IVGLTDQWVQ DKITQMKYVT 240
 DVGVLQRHVS RHNHRNEDEE NTLSDVCTRI SFEYDLRLVL YQHWSLHDSL CNTSYTAARF 300
 KLWSVHGQKR LQEFADMDGL PLKQVKQKQFQ AMDISLKENL REMIEESANK FGMKDMRVQT 360
 FSIHFGPKHK FLASDVVPAT MSIMESPEKD GSGTDHFIQA LDSLSRSNLD KLYHGLELAK 420
 KQLRATQQT IASCLTNLVI SQGPFLYCSL MEGTDPVMLF SRPASLSLLS KHLKSFVCS 480
 TKNRCKLLP LVMAAPLSME HGTVTVVGIP PETDSSDRKN FFGRAFEKAA ESTSSRMLHN 540
 HFDLSVIELK AEDRSKFLDA LISLLS

Seq ID NO: 254 DNA sequence
 Nucleic Acid Accession #: NM_022337
 Coding sequence: 48..683

1 11 21 31 41 51
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 ACAAGAGCA CTTGTACAG TTGCTGGTGA TTGGCGACCT GGGCGTGGGG AAGACCAGTA 120
 TCAATCAAGC CTACGTGCAC CAGAACTTCT CCTCGCACTA CCGGGCCACA ATCGGCGTGG 180
 ACTTCGCGCT CAAGGTGCTC CACTGGGACC CGGAGACTGT GGTGCGCCTG CAGCTCTGGG 240
 ATATCGCAGG TCAAGAAAGA TTTGGAAACA TGACGAGGGT CTATTACCGA GAAGCTATGG 300
 GTGCAATTTAT TGTCTTCGAT GTCACCAGGC CAGCCACATT TGAAGCAGTG GCAAAGTGGG 360
 AAAATGATTT GGACTCCAAG TTAAGTCTCC CTAATGGCAA ACCGGTTTCA GTGGTTTTGT 420
 TGCCCAACAA ATGTGACCA GGAAGGATG TGCTCATGAA CAATGGCCTC AAGATGGACC 480
 AGTTCGCAA GGAGCAGCGT TTCGTAGGAT GGTTTGAAAC ATCAGCAAAG GAAATATAA 540
 ACATTGATGA AGCCTCCAGA TGCCTGGTGA AACACATACT TGCAATGAG TGTGACCTAA 600
 TGAGTCTAT TGAGCCGAGC GTCGTGAAGC CCCATCTCAC ATCAACCAAG GTTGCCAGCT 660
 GCTCTGGCTG TGCCAAATCC TAGTAGGCAC CTTTGTCTGGT GTCTGGTAGG AATGACCTCA 720
 TTGTTCCACA AATTGTGCTT CTATTTTAC CATTITGGGT AAACGTCAGG ATAGATATAC 780
 CACATGTGGC AAGCCAAAGA TCTATGCCTC TGTITTTTCA ATGAGAGAGA AATAGCAAAT 840
 GTTCTTTCTA TGCTTTCTC ACCATCATCA CAGTGTITAC AAACCTTTGA AATATTTAG 900
 TCTGTTACAA ACTTCTGTA TGTAGCTGAC CAAATCCTG CAGGGCCACA GTCGGCACTG 960
 TTATTGCTT CTTTATATCA GCAAAGGCCT CAAGTCTTAA AATAAAGGG GAGAAGAA 1020
 AACTAGCTGT CAAGTCAAGG ACTGGCTTTC ACCTTGCCCT GGTGTCTTTT TCCAGATTTC 1080
 AATATATTCT CTGATGGCCT GACAGGCCTA TTAAGTAGAT GTGATATTTT CTTCGAAGAT 1140
 GACCTCCATT CTCGGCAGAC CTAAGAGTGT CCTCTGAGTT AGCTCTTTGG AATCGTGAAC 1200
 ACAGGTGTGC TATATTGTCC TTGTCTTAAC TGTCACTTGC CATGGCCTGA ATGTTGGCTT 1260
 AACTGAATAT TGTATGAAA GACATGCCTC CATATGTGCC TTTCTGTTAG CTCTCTTTGA 1320
 CTAAGCTGT GGGGCTCCTC TATACATGCT ATACATGTAA TATATATTAT ATATATTTT 1380
 GCAAGTGAAC AATAAACAT TAAAAGATAA AA

Seq ID NO: 255 Protein sequence:
 Protein Accession #: NP_071732

1 11 21 31 41 51
 MQAPHKEHLY KLLVIGDLGV GKTSIIKRYV HQNFSSHYRA TIGVDFALKV LHWDPETVVR 60
 LQLWDIAGQE RFGNMTRVYV REAMGAFIVF DVTRPATFEA VAKWKNDLDS KLSLPNGKPV 120
 SVVLLANKCD QGKDVLMNNG LKMDQFCKEH GFVGWFETSA KENINIDEAS RCLVKHILAN 180
 ECDLMESIEP DVVKPHLTST KVASCSCGAK S

Seq ID NO: 256 DNA sequence
 Nucleic Acid Accession #: NM_016321
 Coding sequence: 25..1464

1 11 21 31 41 51
 GGAACGCGCC GTCGCCAGCC CGGCCAGGCA CCCCTGCAGC ATGGCCTGGA ACACCAACCT 60
 CGCTGGCGG CTGCCGCTCA CCTGCCTGCT CCTGCAGGTG ATTATGGTGA TTCTCTTCGG 120
 GGTGTTCTGT CGCTACGACT TCGAGGCCGA CGCCCACTGG TGGTCAGAGA GGACGCACAA 180
 GAACCTTGAGC GACATCTTCT ACGAATTCTA CTATCGCTAC CCAAGCTTCC AGGACGTGCA 240
 CGTGATGGTC TTGCTGGGCT TCGGCTTCTT CATGACTTTC CTGCAGCGCT ACGGCTTCAG 300
 CGCCGTGGGC TTCAACTTCC TGTGGGCAGC CTTGCGCATC CAGTGGCGGC TGCTCATGCA 360
 GGGCTGGTTC CACTTCTTAC AAGACCGCTA CATCGTCGTG GGGCTGGAGA ACCTCATCAA 420
 CGCTGACTTC TCGTGGCCT CTGTCTGCGT GGCCTTGGG GCAGTCTTGG GTAAAGTCAG 480
 CCCCATTCAG CTGCTCATCA TGACTTCTT CCAAGTGACC CTCTTCGCTG TGAATGAGTT 540
 CATCTCTCTT AACCTGCTAA AGGTGAAGGA TGCAGGAGGC TCCATGACCA TCCACACATT 600
 TGGGCGCTAC TTGGGCTCA CAGTGACCCG GATCCTCTAC CGACGCAACC TAGAGCAGAG 660
 CAAGGAGAGA CAGAACTCTG TGTACCAGTC GGACCTCTTT GCCATGATTG GCACCCTCTT 720
 CCGTGGGATG TACTGGCCCA GCTTCAACTC AGCCATATCC TACCATGGGG ACAGCCAGCA 780
 CCGAGCGGCC ATCAACACCT ACTGCTCCTT GGCAGCCTGC GTGCTTACCT CGGTGGCAAT 840

ATCCAGTGCC CTGCACAGA AGGGCAAGCT GGACATGGTG CACATCCAGA ATGCCACGCT 900
 CGCAGGAGGG GTGGCCGTGG GTACCGCTGC TGAGATGATG CTCATGCCCTT ACGGTGCCCT 960
 CATCATCGGC TTGCTCTGGC GCATCATCTC CACCTGGGT TTTGTATACC TGACCCCAT 1020
 CCTGGAGTCC CGGCTGCACA TCCAGGACAC ATGTGGCATT AACAACTGCG ATGGCATTCC 1080
 5 TGGCATCATA GCGGCGATCG TGGGTGCTGT GACAGCGGCC TCCGCCAGCC TTGAAGTCTA 1140
 TGGAAAAGAA GGGCTTGTC ATTCTTTGA CTTCAGAGT TTCAACGGGG ACTGGACCGC 1200
 AAGAACACAG GGAAGTTCC AGATTTATGG TCTCTGGTG ACCCTGGCCA TGGCCCTGAT 1260
 GGGTGGCATC ATTGTGGGCG TCATTTTGAG ATTACCATTC TGGGGACAAC CTTCAGATGA 1320
 10 GAATGCTTT GAGGATGCGG TCTACTGGGA GATGCCTGAA GGAACAGCA CTGTCTACAT 1380
 CCCTGAGGAC CCCACCTTCA AGCCTCAGG ACCCTCAGTA CCCTCAGTAC CCATGGTGTG 1440
 CCCACTACCC ATGGCTTCTT CGGTACCTCT GGTACCTTAG GCTCCAGGG CAGGTGAGGA 1500
 GCAGGCTCCA CAGACTSTCC TGGGGCCAG AGGAGCTGGT GCTGACCTAG CTAGGGATGC 1560
 AAGAGTGAGC AAGCAGCACC CCCACCTGCT GGCTTGGCCT CAAGGTGCCT CCACCCCTGC 1620
 CCTCCCTTC ATCCAGGGG GTCTGMCTGA GAATGGAGAA GGAGAAGCTA CAAAGTGGGC 1680
 15 ATCCAAGCGG GGTCTGGCT GCAGAAAGTTC TGCCTCTGCC TGGGGTCTTG GCCACATTGG 1740
 AGAAAAACAG GCTCAAAGTG GGGCTGGGAC CTGGTGGGTG AACCTGAGCT CTCCAGGAG 1800
 ACAACTTAGC TGCCAGTCAC CACCTATGAG GCTCTTCTAC CCGTGCCTG CACCTGGGCC 1860
 AGCATCTCCT ATGCTCCCTG GGTCCCCCAG ACCTCTCTGT GTGTGTGTGCG TGGCAGCCTC 1920
 20 CAGGAATAAA CATTCTTGTT GTCCTTTGTA AAAAAAAAAA AAAAAAAAAA

Seq ID NO: 257 Protein sequence:

Protein Accession #: NP_057405

1 11 21 31 41 51
 MAWNTNLRWR LPLTCLLLQV IMVILEGVFV RYDFEADAHW WSEETHKNLS DMENEFYRY 60
 PSFQDVHVMV FVGFGLMTF LQRYGFSAVG FNFLAAFGI QWALLMQGWF HFLQDRYIVV 120
 GVENLINADF CVASVCVAFG AVLKGVSPIQ LLIMTFEQVT LFAVNEFILL NLLKVKDAGG 180
 SMTIHTFGAY FGLTVTRILY RRNLBQSKER QNSVYQSDLP AMIGTLFLWM YWPSFNSAIS 240
 30 YHGD SQHRAA INTYCSLAAC VLTSVAISSA LHKKGKLDLV HIGNATLAGG VAVGTAEMM 300
 LMPYGALIIG FVCGIISTLG FVYLTPPLES RLHIQDTCGI NNHIGIPGII GGIVGAVTAA 360
 SASLEVYGKE GLVHSFDFQG FNGDWTARTQ GKFIYGLLV TLAMALMGGI IVGLILRLPF 420
 WQPSDENCFC EDAVIWEMPE GNSTVYIPED PTFKPSGSPV PSVPMVSPLP MASSVPLVP

Seq ID NO: 258 DNA sequence

Nucleic Acid Accession #: NM_002358.2

Coding sequence: 75..692

1 11 21 31 41 51
 GGGAAGTGCT GTTGGAGCCG CTGTGGTTGC TGTCGCGGGA GTGGAAGCGC GTGCTTTTGT 60
 TTGTGTCCCT GGCCATGGCG CTGCAGCTCT CCCGGGAGCA GGAATCACC CTGCGCGGGA 120
 GCGCCGAAAT CGTGCCCGAG TTCTTCTCAT TCGGCATCAA CAGCATTTTA TATCAGCGTG 180
 45 GCATATATCC ATCTGAAACC TTTACTCGAG TGCAGAAATA CGGACTCACC TTGCTTGTA 240
 CTACTGATCT TGAGCTCATA AAATACCTAA ATAATGTGGT GGAACAACTG AAAGATTGGT 300
 TATACAAGTG TTCAGTTCAG AAACCTGGTTG TAGTTATCTC AAATATTGAA AGTGGTGAGG 360
 TCCTGGAAAG ATGGCAGTTT GATATTGAGT GTGACAAGAC TGCAAAAGAT GACAGTGCAC 420
 CCAGAGAAAA GTCTCAGAAA GCTATCCAGG ATGAAATCCG TTCAGTGATC AGACAGATCA 480
 50 CAGCTACGGT GACATTTCTG CCACTGTTGG AAGTTTCTTG TTCAATTGAT CTGCTGATT 540
 ATACAGACAA AGATTTGGTT GTACCTGAAA AATGGGAAGA GTCGGGACCA CAGTTTATTA 600
 CCAATTTCTG GGAAGTCCGC CTTCGTTTCT TACTACTTAC AATCCACAAA GTAAATAGCA 660
 TGGTGGCCTA CAAAATTCCT GTCAATGACT GAGGATGACA TGAGGAAAAA AATGTAATTG 720
 TAATTTTGAA ATGTGGTTTT CCTGAAATCA GGTCACTTAT AGTTGATATG TTTTATTTC 780
 55 TTGGTTAATT TTTACATGGA GAAAACCAAA ATGATACTTA CTGAACGTG TGTAATTGTT 840
 CCTTATTTTT TTTGGTACCT ATTTGACTTA CCATGGAGTT AACATCATGA ATTTATTGCA 900
 CATTGTTCAA AAGGAACCAG GAGGTTTTTT TGTCAACATT GTGATGTATA TTCCTTTGAA 960
 GATAGTAATC GTAGATGGAA AAACCTGTGC TATAAAGCTA GATGCTTTCC TAAATCAGAT 1020
 GTTTGGTCA AGTAGTTTGA CTCAGTATAG GTAGGAGAT ATTTAAGTAT AAAATACAAC 1080
 60 AAAGGAAGTC TAAATATTCA GAATCTTTGT TAAGTCCCTG AAAGTAACCTC ATAATCTATA 1140
 AACATGAAA TATTGCTGTA TAGCTCCTTT TGACCTTCAT TTCATGTATA GTTTTCCCTA 1200
 TTGAATCAGT TTCCAATTAT TTGACTTTAA TTTATGTAAC TTGAACCTAT GAAGCAATGG 1260
 ATATTGTAC TGTTTAATGT TCTGTGATAC AGAACTCTTA AAAATGTTT TTCAATGTGT 1320
 65 TTATAAAATC AAGTTTAAAG TGAAAGTGAG GAAATAAAGT TAAGTTTGTT TTAATAAAAA 1380
 AAAAAAAAAA

Seq ID NO: 259 Protein sequence:

Protein Accession #: NP_002349.1

1 11 21 31 41 51
 MALQLSREQQ ITLRGSARIV AEFFSFGINS ILYQRGIYPS ETPTRVQXYG LTLVTTDLE 60
 LIKILNNVVE QLKDLNLYKCS VQKLVVVISN IESGEVLERW QFDIECDKTA KDSDAPREKS 120
 75 QKAIQDEIRS VIRQITATVT FLPLLEVSCS FDLIIYTDKD LVVPEKWEES GPQFITNSEE 180
 VRLRSFTTTI HKVNSMVAYK IPVND

Seq ID NO: 260 DNA sequence

Nucleic Acid Accession #: NM_001211

Coding sequence: 43..3195

1 11 21 31 41 51
 AAAGGCTGCG AGCAGGACGA GGACCTGAGC CAGGAATGCA GGATGGCGGC GGTGAAGAAG 60
 GAAGGGGGTG CTCTGAGTGA AGCCATGTCC CTGGAGGGAG ATGAATGGGA ACTGAGTAAA 120
 85 GAAAAATGTAC AACCTTTAAG GCAAGGGCGG ATCATGTCCA CGCTTCAGG AGCACTGGCA 180
 CAAGAATCTG CCTGTAACAA TACTCTTCAG CAGCAGAAAC GGGCATTGTA ATATGAAATT 240

	CGATTTTACA	CTGGAAATGA	CCCTCTGGAT	GTTTGGGATA	GGTATATCAG	CTGGACAGAG	300
	CAGAACTATC	CTCAAGGTGG	GAAAGAGAGT	AATATGTCAA	CGTTATTAGA	AAGAGCTGTA	360
	GAAGCACTAC	AAGGAGAAAA	ACGATATTAT	AGTGATCCTC	GATTTCTCAA	TCTCTGGCTT	420
5	AAATTAGGGC	GTTTATGCAA	TGAGCCTTTG	GATATGTACA	GTTACTTGCA	CAACCAAGGG	480
	ATTGGTGTIT	CAGTTGCTCA	GTTCATATATC	TCATGGGCAG	AAGAATATGA	AGCTAGAGAA	540
	AACTTTAGGA	AAGCAGATGC	GATATTTCAG	GAAGGGATTG	AACAGAAGGC	TGAACCACTA	600
	GAAAGACTAC	AGTCCCAGCA	CCGACAATTC	CAAGCTCGAG	TGTCTCGGCA	AACTCTGTTG	660
	GCACCTTGAGA	AAGAAGAAGA	GGAGGAAGTT	TTTGAGTCTT	CTGTACCACA	ACGAAGCACA	720
10	CTAGCTGAAC	TAAAGAGCAA	AGGGAAAAAG	ACAGCAAGAG	CTCCATCAT	CCGTGTAGGA	780
	GGTGCTCTCA	AGGCTCCAAG	CCAGAACAGA	GGACTCCAAA	ATCCATTTC	TCAACAGATG	840
	CAAAATAATA	TAGAAATATC	TGTTTTTGAT	GAAAATGCTG	ATGAGGCTTC	TACAGCAGAG	900
	TTGTCTAAGC	CTACAGTCCA	GCCATGGATA	GCACCCCA	TGCCCAGGGC	CAAAGAGAAT	960
	GAGCTGCAAG	CAGGCCCTTG	GAACACAGGC	AGGTCTCTTG	AACACAGGCC	TCGTGGCAAT	1020
	ACAGCTTCA	TGATTAGTGT	ACCCGCTGTG	CTTCCAGTT	TCACTCCATA	TGTGGAAGAG	1080
15	ACTGCACAAC	AGCCAGTTAT	GACACCATGT	AAAATTGAAC	CTAGATATAA	CCACATCCTA	1140
	AGCACCAGAA	AGCCTGGAAA	GGAGGAAGGA	GATCCTCTAC	AAAGGGTTCA	GAGCCATCAG	1200
	CAAGCGTCTG	AGGAGAAGAT	AGAGAAGATG	ATGTATTGTA	AGGAGAAGAT	TTATGCAGGA	1260
	GTAGGGGAAT	TCTCCTTTGA	AGAAATTCGG	GCTGAAGTTT	TCCGGAAGAA	ATTAAAAGAG	1320
	CAAAGGGGAG	CCGAGCTATT	GACCAGTGCA	GAGAAGAGAG	CAGAAATGCA	GAACACAGATT	1380
20	GAAGAGATGG	AGTGAAGATG	AAAGAAATC	CAAACTACT	AGCAAGAAAG	AACAGGTGAT	1440
	CAGCAAGAAG	AGACGATGCC	TACAAAGGAG	ACAACTAAAC	TGCAAAATGC	TTCCGAGTCT	1500
	CAGAAAATAC	CAGGAATGAC	TCTATCCAGT	TCTGTTTGTC	AAGTAAACTG	TTGTGCCAGA	1560
	GAAACTCTAC	TTGCGGAGAA	CATTGGCAG	GAACAACCTC	ATTCTAAAGG	TCCAGTGTA	1620
25	CCTTTCTCCA	TTTTTGATGA	GTTTCTTCTT	TCAGAAAAGA	AGAATAAAAG	TCTCCTGCA	1680
	GATCCCCCAC	GAGTTTTCAG	TCAACGAAGA	CCCTTGCAG	TTCTCAAAAC	CTCAGAAAGC	1740
	ATCACCTCAA	ATGAAGATGT	GTCTCCAGAT	GTTTGTGATG	AATTACAGG	AATTGAACCC	1800
	TTGAGCGAGG	ATGCCATTAT	CACAGGCTTC	AGAAATGTAA	CAATTGTGCC	TAACCCAGAA	1860
	GACACTTGTG	ACTTTGCTCAG	AGCAGCTCGT	TTTGTATCCA	CTCCTTTTCA	TGAGATAATG	1920
30	TCCTTGAAGG	ATCTCCCTTC	TGATCCTGAG	AGACTGTTAC	CGGAAGAAGA	TCTAGATGTA	1980
	AAGACCTCTG	AGGACCAGCA	GACAGCTTGT	GGCACTATGT	ACAGTCAGAC	TCTCAGCATC	2040
	AAGAAGCTGA	GCCCAATTAT	TGAAGACAGT	CGTGAAGCCA	CACACTCTCT	TGGCTTCTCT	2100
	GGTCTCTCTG	CTCCGTTTCG	AAGCACCTCC	TCCATCAAA	GTCTTCAAA	TCCTGAGAAA	2160
	CTAGAACTTA	CTAATGAGAC	TTCAGAAAAC	CCTACTCAGT	CACCATGGTG	TTACAGTAT	2220
	CGCAGACAGC	TACTGAGATC	CCTACCAGAG	TTAAGTGCCT	CTGCAGAGTT	GTGTATAGAA	2280
35	GACAGACCAA	TGCCTAAGTT	GGAAATTGAG	AAGGAAATTG	AATTAGGTAA	TGAGGATTAC	2340
	TGCATTAAAC	GAGAATACCT	AATATGTGAA	GATTACAAGT	TATTCTGGGT	GGCGCCAAGA	2400
	AACTCTGCAG	AATTAACAGT	AATAAAGGTA	TCTTCTCAAC	CTGTCCCATG	GGACTTTTAT	2460
	ATCAACCTCA	AGTTAAAGGA	ACGTTTAAAT	GAAGATTTTG	ATCATTTTGT	CAGCTGTTAT	2520
	CAATATCAAG	ATGGCTGTAT	TGTTTGGCAC	CAATATATAA	ACTGCTTCAC	CCTTCAGGAT	2580
40	CTTCTCCAA	ACAGTGAATA	TATTACCCAT	GAAATAACAG	TGTTGATTAT	TTATAACCTT	2640
	TTGACAAATG	TGGAGATGCT	ACACAAAGCA	GAAATAGTCC	ATGGTGACTT	GAGTCCAAGG	2700
	TGTCTGATTC	TCAGAAACAG	AATCCAGCAT	CCCTATGATT	GTAACAAGAA	CAATCAAGCT	2760
	TTGAAGATAG	TGGACTTTTC	CTACAGTGTT	GACCTTAGGG	TGCAGCTGGA	TGTTTTTACC	2820
45	CTCAGCGGCT	TTCCGACTGT	ACAGATCCTG	GAAGACAAA	AGATCCTGGC	TAACGTGTTCT	2880
	TCTCCCTACC	AGGTAGACCT	GTTTGGTATA	GCAGATTTAG	CACATTTACT	ATTGTTCAAG	2940
	GAACACCTAC	AGGCTTCTG	GGATGGGTCC	TTCTGGAAAC	TTAGCCAAA	TATTCTCGAG	3000
	CTAAAGATG	GTGAATGTG	GAATAAATTC	TTTGTGCGGA	TTCTGAATGC	CAATGATGAG	3060
	GCCACAGTGT	CTGTTCTTGG	GGAGCTTGCA	GCAGAAATGA	ATGGGGTTTT	TGACACTACA	3120
	TTCCAAAGTG	ACCTGAACAA	AGCCTTATGG	AAGGTAGGGA	AGTTAACTAG	TCCTGGGGCT	3180
50	TTGCTCTTTC	AGTGAGCTGT	GCAATCAAGT	CTCACAGATT	GCTGCCTCAG	AGCAATGGTT	3240
	GTATTGTGGA	ACACTGAAAC	TGTATGTGCT	GTAATTTAAT	TTAGGACACA	TTTAGATGCA	3300
	CTACCATTGC	TGTTCTACTT	TTTGGTACAG	GTATATTTTG	ACGTCACTGA	TATTTTTTAT	3360
	ACAGTGATAT	ACTTACTACT	GGCCTTGCTT	AACTTTGTG	AAGAACTATT	TTATCTATAA	3420
55	CAGACTCATT	ACAAATGGTT	ACCTTGTTAT	TTAACCATT	TGTCTCTACT	TTTCCCTGTA	3480
	CTTTTCCCAT	TTGTAATTG	TAAATGTTT	TCTTATGATC	ACCATGTATT	TTGTAAATAA	3540
	TAAATAGTA	TCTGTTAAAA	AAAAAAAAAA	AAAAAAAAAA	AAA		

Seq ID NO: 261 Protein sequence:

Protein Accession #: NP_001202

60	1	11	21	31	41	51	
	MAAVKKEGGA	LSEAMSLEGD	EWELSKENVQ	PLRQGRIMST	LQGALAQESA	CNNTLQQQKR	60
	AFEYEIRFYT	GNDPLDVWDR	YISWTEQNY	QGGKESNMST	LLERAVEALQ	GKRYYS DPR	120
65	FLNLWLKLR	LCNEPLDMYS	YLNQIGIGVS	LAQFYISWAE	EYEARENFRK	ADAIFQEGIQ	180
	QKAEPLELRQ	SQHRQFQARV	SRQTLLEALEK	EEEEVFESS	VPQRSTLAE	LKSKGKKTARA	240
	PIIRVGGALK	APSNRGLQ	PPQQMQNNS	RITVFDENAD	EASTAELSKP	TVQPIWAPPM	300
	PRAKENELQA	GPWNTGRSLE	HRPRGNTASL	IAVPAVLPSF	TPYVEETAQQ	PVMTPKIEP	360
70	SINHILSTRK	PGKEEGDPLQ	RVQSHQQASE	EKKEKMMYCK	EKIYAGVGEF	SFEIRAIEVF	420
	RKKLKEQREA	ELLTSAEKRA	EMQKQIEEME	KKLKEIQTTQ	QERTGDQQEE	TMPTKETTKL	480
	QIASESQKIP	GMTLSSSVQC	VNCCARETSL	AENIWQEQPH	SKGPSVPFSI	FDEPLLSEKK	540
	NKSPPADPPR	VLAQRRPLAV	LKTSESITSN	EDVSPDVCDE	FTGIEPLSED	AIITGFRNVT	600
	ICPNPEDTCD	PARAARFVST	PFHEIMSLKD	LPSDPERLLP	EEDLDVKTSE	DQQTACGTY	660
75	SQTLSEIKLS	PIIEDSREAT	HSSGFSGSSA	SVASTSSIKC	LQIPEKLELT	NETSENPTQS	720
	PWCSQYRRQL	LKSLPELSAS	AELCIEDRPM	PKLEIEKEIE	LGNEDYCIKR	EYLICEDYKL	780
	FWVAPRNSAE	LTVIKVSSQP	VPWDFYINLK	LKERLNEFD	HFCSCYQYQD	GCIVVHQVIN	840
	CFTLQDLQSH	SEYITHEITV	LIYNNLLTIV	EMLHKAIEIVH	GDLSPRCLIL	RNRIDHPYDC	900
	NKNNQALKIV	DFSYSVDLRV	QLDVFTLSGF	RTVQILEGQK	ILANCSSPYQ	VDLFGIADLA	960
80	HLLLFKEHLQ	VFWDGSPFKL	SQNISELKDG	ELWNKFFVRI	LNANDEATVS	VLGELAAEMN	1020
	GVFDTTFQSH	LNKALWKVGK	LTSPGALLFQ				

Seq ID NO: 262 DNA sequence

Nucleic Acid Accession #: NM_003784

Coding sequence: 365..1507

85	1	11	21	31	41	51
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	GTCTACTTAT	CAATAAGCAG	CTGCCTGTGC	AGAGTGCAGG	CTGCACCTTT	GGACAGCCTT	60
	TAAAACTGAA	TTCTCAGAAT	TTTAGAACAA	ATTTTGTGCT	AGAAATGCTG	ACTTTGGTTC	120
5	ATTAGGTAGT	GGTAAACAG	GCTCCCTTCG	AAGCTCTCCT	TCATCACCTT	CCTAAGTGCA	180
	TGTACAGGGA	AGCTCTCCTT	CATCACCTTC	CTAAGTGCAT	GGGGGAAAAT	ACCTAGGGCT	240
	CAACAGTCTT	GAGAACTGTG	GAAACATTTT	CTTTGTGAGT	GAGAACAGAT	CACCTAGAGA	300
	AAGGAAACCA	GATTCCTATC	ACTGCTTCTG	GGTATCAGAT	GCTAGCGCTG	CACTCCATTT	360
	TGCAATGGCC	TCCCTTGCTG	CAGCAAATGC	AGAGTTTTCG	TTCAACCTGT	TCAGAGAGAT	420
10	GGATGACAAT	CAAGGAAATG	GAAATGTGTT	CTTTCTCTCT	CTGAGCCTCT	TCGCTGCCCT	480
	GGCCCTGGTC	CGCTTGGGCG	CTCAAGATGA	CTCCCTCTCT	CAGATTGATA	AGTTGCTTCA	540
	TGTTAACACT	GCCTCAGGAT	ATGGAAACTC	TTCTAATAGT	CAGTCAGGGC	TCCAGTCTCA	600
	ACTGAAAAGA	GTTTTTCTG	ATATAAATGC	ATCCCAACAG	GATTATGATC	TCAGCATTTG	660
	GAATGGGCTT	TTTGCTGAAA	AAGTGTATGG	CTTTCATAAG	GACTACATTG	AGTGTGCCGA	720
15	AAAAATTATAC	GATGCCAAGG	TGGAGCGAGT	TGACTTTACG	AATCATTTAG	AAGACACTAG	780
	ACGTAAATAT	AATAAGTGGG	TTGAAAATGA	AACACATGGC	AAAATCAAGA	ACGTGATTGG	840
	TGAAGGTGGC	ATAAGCTCAT	CTGCTGTAAT	GGTGTGGTGG	AATGCTGTGT	ACTTCAAAGG	900
	CAAGTGGCAA	TCAGCCTTCA	CCAAGAGCGA	AACCATAAAT	TGCCATTTC	AATCTCCCAA	960
	GTGCTCTGGG	AAGGCAGTCG	CCATGATGCA	TCAGGAACGG	AAGTTCATTT	TGCTGTATT	1020
20	TGAGGACCCA	TCAATGAAGA	TTCTTGAGCT	CAGATACAAT	GGTGGCATAA	ACATGTACGT	1080
	TCTGCTGCCT	GAGAAATGAC	TCTCTGAAAT	TGAAAACAAA	CTGACCTTTC	AGAATCTAAT	1140
	GGAAATGGACC	AATCCAAGGC	GAATGACCTC	TAAATATGTT	GAGGTATTTT	TTCCCTCAGT	1200
	CAAGATAGAG	AAGAATTATG	AAATGAAACA	ATATTTGAGA	GCCCTAGGGC	TGAAAGATAT	1260
	CTTTGATGAA	TCCAAGCAG	ATCTCTCTGG	GATTGCTTCG	GGGGGTCGTC	TGTATATATC	1320
25	AAGGATGATG	CACAAATCTT	ACATAGAGGT	CACGTAGGAG	GGCACCAGAG	CTACTGCTGC	1380
	CACAGGAAGT	AATATTGTAG	AAAAGCAACT	CCCTCAGTCC	ACGCTGTTTA	GAGCTGACCA	1440
	CCCATTCCTA	TTTGTATCA	GGAAGGATGA	CATCATCTTA	TTCAAGTGGCA	AAGTTTCTTG	1500
	CCCTTGAAAA	TCCAATTGTT	TTCTGTTATA	GCAGTCCCCA	CAACATCAAA	GRACCACCAC	1560
	AAGTCAATAG	ATYTGRTGTT	AATTGGAAAA	ATGTGGTGT	TCCTTTGAGT	TTATTTCTTC	1620
30	CTAACATTGG	CAGACATGAC	ACACTGGTGA	CTTGACCTTT	CCTAGACACC	TGGTTGATTG	1680
	TCCTGATCCC	TGCTCTTAGC	ATTCTACCAC	CATGTGCTCT	ACCCATTCTT	AATTTCAATG	1740
	TCCTTCTTCC	CACGCTCATT	TCTATCATTC	TCCCCATGA	CCCGTCTGGA	AATTATGGAG	1800
	RGTGCTCAAC	TGGTAAGGAG	AACCTAGAAG	TAGCCCTAGG	GATCCTTTT	GAAACTCTAC	1860
	AGTTATCGCA	GATATTCTAG	CTTCATTGTA	AGCAATCTAG	GAAATAAGCC	CTGCTGCTTT	1920
35	CTAGAAATAA	GTGTGAAGGA	TAAATTTTCT	TTGTTGACCT	ATGAAGATT	TAGAGTTTAC	1980
	CTTCATATGT	TTGATTTTAA	ATCAGTGTAT	AATCTAGATG	GTAAAAAATG	TGAAATTGGG	2040
	ATTAGGGACC	TACCAAAATA	TTTCATTAAT	GCITTCATTT	GACAAATTTT	GGCCTTTCTT	2100
	TGATAAGACA	ATATGTACAT	GTTTTTTCAA	ATATTAAAGA	TCITTTAACT	GTGGCAGTT	2160
40	GTATCTACA	GAATCATATT	TCATATGCTG	TGTAGTTTAT	AAGTTTTTCC	TCTATTTATC	2220
	AGAATAAAGA	AATACAACAT	ACCTGTAAA				

Seq ID NO: 263 Protein sequence:
Protein Accession #: NP_003775

45	1	11	21	31	41	51	
	MASLAAANAE	FCPNLFREMD	DNQNGNVFF	SSLSLPAALA	LVRIGAQDD	LSQIDKLLHV	60
	NTASGYGNSS	NSQSLQSQL	KRVFSDINAS	HKDYDLSIVN	GLFAEKVYGF	HKDYIECAEK	120
50	LYDAKVERVD	FTNHLEDTTR	NINKWVENET	HGKIKNVIGE	GGISSAVMV	LVNAVYFKGK	180
	WQSAFTKSET	INCHFKSPKC	SGKAVAMMHQ	ERKFNLSVIE	DPSMKILELR	YNGGINMYVL	240
	LPENDLSEIE	NKLTQNLME	WTNPRRMTSK	YVEVFPPQFK	IEKNYEMKQY	LRALGLKDIF	300
	DESKADLSGI	ASGGRLYISR	MMHKSYLEVT	EEGTEATAAT	GSNIVEKQLP	QSTLPRADHP	360
	FLFVIRKDDI	ILFSKGVSCP					

55 Seq ID NO: 264 DNA sequence
Nucleic Acid Accession #: AB052906
Coding sequence: 74-814

60	1	11	21	31	41	51	
	AAAACCTTGA	GGTGATTCAT	CTTCCAGGCT	CTCCTTCCAT	CAAGTCTCTC	CTCCCTAGCG	60
	CTCTGGGTCC	TTAATGCCAG	CAGCCGCGCG	TACCAAGATC	CTTCTGTGCC	TCCCGCTTCT	120
	GCTCCTGCTG	TCCGCTGGT	CCCGGCTGG	GCGAGCCGAC	CCTCCTCTC	TTTGCTATGA	180
65	CATCACCGTC	ATCCCTAAGT	TCAGACCTGG	ACCACGGTGG	TGTGCGGTTC	AAGGCCAGGT	240
	GGATGAAAAA	ACTTTTCTTC	ACTATGACTG	TGGCAACAAG	ACAGTCACAC	CTGTCACTCC	300
	CCTGGGGAAG	AACTAAATG	TCACAACGGC	CTGGAAAGCA	CAGAACCAG	TACTGAGAGA	360
	GGTGGTGGAC	ATACTTACAG	AGCAACTGCG	TGACATTGAG	CTGGAGAAAT	ACACACCCAA	420
	GGAAACCCCT	ACCCTGCAGG	CCAGGATGTC	TTGTGAGCAG	AAAGCTGAAG	GACACAGCAG	480
70	TGGATCTTGG	CAGTTCAGTT	TCGATGGGCA	GATCTTCTCT	CTCTTGGACT	CAGAGAAGAG	540
	AATGTGGACA	ACGGTTTATC	CTGGAGCCAG	AAAGATGAAA	GAAAAGTGGG	AGAATGACAA	600
	GGTTGTGGCC	ATGTCTTCTC	ATTACTTCTC	AATGGGAGAC	TGTATAGGAT	GGCTTGAGGA	660
	CTTCTTGATG	GGCATGGACA	GCACCCTGGA	GCCAAGTGCA	GGAGCACCAC	TCGCCATGTC	720
	CTCAGGCACA	ACCCAATCA	GGGCCACAGC	CACCACCTCT	ATCCTTTGCT	GCCTCCTCAT	780
75	CATCTTCCCC	TGCTTCTATC	TCCCTGGCAT	CTGAGGAGAG	TCCTTTAGAG	TGACAGGTTA	840
	AAGCTGATAC	CAAAAGGCTC	CTGTGAGCAC	GGTCTTGATC	AAACTCGCCC	TTCTGTCTGG	900
	CCAGCTGCCC	ACGACCTACG	GTGTATGTCC	AGTGGCCTCC	AGCAGATCAT	GATGACATCA	960
	TGAGCCCAAT	CTGCTATTCA	CTGCCCTGAT	TCCTTTTGCC	AACAATTTTA	CCAGCAGTTA	1020
80	TACCTAACAT	ATTATGCAAT	TTTCTCTTGG	TGCTACCTGA	TGGAATTCCT	GCACTTAAAG	1080
	TTCTGGCTGA	CTAAACAAGA	TATATCATTT	TCITTTCTCT	CTTTTGTGTT	GGAAAAATCAA	1140
	GTACTTCTTT	GAATGATGAT	CTCTTCTTGG	CAAAATGATAT	TGTCAGTAAA	ATAATCACGT	1200
	TAGACTTCAG	ACCTCTGGGG	ATTCTTTCCG	TGCTCTGAAA	GAGAAATTTT	AAATTATTTA	1260
	ATAAGAAAAA	ATTTATATTA	ATGATTGTTT	CCTTTAGTAA	TTTATTGTTT	TGTACTGATA	1320
85	TTTAAATAAA	GAGTTCATTT	TCCCAAAAAA	AAAAAATAAA	A		

Seq ID NO: 265 Protein sequence:
Protein Accession #: BAB61048.1


```

1      11      21      31      41      51
|      |      |      |      |      |
MAAAAATKIL LCLPLLLLLS GWSRAGRADP HSLCYDITVI PKFRPGPRWC AVQGGVDEKT 60
FLHYDCGNKT VTPVSPGLGKK LNVTTAWKAO NPVLREVVDI LTELRLDIQL ENYTPKEPLT 120
5 LQARMSCEQK AEGHSSGSQW FSPDGGQIFLL FDSEKRMWTT VHPGARKMKE KWENDKVVAM 180
SPHYFSMGDC IGWLEDFLMG MDSTLEPSAG APLAMSSGTT QLRATATTLLI LCCLLIILFC 240
FILPGI

```

Seq ID NO: 266 DNA sequence
Nucleic Acid Accession #: XM_084853.1
Coding sequence: 127-444

```

1      11      21      31      41      51
|      |      |      |      |      |
ATTGATGATA TATTAAACGA AATCAAATTT GGTGAATATG TGGACACTGG AAAGCTAATC 60
GACAAGATCA ACTTACCAGA TTTCTTAAAA GTGTACCTTA ACCACAAGCC ACCTTTTGGT 120
AACACCATGA GTGGCATCCA CAAGAGCTTT GAGGTGCTCG GTTATACCAA CTCCAAAGGG 180
AAAAAGGCCA TTCGAAGAGA GGACTTCTCG AGACTGCTCG TTAATAAAGG TGAGCATATG 240
ACGGAGGAGG AGATGTTGGA TTGCTTTGCT TCACTGTTTG GCCTGAATCC CGAGGGATGG 300
20 AAATCCGAGC CTGCAACCTG CTCGTCAGAA GGTTCAGAAA TTGCCTTGA AGAAGAACTT 360
CCAGACGAAA TCACTGCAGA AATATTCGCG ACTGAAATTC TTGGCTTAAC CATTTTCAGAA 420
GATTCGGGCC AGGATGGTCA GTGAAGTTAC CAGGAATGTT TAAAGCACAA AGGACTTTGG 480
GTGTGTGTGC ATGCACATGT GTGTGTTTTC CATGAGGCAC TGCTTTTAT GCATTTCCCT 540
25 CCCCCCTCTC ATCTTTAGAA CATTTAGACA TTAAAGCAAG TTTCTGGTGA GCAATG

```

Seq ID NO: 267 Protein sequence:
Protein Accession #: XP_084853.1

```

1      11      21      31      41      51
|      |      |      |      |      |
MSGIHKSFEV LGYNSKGKK AIRREDLRL LVTKEHMT EEMLD CFASL FGLNPEGWKS 60
EPATCSVKGS EICLEELPD EITAEIPATE ILGLTISED S GQDQG

```

Seq ID NO: 268 DNA sequence
Nucleic Acid Accession #: NM_001898
Coding sequence: 57-482

```

1      11      21      31      41      51
|      |      |      |      |      |
GGCTCTCACC CTCCTCTCCT GCAGCTCCAG CTTTGTGCTC TGCTCTGAG GAGACCATGG 60
CCCGATATCT GAGTACCCTG CTGCTCCTGC TGGCCACCCT AGCTGTGGCC CTGGCTTGA 120
GCCCCAAGGA GGAGGATAGG ATAATCCCGG GTGGCATCTA TAACGCAGAC CTCAATGATG 180
45 AGTGGGTACA GCGTGCCCTT CACTTCGCCA TCAGCGAGTA TAACAAGGCC ACCAAAGATG 240
ACTACTACAG ACGTCCGCTG CGGTACTAA GAGCCAGGCA ACAGACCGTT GGGGGGGTGA 300
ATTACTTCTT CGAGCTAGAG GTGGGCGGCA CCATATGTAC CAAGTCCCAG CCCAACTTGG 360
ACACCTGTGC CTTCATGATA CAGCCAGAAC TGCAAGAA ACAGTTGTGC TCTTTCGAGA 420
TCTACGAAGT TCCCTGGGAG AACAGAAGGT CCCTGGTGAA ATCCAGGTGT CAAGAATCCT 480
AGGGATCTGT GCCAGGCCAT TCGCACCAGC CACCACCAC TCCACCCCC TGTAAGTCTC 540
50 CCACCCCTGG CTGGTGGCC CCCACCCTGC GGGAGGCTC CCATGTGCC TCGCCCAAGA 600
GACAGACAGA GAAGGCTGCA GGAGTCTTT GTTGCTCAGC AGGCGCTCT GCCCTCCCTC 660
CTTCTTCTT GCTTCTAATA GCCCTGTGAC ATGGTACACA CCCCCCACC TCCTGCAATT 720
AAACAGTAGC ATCGCC

```

Seq ID NO: 269 Protein sequence:
Protein Accession #: NP_001889.1

```

1      11      21      31      41      51
|      |      |      |      |      |
MAQYLSLTL LLAVALA WSPKEEDRII PGGIYNADLN DEWVQRALHF AISEYNKATK 60
DDYYRPLRV LRARQQTGG VNYFFDVEVG RTICTKSQPN LDTCAFHEQP ELQKKQLCSF 120
EIYEVWENR RSLVKSRCQES

```

Seq ID NO: 270 DNA sequence
Nucleic Acid Accession #: XM_093210
Coding sequence: 13-1854

```

1      11      21      31      41      51
|      |      |      |      |      |
ATGGCAAGCG CCGGAATCTC CTCAGCTGCC GTTTCACAAA AGAGGTACCA GGTCCGCACC 60
AAACGAGCAC ACAAGCAGCA CCAGGAGCTG CAGAAGAAGG AGGCGGCAGC GATGGACCAG 120
GGCAGAGGGA ATGGGAGGG GGCATCTTAC CCCATATCTG AGGTGCGACT GCGGGACGTA 180
GAGCGGACTG GGCCTTTCCC GTTGGCGCGT GGCCTCAATC AGGACTTCTT GCCCAGCTGC 240
75 GCCTTCAAAA CGTTAAGAGC TGCAACTGAA CGTGTGAGAC ATGGTGACAG TAGGCTGAGA 300
GGCGGCGGGA GAGATGCCCA TGAACCTAAG TACCCGAGCA CGCCCTCCAC TTCTACCACC 360
ACGAGTAACA CCGCCCCCAC GGGACCGCTC TCGAGGTCCC CCAAGCCAAG GACGCAAGGA 420
GGAACGCCCC GGCGGCGGCG CAGCAGCGGC GGGCACCAGC CCAATGGCCA CGGAACCTAG 480
CACTGGCAGT CGGCCCTCTC CACACCGCAG GCGTGCAAGT TGGCCGACGG AGCCTCCCGG 540
GCGGAGGACC CAGCTAGGCC GTCAACCCGG TTGCTCCAC GGGGAAGGGC ACCAGGCAAA 600
80 CTGCCAAGG CCCGAGGCC AGGTCCCTG GCGGAGGCTC CCGCTGGTCC CGCCAGATC 660
ATGGCCGCCA CCAGGCTCCC GAGCCATGGC TTCCTGTCCG GGAACGGCCC GCGCTCCTGG 720
CTGTCCAGCT AG

```

Seq ID NO: 271 Protein sequence:
Protein Accession #: XP_093210

```

1      11      21      31      41      51

```


MLRHGEQKRK RARKKWFDFLP TCAFKTVRAA TERVRHGADR LRGGGRDAHE LKYPDTPSTS 60
 TTTSNTAPTG PLRSRSPKPRP QGGTPRRRPA AAGTRANGHG TQHWQSALLT PQACSVADGA 120
 SRAEDPARPS PRLLPREGAP GKLPKAPSPG SLAEASAGLL AHVRLQNADA QRVSIQALP 180
 PNSSVGRKEE RPGAGQRRRA PAPMATELST GSRPSSHRRR AVWPTEPPGP RTQLEPSRL 240
 LPREGAPGKL PKAPSPGSLA EASAGPAQIM AATRLPSRGP LSGNGPASWL SS

Seq ID NO: 272 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 1..732

1 11 21 31 41 51
 GGATACTGTG TCACTCAAAG TAATGGGAGG GAGAGAGAAC AGGGAGGGTA GGGATGCTTT 60
 TGAAAAAGCT TTTTTCCTCA CTTTAACTT GCTTTAGCGT TAAGAGTACT TACCAGCTAA 120
 TAATGTGGAG GAAATATTTC TTTCTCATTG GAGATTACAG AATATATCTA TTCTCTTGA 180
 ATACCCACTT GAAGCCTCTG TAGAAATGTC TCGTCCTCCG GTTGTATTTC TAAACCTAC 240
 ATGATTTTGT CTGTCTCTG CAGTGAGAAA TTACATCCAT AGCAAAGACA AAAGTCTTTT 300
 TAAATTATTT TTATTATCT TCCATATAGT TCTTACAATT TCTAAAAAAT TAACACTCAT 360
 TTAGTATCAC AATTTATGGG AGAGGGTTTT TTGTATTTTT AAGCATATGT GGCTTATATA 420
 AAAATTGCAG AAGTCATAGG ACTGTCATGT ATTGCAGCTC TGAGAACCAA TGCCTGAAAC 480
 TTAAGCC

Seq ID NO: 273 Protein sequence:

Protein Accession #: Eos sequence

1 11 21 31 41 51
 MGGRENREGR DAFEKAFPT FNLL

Seq ID NO: 274 DNA sequence

Nucleic Acid Accession #: NM_003976.2

Coding sequence: 299-961

1 11 21 31 41 51
 CTCTGAGCTT CTCTGAGCCT TGTGTGCTCA TCTGGAAAAA GGGGATTAAA CCATTTACCT 60
 CATGGAGTTG TGAAAGAATA GCTGCAAAGC ACCTAACACA TAGTAAGGTT CCCAGTGCAG 120
 CTACTTCTGC TGGTTGAGT CTAGCTGTGT AGGCCCTTG TTCCTCACCT GGAGAACTG 180
 GGGTGGCAGG CCGGTCCCCC ACAAAAGATA ACTCATCTCT TAATTGCAA GCTGCCTCAA 240
 CAGGAGGGTG GGGGAACAGC TCAACAATGG CTGATGGGCG CTCCTGGTGT TGATAGAGAT 300
 GGAACCTGGA CTGGAGGCC TCTCCACGCT GTCCCACTGC CCCCTGGCTA GCGGCGAGCC 360
 TGCCCTGTGG CCGCTCTGGC TCTGCTGAGC AGCGTCGAG AGGCCTCCCT 420
 GGGCTCCGG CCGCGCAGCC CTGCCCCCG CGAAGGCCCG CCGCTGTCC TGGCGTCCCC 480
 CGCCGCCAC CTGCGGGGG GACGCACGGC CCGCTGGTGC AGTGAAGAG CCGCGCGGCC 540
 GCGCGCGCAG CCTTCTCGGC CCGCGCCCCG GCGCGCTGCA CCCCCTCTG CTCTTCCCCG 600
 CGGGGGCGCG GCGGGCGGG CTGGGGGCC GGGCAGCCGC GCTCGGGCAG CGGGGGCGCG 660
 GGGCTGCCG CTGCGCTCGC AGCTGGTGCC GGTGCGCGCG CTCGGCTTGG GCCACCGCTC 720
 CGACGAGCTG TGGCGTTTCC GCTTCTGAG CCGCTCTGCA CGCGCGCGC GCTCTCACCA 780
 CGACCTCAGC CTGGCCAGCC TACTGGGCGC CGGGGCCCTG CGACCGCCCC CGGGCTCCCC 840
 GCCGTCAGC CAGCCCTGCT GCCGACCCAC GCGCTACGAA GCGGTCTCCT TCATGGACGT 900
 CAACAGCACC TGGAGAACC TGGACCGCCT CTCGCCACC GCCTGCGGCT GCCTGGGCTG 960
 AGGGCTCGCT CCAGGGCTTT GCAGACTGGA CCCTTACCGG TGGCTCTTCC TGCTGGGAC 1020
 CCTCCGCGAG AGTCCCACTA GCCAGCGGCC TCAGCCAGGG ACGAAGGCCT CAAAGCTGAG 1080
 AGGCCCTTAC CCGTGGGTGA TGGATATCAT CCCCAGACAG GTGAAGGAC AACTGACTAG 1140
 CAGCCCCAGA GCCCTCACCC TGCGGATCCC AGCCTAAAG ACACCAGAGA CCTCAGCTAT 1200
 GGAGCCCTTC GGACCCACTT CTCACAGACT CTGGCACTGG CCAGGCCTCG AACCTGGGAC 1260
 CCTCTCTCTG ATGAACACTA CAGTGGCTGA GGCATCAGCC CCGGCCAGG CCCTGTAGGG 1320
 ACAGCATTG AAGGACACAT ATTGCAGTTG CTTGTTGAA AGTGCCTGTG CTGGAAGTGG 1380
 CCTGTACTCA CTCATGGGAG CTGGCCCC

Seq ID NO: 275 Protein sequence:

Protein Accession #: NP_003967.1

1 11 21 31 41 51
 MELGLGGLST LSHCPWPRRQ PALWPTLAAL ALLSSVAEAS LGSAPRSPAP REGPPPVLAS 60
 PAGHLPGGRT ARWCSSRRARR PPPQSRPAP PPPAPPSALP RGGRAARAGG PGRSARAAGA 120
 RGCRRLRSQIV PVRALGLGHR SDELVRFRFC SGSCRRARSP HDLSLASLLG AGALRPPPGS 180
 RPSVQPCCRP TRYEAVSFMD VNSTWRTVDR LSATACGLG

Seq ID NO: 276 DNA sequence

Nucleic Acid Accession #: NM_057091.1

Coding sequence: 783-1445

1 11 21 31 41 51
 ACTGGCCGCT GAGAGAAGAA TCGGGTGGAG CAGAGAGCAG CTGCTGCAGG GCAGACAGCC 60
 GACCCCCAA ATCTGCAGT ACCAGCAGTC AGCCGCCCA CGCAGGGACC GGCTTACCCC 120
 TCGCTCCCG CCCTCACTCA CTTTCTCCG CCCTCGGCC GGCCTCCAG CTCTCTACTT 180
 CGCGTGTCTA CAAACTCAAC TCCCGGTTTC CGTGCCTCTC CACGCTCGA GTTCTCTACT 240
 CTCATATCCC GAGGGGCCCC TCCAGCATC TACCCCTCT CCAACCTCG GGGACCTAGC 300
 CAGCTAGGG GGGACTGGAT CCGACGGGTG GAGCAGCCAG GTGAGCCCG AAAGGTGGGG 360
 CGGGGAGGG GCGTCTCCAG CCCACCCCG GATCTGGTG ACGCTGGGG TGAATTTGA 420
 CACCGGACGG CTGCGGCGGC GGGCAGGAG CTGCTGAGG ATGGAGTTG GCCCGGCC 480
 CAGACAAGGC CCGGGGGCTC CGCCAGCAGC AGTCCCTCG GCGCCAGCC CTGCTGCCA 540

CCGGGGCTG GAGCCCAACA CCGAGGGGTG CAGACTGGCT GCCAAGGCCA CACTTTTGGC 600
 TAAAAGAGGC ACTGCCAGGT GTACAGTCCT GGGCATGCGC TGTTTGAGCT TCGGGGGAGA 660
 GCCCAGCACT GGTCCCCCGA AAGGTGCCTA GAAGAACAAG GTGCAGGACC CCGTGCTGCC 720
 TCAACAGGAG GGTGGGGGAA CAGCTCAACA ATGGCTGATG GGCCTCTCTG GTGTTGATAG 780
 5 AGATGGAAGT TGGACTTGGG GGCCTCTCCA CGCTGTCCCA CTGCCCCTGG CCTAGGCGGC 840
 AGCCTGCCCT GTGGCCCACT CTGGCCGCTC TGGCTCTGCT GAGCAGCGTC GCAGAGGCCT 900
 CCCTGGGCTC CGCGCCCGCG AGCCCTGCCG CCGCGAAGG CCCCCTGCTT GTCTGGCGT 960
 CCCCCTGGG CCACTGTCCG GGGGACGCA CGGCCCGCTG GTGCAGTGGG AGAGCCCGGC 1020
 10 GCGCCGCGCC GCAGCTTCTT CCGCCCGCGC CCCCCTGCTG TGACCCCTCA TCTGCTCTTC 1080
 CCGCGGGGG CCGCGCGGGG CGGGCTGGGG GCGCGGGCAG CCGCGCTCGG GCAGCGGGGG 1140
 CGCGGGGCTG CCGCTGTCCG TCGCAGCTGG TGCCGGTGGC CGCGCTCGGC CTGGGCCACC 1200
 GCTCCGACGA GCTGTGCGT TTCCGCTTCT GCAGCGGCTC CTGCGCGCGC GCGCGCTCTC 1260
 CACACGACCT CAGCCTGGCC AGCCTACTGG GCGCCGGGGC CCGCGACCG CCCCCTGGCT 1320
 CCGGCCCGT CAGCCAGCCC TGCTGCCGAC CCACGCGCTA CGAAGCGGTC TCCTTCATGG 1380
 15 AGCTCAACAG CACCTGGAGA ACCGTGGACC GCCTCTCCGC CACCGCTGCG GGCTGCTTGG 1440
 GCTGAGGGCT CGCTCCAGGG CTTTGCAGAC TGGACCCCTT CCGGTGGCTC TTCTGCTCTG 1500
 GGACCTTCCC GCAGAGTCCC ACTAGCCAGC GGCCTCAGCC AGGGACGAAG GCCTCAAAGC 1560
 TGAGAGGCCC CTACCGGTGG GTGATGGATA TCATCCCGGA ACAGGTGAAG GGACAACTGA 1620
 CTAGCAGCCC CAGAGCCCTC ACCCTGCGGA TCCCAGCCTA AAAGACACCA GAGACCTCAG 1680
 20 CTATGGAGCC CTTGCGACCC ACTTCTACA GACTCTGGCA CTGGCCAGGC CTCGAACCTG 1740
 GGACCCCTCC TCTGATGAAC ACTACAGTGG CTGAGGCATC AGCCCCCGCC CAGGCCCTGT 1800
 AGGACAGCA TTTGAAGGAC ACATATTGCA GTTGTCTGGT TGAAGTGCC TGTGCTGGAA 1860
 CTGGCTGTA CTCACCTATG GGAGCTGGCC CC

25 Seq ID NO: 277 Protein sequence:
 Protein Accession #: NP_003967.1

1 11 21 31 41 51
 | | | | |
 30 MELGLGLST LSHCPWPRRQ PALWPTLAAL ALLSSVAEAS LGSAPRSPAP REGPPPVLAS 60
 PAGHLPGGRT ARWCSGRARR PPPQPSRPAP PPPAPPSALP RGGRAARAGG PGSRRARAAGA 120
 RGRCLRSQVL PVRALGLGHR SDELVRFRFC SGSCRRRASP HDLSLASLLG AGALRPPPGS 180
 RPSVQPCCRP TRYEAVSFMD VNSTWRTVDR LSATACGCLG

35 Seq ID NO: 278 DNA sequence
 Nucleic Acid Accession #: NM_057160.1
 Coding sequence: 1-714

1 11 21 31 41 51
 | | | | |
 40 ATGCCCGGCC TGATCTCAGC CCGAGGACAG CCCCTCCTTG AGGTCCCTTC TCCCCAAGCC 60
 CACCTGGGTG CCCTCTTTCT CCCTGAGGCT CCACTTGGTC TCTCCGCGCA GCCTGCCCTG 120
 TGGCCCAACC TGCCGCTCTT GGCTCTGCTG AGCAGCGTCG CAGAGGCTC CTGGGGCTCC 180
 GCGCCCGGCA GCCCTGCCCC CCGCGAAGGC CCCCCTGCTG TCCTGGCGTC CCCCCTGGGC 240
 45 CACCTGCGCG GGGGCGCAC GGGCCGCTGG TGCAGTGGAA GAGCCCGCGC GAGCCCGCGC 300
 CAGCCTTCTC GCGCCGCGCC CCGCGCGCTT GCACCCCAT CTGCTCTTCC CCGCGGGGGC 360
 CGCGCGGCGC GGGCTGGGGG CCGGGGCGAG CGCGCTCGGG CAGCGGGGGC GCGGGGCTGC 420
 CGCCTGCGCT CGCAGCTGCT GCGGTGCGC GCGCTCGGCC TGGGCCACCG CTCCGACGAG 480
 CTGGTGGGTT TCGCTTCTG CAGCGGCTCC TGCCGCGCGC CGCGCTCTCC ACACGACCTC 540
 50 AGCCTGGCCA GCCTACTGGG CGCCGGGGCC CTGCGACCGC CCCCCTGGCT CCGGCCCTGC 600
 AGCCAGCCCT CCTGCGGACC CACGCGCTAC GAAGCGGTCT CCTTCATGGA CGTCAACAGC 660
 ACCTGGAGAA CCGTGGACCG CTTCTCCGCC ACCGCTCGCG GCTGCTGGG CTGAGGGCTC 720
 GCTCCAGGGC TTTGCAGACT GGACCTTAC CGGTGGCTCT TCCTGCTTGG GACCTCCCG 780
 CAGAGTCCCA CTCTGCGAGC GGCAGGCGC CCTCAAAGCT GAGAGGCCCC 840
 TACCGTGGG TGATGGATAT CATCCCCGAA CAGGTGAAGG GACAACTGAC TAGCAGCCCC 900
 55 AGAGCCCTCA CCTGCGGAT CCCAGCCTAA AAGACACCAG AGACCTCAGC TATGGAGCCC 960
 TTCGGAACCA CTTCTCAGC ACTCTGGCAC TGGCCAGGCC TCGAACCTGG GACCCCTCT 1020
 CTGATGAACA CTACAGTGGC TGAGGCATCA GCCCCGCCC AGGCCCTGTA GGGACAGCAT 1080
 TTGAAGGACA CATATTGCAG TTGCTTGGTT GAAAGTGCCT GTGCTGGAAC TGGCCTGTAC 1140
 TCACTCATGG GAGCTGGCCC C

60 Seq ID NO: 279 Protein sequence:
 Protein Accession #: NP_476501.1

1 11 21 31 41 51
 | | | | |
 65 MPGLISARGQ PLLEVLPQA HLGALFLPEA PLGLSAQPAL WPTLAALALL SVAEASLGSS 60
 APRSPAPREG PPPVLASAPG HLPGGRTARW CSGRARRPPP QPSRPAPPPP APPSALPRGG 120
 RAARAGGPGS RARAAGARGC RLRSQVLPVR ALGLGHRSD E LVRFRFCSGS CRRARSPHDL 180
 SLASLLGAGA LRPPPGSRPV SQPCCRPTRY EAVSFMDVNS TWRTVDRLSA TACGCLG

70 Seq ID NO: 280 DNA sequence
 Nucleic Acid Accession #: NM_057090.1
 Coding sequence: 29-715

1 11 21 31 41 51
 | | | | |
 75 CTGATGGGCG CTCTGGTGT TGATAGAGAT GGAACCTGGA CTTGGAGGCC TCTCCACGCT 60
 GTCCCACTGC CCTGGCCCTA GCGCGCAGGC TCCACTTGGT CTCTCGCGC AGCCTGCCCT 120
 80 GTGGCCCACT CTGGCCGCTC TGGCTCTGCT GAGCAGCGTC GCAGAGGCGT CCGTGGGCTC 180
 CGCGCCCGCG AGCCCTGCCC CCGCGAAGG CCCCCTGCTG GTCTTGGCGT CCGCGCGCG 240
 CCACCTGCGG GGGGACGCA CCGCCGCTG GTGCAGTGGG AGAGCCCGGC GCGCGCGGCC 300
 GCAGCTTCTT CCGCCCGCGC CCGCCCGGCC TGCACCCCA TCTGCTCTTC CCGCGGGGG 360
 CCGCGCGGCG CCGGCTGGGG GCGCGGCGAG CCGCGCTCGG GCAGCGGGGG CCGGGGGCTG 420
 CCGCTGCGC TCGCAGCTGG TGCCGGTGGC CGCGCTCGGC CTGGGCCACC GCTCCGACGA 480
 85 GCTGGTGGCT TTCCGCTTCT GCAGCGGCTC CTGCCGCGC GCGCGCTCTC CACACGACCT 540
 CAGCCTGGCC AGCCTACTGG GCGCGGGGCG CCGCGGACCG CCCCCTGGCT CCGCGCGCGT 600
 CAGCCAGCCC TGCTGCCGAC CACGCGCTA CGAAGCGGTC TCCTTCATGG ACGTCAACAG 660

CACCTGGAGA ACCGTGGACC GCCTCTCCGC CACCGCCTGC GGCTGCCTGG GCTGAGGGCT 720
 CGCTCCAGGG CTTTGCAGAC TGGACCCCTA CCGGTGGCTC TTCTGCCTG GGACCCCTCC 780
 GCAGAGTCCC ACTAGCCAGC GGCTCTAGCC AGGGACGAAG GCCTCAAAGC TGAGAGGGCCC 840
 CTACCGGTGG GTGATGGATA TCATCCCGA ACAGGTGAAG GGACAACTGA TAGCAGGCC 900
 CAGAGCCCTC ACCCTGCGGA TCCAGCCTA AAAGACACCA GAGACCTCAG CTATGGAGCC 960
 CTTCGGACCC ACTTCTCAG GACTCTGGCA CTGGCCAGGC CTGAACTCTG GGACCCCTCC 1020
 TCTGATGAAC ACTACAGTGG CTGAGGCATC AGCCCCGCC CAGGCCCTGT AGGGACAGCA 1080
 TTTGAAGGAC ACATATTGCA GTTGCTTGGT TGAAAGTGCC TGTGCTGGAA CTGGCCTGTA 1140
 CTCATCATG GGAGCTGGCC CC

Seq ID NO: 281 Protein sequence:
 Protein Accession #: NP_476431.1

1 11 21 31 41 51
 MELGLGLST LSHCPWPRRQ APLGLSAQPA LWPTLAALAL LSSVAEASLG SAPRSPAPRE 60
 GPPFVLASPA GHLPGGRTAR WSGRRARRPP PQPSRPAPPP PAPPSPALPRG GRAARAGGPG 120
 SRARAAGARG CRLRSQVLVPV RALGLGHRSD ELVRFRFCSG SCRRARS PHD LSLASLLGAG 180
 ALRPPPGSRP VSQPCCRPRR YEAVSFMDVN STWRTVDRLS ATACGCLG

Seq ID NO: 282 DNA sequence
 Nucleic Acid Accession #: Eos sequence

1 11 21 31 41 51
 CTACTGCACC TGCCCTCTGT TTCCTTTGGA AATCTCTTAC CTTCATTAG GGTTCCTTTC 60
 ATAGCAATTT CCTTTGGTTT TTAAGACTTC TACATTGCTT TTCTTTTAT TATCTGTGCT 120
 CCGTGAACCT TATGAATGCT GCTTAAAAAT AATGTCAAAA TATGTTTATG CTGCCTACTC 180
 AGGTAACGTT TTCTTTTGTG CTCATCTTGG TTTCCATATA CTATTTTGG TTTTGTGTA 240
 GACTTAATCA ATGATCTAGT CAGAGGTAC TTTACTGGCT AACAGTGATC ATGTTCATGT 300
 GCTAAAAATG AACTTGA AACGGAAGTAG TGGTTGGTCC AGTTTGAAG CTCTTATTAG 360
 TATTCTTCAT CCTGGCTGTA ATAATAGCCA TTATTTGTTA TGCCTTTGTT ATGTAGCAGA 420
 CACTCTTAAG GATTTTATGT GTATTATTCA AATTGCTATT ACTGTTCTTT TTATAGTTGA 480
 GAATCTCAGG ATACCTACAT TTATCACTTT TTCATATAT ATGTATTCT TATT

Seq ID NO: 283 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 564-1481

1 11 21 31 41 51
 GAGACTTTTA ATCATCTATC CCTTGTGCTT TACGCAGACC CTACAATACA CTAGAGGCTT 60
 CAAAGAGGTC AAAAAATTCAC ATGTGTAGAC AAATTAGGTC CCTTAAGATG CCAGGCAAAAC 120
 GAAGTGCTAC CAAAACACGC AATGACTGTC CTAAGATGTC GTTCTGGGAT ACACCTGTAA 180
 ACTTGATACA AGTTCCCTCC CCTCTCCTCA AAATATATCG ACTTGTGCTG AAAGAAATCA 240
 CGACCGATGC TCACAATTCT GACCTCGTAA TTATATAGGG GGTGGTTTGG GTTCTGCGT 300
 CTTTCCCTGA TTCAGTGCCA GGTAAACATAT TTCATGTACA AAATGAACTG CAACACCACG 360
 GCAACAAGG GACAGGCCCT CAAAGTTGTC GGTAGGGAGC CAGGACCCCG CCAGTGGCGT 420
 GGGGAGACAC CGTACTAAAC AAGCTTGCAA ACAGCAGGCA CCTTCTGCC ACTGAGGAGG 480
 AAGGGCTGGC TAAGGGAGGC CGGGGCGGAG GAAGCCAAGC TCTGCAGGCC CTGACAAAGT 540
 CTCTCCGGCC TCCACCGCTC GCCATGGCAA CGCGGGGTCT GTGCTGGCCG GGATTTGGCCG 600
 GCTGGCGCG CGCACGTGGC GCTGGGAAAG CGCGTCCCG CGCGGCTCC GCCAGTTTGA 660
 ACTTGGCGGG CCAGATGTGG GCGGCGGGGC GCTGGGGGCC TACTTTTCCC TCTTCTACG 720
 CCGGTTTCTC TGCTGACTGC AGACCCAGGT CTCGGCCCTC CTGCGACTCC TGCTCAGTCC 780
 CTATGACGG GGCACGTGGC CAGGGGCTGG AGGTGGTGGC CTCGCGTCC CCGCGCTGC 840
 CGCTGAGCTG CAGCAATTCC ACCAGSTGCG TGTGTGCTCC CCTTGGCCAC CAGAGCTTCC 900
 AGTTTGACGA GGACGACGGT GACGGGGAGG ATGAGGAAGA CGTGGATGAT GAGGAAGACG 960
 TGGATGAAGA GCTGCAATAT TCAGAGGCCA AAGTGGCGAG CCTGAGAGGA ATGGAGTTAC 1020
 AGGGGTGCGC CAGCACTCAG GTTGAATCAG AAAATAACCA AGAAGAACAG AAACAGGTGC 1080
 GCTTACCAGA AAGCCGCTCG ACACCATGGG AGGTGTGGTT TATTTGCAAA GAAAAAGAA 1140
 AACGTGACCG CTGCAACTAG AAGCTCTAG AGGAATTAA TCAACAATA GAAAAAGAA 1200
 AAGAAATGGA AGAAGCTGAA AAAAGAAAGA TAATTGCTGA AGAAAAGCAC AAGGAATGGG 1260
 TCGAAAAA GAATGAGCAA AAAAGAAAG AAAGAGACA AAAAATTAAT AAAGAAATGG 1320
 AGGAAAAAGC AGCAAGAGAA CTGGAGAAAG AATACTTGCA AGAAAAAGCA AAAGAAAAAT 1380
 ATCAAGAATG GTTAAAGAAA AAAAATGCTG AAGAATGTGA GAGGAAGAAG AAAGAAAAA 1440
 AAAACAACAG CAAGCTGAAA TACAGGAGAA AAAGGAAATA GCAGAAAAA AGTTTCAAGA 1500
 ATGGTTGAAA AATGCGAAAC ATAAACCTCG TCCAGCTGCA AAGAGCTATG GTTATGCCAA 1560
 TGGAAAACTT ACAGGTTTTT ACAGTGGAAA TTCCTATCCA GAACGAGCCT TTTATAATCC 1620
 AATTCCGTGG AAACCAATTC ATATGCCACC TCCCAAAGAA GCTAAGGATC TATCAGGAAG 1680
 GAAGAGTAAA AGACCTGTGA TAAGTCAGCC ACACAAGTCA TCATCTCTGG TAATTCATAA 1740
 AGCCAGGAGC AATCTTTGCC TTGGAATCT GTGCAGAATA CAAAGATAGC GTATGTGGAA 1800
 AATAACATGC TTTTATCTGG AGCTATTTAA TTTAAAAATC AGAAATTTGT TTTTACTGCT 1860
 CAGTCAATAA CTCAACACTT AATGTGATTA TTGACAAATA GCAATTTTGT CATTTGTATA 1920
 TGGAGTCTCT AGAGTTGAGG AAGATATTTT CTGGATTTTG GTTTTTATAA ACTTTTTAAG 1980
 GTTGATCTTG GCATGTTGTT TTGCAGAAATA AGTGGCTGAA TATGTAAGAA TTGTGTTTGT 2040
 ATTTAGCTTG TATTAAAAAGT AACTGTAAAT ACCAATAAAA CTAACAATTT TTCTTG

Seq ID NO: 284 Protein sequence:
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 MATRGLCPWP LAGLARAGPA GKARPRRGS SLNLAGQMW AGRWGPFFPS SYAGFSADCR 60
 PRSRPSSDSC SVPMTGARQ GLEVVRSPP PLPLSCSNST RSLSPGLHQ SFQFDEDDGD 120
 GEDEEDVDDE EDVDEDAHDS EAKVASLRGM ELQGCSTQV ESENNEEQEQ QVRLPESRLT 180
 PWEVWFIGKE KEERDRLQLE ALEELNQQLE KRKEMEEREK RKI IAEKHK ENVQKQNEQK 240
 RKEREQKINK EMEERAAKEL EKEYLQEKAK EKYQEWLKKK NAECEKRRK EKNNSKLLKY 300

RRRRK

Seq ID NO: 285 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1-1746

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1	11	21	31	41	51	
ATGCCACTGA	AGCATTATCT	CCTTTTGCTG	GTGGGCTGCC	AAGCCTGGGG	TGCAGGGTTG	60
GCCTACCATG	GCTGCCCTAG	CGAGTGTACC	TGCTCCAGGG	CCTCCAGGT	GGAGTGCACC	120
GGGGCACGCA	TGTGTGGCGT	GCCCAACCCCT	CTGCCCTGGA	ACGCCATGAG	CCTGCAGATC	180
CTCAACACGC	ACATCACTGA	ACTCAATGAG	TCCCCGTTC	TCAATATCTC	AGCCCTCATC	240
GCCCTGAGGA	TTGAGAAGAA	TGAGCTGTCT	CGCATCACGC	CTGGGGCCTT	CCGAAACCTG	300
GGCTCGCTGC	GCTATCTCAG	CCTCGCCAAC	AACAAGCTGC	AGGTTCTGCC	CATCGGCCCTC	360
TTCCAGGGCC	TGACAGCCCT	TGAGTCTCTC	CTTCTGTCCA	GTAACCAAGCT	GTTGCAGATC	420
CAGCCGGCCC	ACTTCTCCCA	GTGCAGCAAC	CTCAAGGAGC	TGCAGTTGCA	CGGCAACCAC	480
CTGGAATACA	TCCCTGACGG	AGCCTTCGAC	CACCTGGTAG	GACTACGAA	GCTCAATCTG	540
GGCAAGAATA	GCCTCACCCA	CATCTCACCC	AGGGTCTTCC	AGCACCTGGG	CAATCTCCAG	600
GTCTCCGGC	TGTATGAGAA	CAGGCTCACG	GATATCCCA	TGGGCACTTT	TGATGGGCTT	660
GTTAACTGCG	AGGAACTGGC	TCTACAGCAG	AACCAGATTG	GACTGCTCTC	CCCTGGTCTC	720
TTCCACAACA	ACCACAACCT	CCAGAGACTC	TACCTGTCCA	ACAACCACAT	CTCCAGCTG	780
CCACCAGCA	TCTTCATGCA	GCTGCCCCAG	CTCAACCGTC	TTACTCTCTT	TGGGAATTCC	840
CTGAAGGAGC	TCTCTCTGGG	GATCTTCGGG	CCCATGCCCA	ACCTGGCGGA	GCTTTGGCTC	900
TATGACAACC	ACATCTCTTC	TCTACCCGAC	AATGTCTTCA	GCAACCTCCG	CCAGTTGCAG	960
GTCTGATTTC	TGACCGGCAA	TCAGATCAGC	TTATCTCTCC	CGGGTGCCTT	CAACGGGCTA	1020
ACGGAGCTTC	GGGAGCTGTC	CCTCCACACC	AACGCACCTG	AGGACCTGGA	CGGGAATGTC	1080
TTCCGCATGT	TGGCCAACCT	GCAGAACATC	TCCCTGCAGA	ACAATCGCCT	CAGACAGCTC	1140
CCAGGGAATA	TCTTCGCCAA	CGTCAATGGC	CTCATGGCCA	TCCAGCTGCA	GAACAAACAG	1200
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TCGCTCTCTT	CTACCACTGA	GCTAACCCAG	CCTGTGGAAG	ACTACACTGA	TCTGACTACC	1560
ATTCAAGTCA	GTGAGTACG	CAGCGTTTGG	GGCATGACCC	AGGCCAGAG	CGGGCTGGCC	1620
ATTGCCGCCA	TTGTAATTGG	CATTGTGCGC	CTGGCCTGCT	CCCTGGCTGC	CTGCGTGGC	1680
TGTTGCTGCT	GCAAGAAGAG	GAGCCAAGCT	GTCTGTATGC	AGATGAAGGC	ACCCAATGAG	1740
TGTTAAAGAG	GCAAGCTGGA	CAGGGCTGG	GGAAATGATG	GACTGGAGGA	CCTGGGAATT	1800
TCATCTTTCT	GCCTCCACCC	CTGGGTCCAT	GGAGCTTTCC	CGTGATTGCT	CTTCTTGCC	1860
CTAGATAAAG	GTGTGCCCTAC	CTCTTCTCTG	CTTGCTGAT	TCTCCCGTAG	AGAAGCAGGT	1920
CGTGCCGGAC	TTTCTCTACA	TCAGGAAGAT	AGATCCAACT	GGCCATGGCA	AAAGCCCTGG	1980
GGATTTCOGA	TTCATACCCC	TGGGCTTCCT	TCGAGAGGGC	TCTTCTCTCA	AATCTCCCC	2040
ACCTGTCTCT	CAAGAACAGC	CTTCCCTCGG	CCCAGGCCCC	CTCCGGGCTT	CTGTAGACTC	2100
AGTTAGTCCA	CAGCCTGTCT	ACTTCGTGGG	AATAGTTCTC	CGCTGAGATA	CGCCCTCTCG	2160
CCTAAGTATT	ATGTAAGTTG	ATTTCCCTTC	TTTGTCTTCT	CTTGTCTGTC	CTATGGCTTG	2220
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TGAGTTCTCT	CCTCAAGTCA	GACTTCAAA	CATTAACTG	GTTTCTTAAG	AGCCCTCAAT	2340
CAGCCTGGTT	TTGGGGATGC	TATGAAGAG	AGAAGGAAA	TCATGCCGCT	CAGTTCCTGG	2400
AGACAGAAGA	GGCGTCATCA	GTGTCTCACT	TGTGATTTTT	ATCTGGAAAA	GGAGAAAAAC	2460
CCCCAGCACA	GCAAGCTCAG	CCTTTTAGAG	AAGGATATTT	CCAAACTGCA	AACTTTGCTT	2520
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TCCCCCACA	GTGAGCTGT	GCAAAGGCC	CGTGGCCAGG	GGTGGAGGAG	AATATGTGGG	2940
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GGGGCATCCC	GGCCCGTACC	CCTCCAGACA	GGAAGCATGG	GTTTGCCAC	AGACCTGTCTG	4200
GGTGCTCCTG	TGAGTGGCCT	CCAGATGTCT	TTGTGCATAG	GCACAAGTGG	GCCAGGGCTG	4260
GAGGGAGGTG	GGAAACCTCA	TCATCCGGTG	GGCCCTGCCA	ATCTTAACCC	AGAACCCTTA	4320
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CCTTATGTGA	ACCTCTTGCC	TCTTCTTTTC	TCCCATCAGA	GTGGTTGGAT	GGAGCCATTG	4500
GCCTCCTTTT	CTTCAGCGGG	CCCTTCAACC	TCTCTGCACC	ATGTTGTCTG	GCTGAGGAGC	4560
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GGGCTGGAAT	GAGCCGGCTG	GTCCCCCAGA	AAGCTGGAGT	GGGGTACAGA	GTTCACTTTT	4680
CCTCTCTGTT	TACAGCTCCT	TGACAGTCCC	ACGCCCATCT	GGAGTGGGAG	CTGGGAGTTA	4740

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5 GGTGTTCAAT AGGCTGGGAG TTTTATTAT CTCTTCAAAC TTTGTACAAG AGCTCATGGC 4980
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20 Seq ID NO: 286 Protein sequence:
Protein Accession #: NP_570843.1

1 11 21 31 41 51
25 MPLKHYLLLL VGCQAWGAGL AYHGCPSECT CSRASQVECT GARIVAVPTP LPWNAMSLQI 60
LNTHITELNE SPFLNISALI ALRIEKNELS RITPGAFRNL GSLRYLSLAN NKLQVLPGL 120
FQGLDSLESL LLSSNQQLQI QPAHFSQCSN LKELQLHGNH LEYIPDGAFL HLVLGLTKLNL 180
GKNSLTHISP RVFQHLGNLQ VLRLYENRLT DIPMGTFDGL VNLQELALQ NQIGLLSPGL 240
30 PNNHNLRL YLSNNHISGL PPSIFMQLPQ LNRLTLFGNS LKELSLGIFG PMPNLRELWL 300
YDNHISSLPD NVFSNLRQLQ VLILSRNQIS FISPGAFNGL TELRELSLHT NALQDLGDNV 360
FRMLANLQNI SLQNNRLRLQ PGNIFANVNG LMAIQLQNNQ LENLPLGIFD HLGKLCLELRL 420
YDNPWRCDSI ILPLRNWLLL NQPRLGTDIV PFCFSPANVR QSLIIINVN VAVPSVHVPE 480
VPSYPETPWY PDTSPYPTDT SVSSTTELS FVEDYTDLT IQVTDDRSVW GMTQAQSGLA 540
35 IAAIVIGIVA LACSLAACVG CCCCKKRSQA VLMQMKAPNE C

Seq ID NO: 287 DNA sequence
Nucleic Acid Accession #: NM_002362
Coding sequence: 1..954

1 11 21 31 41 51
40 ATGTCTTCTG AGCAGAAGAG TCAGCACTGC AAGCCTGAGG AAGGCGTTGA GGCCCAAGAA 60
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45 GGTCTCTCCC AGAGTCTCTA GGGAGCCTCT GCCTTACCCA CTACCATCAG CTTCACCTGC 240
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GACGCAGAGT CTTTGTTCGG AGAAGCACTC AGTAACAAGG TGGATGAGTT GGCTCATTTT 360
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50 ATCAAAATTT ACAAGCGCTG CTTTCTGTG ATCTTCGGCA AAGCCTCCGA GTCCCTGAAG 480
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GGCCTTCTGA TAATCGTCTT GGGCACAAAT GCAATGGAGG GCGACAGCGC CTCTGAGGAG 660
GAAATCTGGG AGGAGCTGGT TGTGATGGGG GTGTATGATG GGAGGGAGCA CACTGTCTAT 720
GGGGAGCCCA GGAAACTGCT CACCAAGAT TGGGTGCAGG AAAACTACCT GGAGTACCGG 780
55 CAGGTACCGG GCAGTAATCC TGCAGCTGAT GAGTTCCTGT GGGGTCCAAG GGCTCTGGCT 840
GAAACCAAGT ATGTGAAGT CCTGGAGCAT GTGGTCAGG TCAATGCAAG AGTTGCAATT 900
GCCTACCCAT CCCTGCGTGA AGCAGCTTTG TTAGAGGAGG AAGAGGGAGT CTGA

60 Seq ID NO: 288 Protein sequence:
Protein Accession #: NP_002353.1

1 11 21 31 41 51
65 MSSEQKSQHC KPEEGVEAQE EALGLVGAQA PTTEEQEAHV SSSSPLVPGT LEEVPAESA 60
GPPQSPQAS ALPTTISFTC WRQPNEGSSS QEEEGPSTSP DAESLFREAL SNKVDELAHF 120
LLRKYRAKEL VTKAEMLERV IKNYKRCPPV IFGKASESLK MIFGIDVKEV DPASNTYTLV 180
TCLGLSYDGL LGNNQIFPKT GLLIIVLGTI AMEGDSASEE EIWEELGVMG VYDGREHTVY 240
70 GEPRKLLTQD WQENYLEYR QVPGSNPARY EFLWGPRALA ETSYVKVLEH VVRVNRVRI 300
AYPSLREAAAL LEEEBGV

Seq ID NO: 289 DNA sequence
Nucleic Acid Accession #: NM_002362
Coding sequence: 46..1344

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CATCAGCGCG GCAGCAGCAC TGCAAGAAA GAAGACATAA ACCTGAGTGT TAGAAGCTA 180
CTCAACAGAC ATAATATTGT GTTTGGTGAT TACACATGGA CTGAGTTTGA TGAACCTTTT 240
85 TTGACCAGAA ATGTGCAGTC TGTGTCTATT ATTGACACAG AATTAAAGGT TAAAGACTCA 300
CAGCCCATCG ATTTGAGTGC ATGCACTGTT GCACCTTACA TTTTCCAGCT GAATGAAGAT 360
GGCCCCAGCA GTGAAAATCT GGAGGAAGAG ACAGAAAACA TAATTGCAGC AAATCACTGG 420
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AAATCCCATC TCCTCGATTA TGTGATGACA ACTTTACTGT TTTGACACAA GAACGTCAAC 540

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AGCAACCTCA TCACCTGGAA CCGGGTGGTG CTGCTCCACG GTCCTCCTGG CACTGGAAAA 600
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TATGGCCAAT TAAATTGAAT AAACAGCCAC AGCCTCTTTT CTAAGTGGTT TTCGAAAAGT 720
GGCAAGCTGG TAACCAAGAT GTTTCAGAAG ATTCAAGATT TGATTGATGA TAAAGACGCC 780
CTGGTGTTCG TGAGCTTGA TGAGGTGGAG AGTCTCACAG CCGCCCGAAA TGCTGCAGG 840
GCGGGCACCG AGCCATCAGA TGCCATCCGC GTGGTCAATG CTGTCTTGAC CCAAATTGAT 900
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GACGTGGCCT TCGTGGACAG GGCTTGACATC AAGCAGTACA TTGGGCCACC CTCTGCAGCA 1020
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Seq ID NO: 290 Protein sequence:
Protein Accession #: NP_004228

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1 11 21 31 41 51
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AANHWWLPAA EFHGLWDSLIV YDVEVKSHLL DYVMTTLFS DKNVNSNLIT WNRVLLHGP 180
PGTGTSLCKL GAGKLTIRL SSRYRYGQLI EINSLSLFSK WFSSEGLKVT KMFQIKQDLI 240
DDKDALVFVL IDEVESLTAA RNACRAGTEP SDAIRVNAV LTQIDQIKRH SNVILITTSN 300
ITEKIDVAVF DRADIKQYIG PPSAAAIFKI YLSLEELMK CQIIYPRQQL LTLRELEMIG 360
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Seq ID NO: 291 DNA sequence
Nucleic Acid Accession #: NM_002658.1
Coding sequence: 77-1372

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CTTACCCTGG ATCCGCGAGT ACACCAAGGA AGAGAATGGC CTGGCCCTCT GAGGGTCCCC 1380
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ATCCCTTCCT TTTAGCTTAT TTCATCCAAT CCTCACTGGG TGGGGTGAGG ACCACTCTCT 2220
ACACTGAATA TTTATATTTC ACTATTTTAA TTTATATTTT TGTAATTTTA AATAAAAGTG 2280

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ATCAATAAAA TGTGATTTT CTGA

Seq ID NO: 292 Protein sequence:
Protein Accession #: NP_002649.1

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HCEIDKSKTC	YBGNHGFYRG	KASTDTMGRP	CLPWSNATVL	QQTYHAHRSD	ALQLGLGKHN	120
YCRNPDRRR	PWCYVQVGLK	PLVQECMVHD	CADGKPKSSP	PEELKFQCGQ	KTLRPRFKII	180
GGFTTIEHQ	WFAAIYRRH	RGGSVTYVCG	GSLISPCWVI	SATHCFIDYP	KKEDYIVYLG	240
RSRLNSNTQG	EMKFEEVNL	LHKDYSADTL	AHNDIALLLK	IRSGEGRCAQ	PSRTIQTICL	300
PSMYNDPQFG	TSCEITGFGK	ENSTDYLYPE	QLKMTVVVKLI	SHRECCQPHY	YGSEVITKML	360
CAADPQWKTD	SCQGDSSGGL	VCSLQGRMTL	TGIVSWGRGC	ALKDKPGVYT	RVSHFLPWIR	420
SHTKEENGLA	L					

Seq ID NO: 293 DNA sequence
Nucleic Acid Accession #: NM_001498
Coding sequence: 93..2006

1	11	21	31	41	51	
GGCACGAGGC	TGAGTGTCCG	TCTCGCGCCC	GGAAGCGGGC	GACCGCCGTC	AGCCCCGAGG	60
AGGAGGAGGA	GGAGGAGGAG	GAGGGGGCGG	CCATGGGGCT	GCTGTCCCAG	GGCTCGCCGC	120
TGAGCTGGGA	GGAAACCAAG	CGCCATGCCG	ACCACGTGCG	GCGGCACGGG	ATCCTCCAGT	180
TCCTGCACAT	CTACCACGCC	GTCAGGACCC	GGCACAAGGA	CGTTCTCAAG	TGGGGCGATG	240
AGGTGGAATA	CATGTTGGTA	TCTTTTGATC	ATGAAAATAA	AAAAGTCCGG	TTGGTCTCTGT	300
CTGGGGAGAA	AGTTCTTGAA	ACTCTGCAAG	AGAAGGGGGA	AAGGACAAAC	CCAAACCATC	360
CTACCCTTTG	GAGACCAGAG	TATGGGAGTT	ACATGATTGA	AGGGACACCA	GGACAGCCCT	420
ACGGAGGAAC	AATGTCCGAG	TTCAATACAG	TTGAGGCCAA	CATGCGAAAA	CGCCGGAAAG	480
AGGCTACTTC	TATATTAGAA	GAAAATCAGG	CTCTTTGCAC	AATAACTTCA	TTTCCAGAT	540
TAGGCTGTCC	TGGGTTTACA	CTGCCCGAGG	TCAAACCCAA	CCCAGTGGAA	GGAGGAGCTT	600
CCAAGTCCCT	CTTCTTTTCA	GATGAAGCAA	TAAACAAGCA	CCCTCGCTTC	AGTACCTTAA	660
CAAGAAATAT	CCGACATAGG	AGAGGAGAAA	AGGTTGTGAT	CAATGTACCA	ATATTTAAGG	720
ACAAGAATAC	ACCATCTCCA	TTTATAGAAA	CATTTACTGA	GGATGATGAA	GCTTCAAGGG	780
CTTCTAAGCC	GGATCATATT	TACATGGATG	CCATGGGATT	TGGAATGGGC	AATTGCTGTC	840
TCACGGTGAC	ATCTCAAGCC	TGCAGTATAT	CTGAGGCCAG	ATACCTTTAT	GATCAGTTGG	900
CTACTATCTG	TCCAATTGTT	ATGGCTTTGA	GTGCTGCATC	TCCCTTTTAC	CGAGGCTATG	960
TGTACAGCAT	TGATTGTCCG	TGGGGAGTGA	TTTCTGCATC	TGTAGATGAT	AGAACTCGGG	1020
AGGAGCGAGG	ACTGAGAGCC	TTGAAGAACA	ATAACTATAG	GATCAGTAAA	TCCCGATATG	1080
ACTCAATAGA	CAGCTATTTA	TCTAAGTGTG	GTGAGAAATA	TAATGACATC	GACTTGACGA	1140
TAGATAAAGA	GATCTACGAA	CAGCTGTTGC	AGGAAGGCAT	TGATCATCTC	CTGGCCACGC	1200
ATGTTGCTCA	TCTCTTTATT	AGAGACCCAC	TGACACTGTT	TGAAGAGAAA	ATACACCTGG	1260
ATGATGCTAA	TGAGTCTGAC	CATTTTGAGA	ATATTCAGTC	CACAAATTGG	CAGACAATGA	1320
GATTTAAGCC	CCCTCCTCCA	AACCTCAGCA	TTGGATGGAG	AGTAGAATTT	CGACCCATGG	1380
AGGTGCAATT	AACACAGCTT	GAGAACTCTG	CCTATGTGGT	GTTTGTGGTA	CTGCTCACCA	1440
GAGTGATCCT	TTCTTACAAA	TTGGATTTTC	TCATTCCACT	GTCAAAGGTT	GATGAGAACA	1500
TGAAGGTAGC	ACAGAAAAGA	GATGCTGTCT	TGCAGGGAAT	GTTTATTTTC	AGGAAAGATA	1560
TTTGCAAAGG	TGGCAATGCA	GTGGTGGATG	GTTGTGGCAA	GGCCAGAAAC	AGCACGGAGC	1620
TCGCTGCAGA	GGAGTACACC	CTCATGAGCA	TAGACACCAT	CATCAATGGG	AAGGAAGGTG	1680
TGTTTCTCTG	ACTGATCCCA	ATTCTGAACT	CTTACCTTGA	AAACATGGAA	GTGGATGTGG	1740
ACACCAGATG	TAGTATTCTG	AACCTACCTA	AGCTAATTAA	GAAGAGAGCA	TCTGGAGAAC	1800
TAATGACAGT	TGCCAGATGG	ATGAGGGAGT	TTATCGCAAA	CCATCCTGAC	TACAAGCAAG	1860
ACAGTGTGAT	AACCTGATGA	ATGAATTATA	GCCTTATTTT	GAAGTGTAAAC	CAAATTGCAA	1920
ATGAATTATG	TGAATGCCCA	GAGTTACTTG	GATCAGCATT	TAGGAAAGTA	AAATATAGTG	1980
GAAGTAAAC	TGACTCATCC	AACCTAGACAT	TCTACAGAAA	GAAAAATGCA	TTATTGACGA	2040
ACTGGCTACA	GTACCATGCC	TCTCAGCCCG	TGTGTATAAT	ATGAAGACCA	AATGATAGAA	2100
CTGTACTGTT	TCTGGGGCCA	GTGAGCCAGA	AATTGATTAA	GGCTTTCTTT	GGTAGGTAAA	2160
TCTAGAGTTT	ATACAGTGTA	CATGTACATA	GTAAGTATT	TTTGATTAAAC	AATGTATTTT	2220
AATAACATAT	CTAAAGTCAT	CATGAACCTG	CTGTACATT	TTTAAATTCT	TACTCTGGAG	2280
CAACCTACTG	TCTAAGCATG	TTTGTAATG	TACTGGTAAT	TGTACAATAC	TTGCATTCCA	2340
GAGTTAAAT	GTTTACTGTA	AATTTTGTG	CTTTTAAAGA	CTACCTGGGA	CCTGATTTAT	2400
TGAAATTTT	CTCTTAAAA	ACATTTCTC	TCGTTAATTT	TCCTTTGTCA	TTTCTTTTGT	2460
TGTTCTACAT	AAATCACTTG	AATCCATTGA	AAGTGCTTCA	AGGGTAATCT	TGGGTTTCTA	2520
GCACCTTATC	TATGATGTTT	CTTTTGCAAT	TGGAATAATC	ACTTGGTCAC	CTTGCCCCAA	2580
GCTTTCCCT	CTGAATAAAT	ACCCATTGAA	CTCTGAAAAA	AAAAAATAAA	AAAA	

Seq ID NO: 294 Protein sequence:
Protein Accession #: NP_001489

1	11	21	31	41	51	
MGLLSQGSPL	SWEETKRHAD	HVRRHGILQF	LHIYHAVKDR	HKDVLKWGDE	VEYMLVSFDH	60
ENKKVRLVLS	GKVLLETQGE	KGERTNPNHP	TLWRPEYGSY	MIEGTPGQPY	GGTMSEFNTV	120
EANMRKRKE	ATSILEENQA	LCTITSFPRL	GCPGFTLPEV	KPNPVEGGAS	KSLFPFDEAI	180
NKHPRFSTLT	RNIRHRRGK	VVINVPFKD	KNTPSPIET	FTEDDEASRA	SKPDHIYMDA	240
MGFGMGNCL	QVTFQACSIS	EARYLYDQLA	TICPIVMALS	AASFPYRGYV	SDIDCRWGI	300
SASVDDRTRE	ERGLEPLKNN	NYRISKSRD	SIDSYLSKCG	EKYNDIDLT	DKEIYBQLLQ	360
EGIDHLLAQH	VAHLFIRDPL	TLFEKIHLD	DANESDHFFEN	IQSTNQWQTM	FKPPPPNSDI	420
GWVFEFRPME	VQLTDFENSA	VVVFVLLTR	VILSYKLDL	IPLSKVDENM	KVAQRDAVL	480
QGMFYPRKDI	CKGGNAVDG	CGKAQNSTEL	AAEYTLMSI	DTIINGKEGV	FPGLIPILNS	540
YLENMEVDVD	TRCSILNYLK	LKKRASGEL	MTVARWMREF	IANHPDYKQD	SVITDEMNYN	600
LILKCNQIAN	ELCECPPELLG	SAFRKVKYSG	SKTDDSSN			

Seq ID NO: 295 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 247-816

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5      1      11      21      31      41      51
      |      |      |      |      |      |
      |      |      |      |      |      |
AGTGTTCGGC TGGGGCAGGC ACGCTGTGGC TGGCTACTTC CCTTCCTCCC ATCCCCCTTG 60
GGCCAAACGG GATCGGTGCT TCTGGTGAGA CGCCTCCCCA TGCACATCAC TCCCAGGTGC 120
CCTAGGGGGC ACATTTCCTCA CACTCTCCAG AGGGCAGGTT TCTAGAAAGT GCCACCAGTG 180
10     GGGAGGCGCC ACAACTTCAC TGCCATTTTG TGAGGTGCCG CCGTCTCTCC TCCAGCAAGG 240
      GAAACAATGA CCGATAAAAC AGAGAAGGTG GCTGTAGATC CTGAAACTGT GTTTAAACGT 300
      CCCAGGGAAT GTGACAGTCC TTCGTATCAG AAAAGGCAGA GGATGGCCCT GTTGGCAAGG 360
      AAACAAGGAG CAGGAGACAG CCTTATTGCA GGCTCTGCCA TGTCCAAAGA AAAGAAGCTT 420
      ATGACAGGAC ATGCTATTTC ACCCAGCCAA TTGGATTCTC AGATTGATGA CTTCAGTGGT 480
15     TTCAGCAAAG ATAGGATGAT GCAGAAACCT GGTAGCAATG CACCTGTGGG AGGAAACGTT 540
      ACCAGCAGTT TCTCTGGAGA TGACCTAGAA TGCAGAGAAA CAGCCTCCTC TCCCAAAAGC 600
      CAACGAGAAA TTAATGCTGA TATAAAACGT AAATTAGTGA AGGAACTCCG ATGCGTTGGA 660
      CAAAAATATG AAAAAATCTT CGAAATGCTT GAAGGAGTGC AAGGACCTAC TGCAGTCAGG 720
      AAGCGATTTT TTGAATCCAT CATCAAGGAA GCAGCAAGAT GTATGAGACG AGACTTTGTT 780
20     AAGCACCTTA AGAAGAACT GAAACGTATG ATTTGAGAAT ACTTGTCCCT GGAGGATTAT 840
      CACACCCCAA ATGCATAATC TCGTTAATGA TTGAGGAGAG AAAAGGATCA GATTGCTGTT 900
      TTCTACAATG GAGCAGGATA TTGCTGAAGT CTCCTGGCAT ATGTTACCGA ATCAAAATAGC 960
      CTTCAGAGG CTAAGAAATT TCTGTTAGTA AAAGATGTTT TTTTCCCAA AGCATTTTAT 1020
      TTGAAGGAT AACTTGTGTT TTGTTTATT TGTATTCCCA CCTGTGCTGG TAGATATTAT 1080
25     TAACCCATTA GGTAAATACT ATTACAGTCG TGGTTTCTGC A

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Seq ID NO: 296 Protein sequence:
Protein Accession #: Eos sequence

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30     1      11      21      31      41      51
      |      |      |      |      |      |
      |      |      |      |      |      |
MTDKTEKVAV DPETVFKRPR ECDSPSYQKR QRMALLARKQ GAGDSLIAGS AMSKEKKLMT 60
GHAIPPSQLD SQIDDFTFGS KDRMMQKPGS NAPVGGNVTS SFGDDLECR ETASSPKSQR 120
35     EINADIKRKL VKELRCVGQK YEKIFEMLEG VQGPTAVRKR FPESIIKEAA RCMRRDFVKH 180
      LKKKLKRLMI

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Seq ID NO: 297 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 247-815

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40     1      11      21      31      41      51
      |      |      |      |      |      |
      |      |      |      |      |      |
AGTGTTCGGC TGGGGCAGGC ACGCTGTGGC TGGCTACTTC CCTTCCTCCC ATCCCCCTTG 60
GGCCAAACGG GATCGGTGCT TCTGGTGAGA CGCCTCCCCA TGCACATCAC TCCCAGGTGC 120
CCTAGGGGGC ACATTTCCTCA CACTCTCCAG AGGGCAGGTT TCTAGAAAGT GCCACCAGTG 180
45     GGGAGGCGCC ACAACTTCAC TGCCATTTTG TGAGGTGCCG CCGTCTCTCC TCCAGCAAGG 240
      GAAACAATGA CCGATAAAAC AGAGAAGGTG GCTGTAGATC CTGAAACTGT GTTTAAACGT 300
      CCCAGGGAAT GTGACAGTCC TTCGTATCAG AAAAGGCAGA GGATGGCCCT GTTGGCAAGG 360
      AAACAAGGAG CAGGAGACAG CCTTATTGCA GGCTCTGCCA TGTCCAAAGA AAAGAAGCTT 420
      ATGACAGGAC ATGCTATTTC ACCCAGCCAA TTGGATTCTC AGATTGATGA CTTCAGTGGT 480
      TTCAGCAAAG ATAGGATGAT GCAGAAACCT GGTAGCAATG CACCTGTGGG AGGAAACGTT 540
      ACCAGCAGTT TCTCTGGAGA TGACCTAGAA TGCAGAGAAA CAGCCTCCTC TCCCAAAAGC 600
      CAACAAGAAA TTAATGCTGA TATAAAACGT AAATTAGTGA AGGAACTCCG ATGCGTTGGA 660
      CAAAAATATG AAAAAATCTT CGAAATGCTT GAAGGAGTGC AAGGACCTAC TGCAGTCAGG 720
      AAACGATTTT TTGAATCCAT CATCAAGGAA GCAGCAAGAT GTATGAGACG AGACTTTGTT 780
      AAGCACCTTA AGAAGAACT GAAACGTATG ATTTGAGAAT ACTTGTCCCT GGAGGATTAT 840
      CACACCCCAA ATGCATAATC TCATTAATGA TTGAGGAGAG AAAAGGATCA GATTGCTGTT 900
      TTCTACAATG GAGCAGGATA TTGCTGAAGT CTCCTGGCAT ATGTTACCGA ATCAACTGGC 960
60     CTTCAGAGG CTAAGAAATT TCTGTTAGTA AAAGATGTTT TTTTCCCAA AGCGTTTAT 1020
      TTGAAGGAT AACTTGTGTT TTGTTTATT TGTATTCCCA CCTGTGCTGG TAGATATTAT 1080
      TAACCCATTA GGTAAATACT ATTACAGTCG TGGTTTCTGC A

```

Seq ID NO: 298 Protein sequence:
Protein Accession #: Eos sequence

```

65     1      11      21      31      41      51
      |      |      |      |      |      |
      |      |      |      |      |      |
MTDKTEKVAV DPETVFKRPR ECDSPSYQKR QRMALLARKQ GAGDSLIAGS AMSKEKKLMT 60
GHAIPPSQLD SQIDDFTFGS KDRMMQKPGS NAPVGGNVTS SFGDDLECR ETASSPKSQ 120
70     EINADIKRKL VKELRCVGQK YEKIFEMLEG VQGPTAVRKR FPESIIKEAA RCMRRDFVKH 180
      LKKKLKRLMI

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Seq ID NO: 299 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 247-815

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75     1      11      21      31      41      51
      |      |      |      |      |      |
      |      |      |      |      |      |
AGTGTTCGGC TGGGGCAGGC ACGCTGTGGC TGGCTACTTC CCTTCCTCCC ATCCCCCTTG 60
GGCCAAACGG GATCGGTGCT TCTGGTGAGA CGCCTCCCCA TGCACATCAC TCCCAGGTGC 120
CCTAGGGGGC ACATTTCCTCA CACTCTCCAG AGGGCAGGTT TCTAGAAAGT GCCACCAGTG 180
80     GGGAGGCGCC ACAACTTCAC TGCCATTTTG TGAGGTGCCG CCGTCTCTCC TCCAGCAAGG 240
      GAAACAATGA CCGATAAAAC AGAGAAGGTG GCTGTAGATC CTGAAACTGT GTTTAAACGT 300
      CCCAGGGAAT GTGACAGTCC TTCGTATCAG AAAAGGCAGA GGATGGCCCT GTTGGCAAGG 360
      AAACAAGGAG CAGGAGACAG CCTTATTGCA GGCTCTGCCA TGTCCAAAGC AAAGAGCTTA 420
      TGACAGGACA TGCTATTCCA CCCAGCCAAT TGGATTCTCA GATTGATGAC TTCAGTGGT 480
85

```


TCAGCAAAGA TAGGATGATG CAGAAACCTG GTAGCAATGC ACCTGTGGGA GGAAACGTTA 540
 CCAGCAGTTT CTCTGGAGAT GACCTAGAAT GCAGAGAAAC AGCCTCCTCT CCCAAAAGCC 600
 AACAAGAAAT TAATGCTGAT ATAAAACGTA AATTAGTGAA GGAACCTCGA TGCCTGGAC 660
 AAAAAATATGA AAAAATCTTC GAAATGCTTG AAGGAGTGCA AGGACCTACT GCAGTCAGGA 720
 AACGATTTTT TGAATCCATC ATCAAGGAAG CAGCAAGATG TATGAGACGA GACTTTGTTA 780
 AGCACCTTAA GAAGAAACTG AAACGTATGA TTTGAGAATA CTTGTCCCTG GAGGATTATC 840
 ACACCCCAAA TGCATAATCT CATTAAATGAT TGAGGAGAGA AAAGGATCAG ATTGCTGTTT 900
 TCTACAATGG AGCAGGATAT TGCTGAAGTC TCCTGGCATA TGTACCGAA TCAACTGGCC 960
 TTCCAGAGGC TAAGAAATTT CTGTTAGTAA AAGATGTTCT TTTTCCCAA GCGTTTTATT 1020
 TGAAGGATA ACTTGTGTTT TGGTTATTT GTATTCCAC CTGTGCTGGT AGATATTATT 1080
 AACCATTAG GTAAATACTA TTACAGTCGT GGTTCCTGCA

Seq ID NO: 300 Protein sequence:
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 | | | | |
 MTDKTEKVAV DPETVFKRPR ECDSPSYQKR QRMALLARKQ GAGDSLIAGS AMSKAKKLMT 60
 GHAIPPSQLD SQIDDPFGPS KDRMMQKPGS NAPVGGNVT SFGDDLECR ETASSPKSQ 120
 EINADIKRKL VKELRCVGQK YEKIFEMLEG VQGPTAVRKR FFESIIEKAA RCMRRDPVKH 180
 LKKLKRMI

Seq ID NO: 301 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 247-812

1 11 21 31 41 51
 | | | | |
 AGTGTTCGGC TGGGGCAGGC ACGCTGTGGC TGGCTACTTC CCTTCCTCCC ATCCCCCTTG 60
 GGCCAAACGG GATCGGTGCT TCTGGTGAGA CGCCTCCCA TGCACATCAC TCCAGGTGC 120
 CCTAGGGGGC ACATTTCCCA CAATCCCAAG AGGGCAGGTT TCTAGAAAGT GCCACCACTG 180
 GGGAGGGGCC ACAACTTCAC TGCCATTTTG TGAGGTGCGG CCGTCTCTCC TCCAGCAAGG 240
 GAAACAATGA CCGATAAAAC AGAGAAGGTG GCTGTAGATC CTGAAACTGT GTTTAAACGT 300
 CCCAGGGAAT GTGACAGTCC TTCGTATCAG AAAAGGCAGA GGATGGCCCT GTTGGCAAGG 360
 AAACAAGGAG CAGGAGACAG CCTTATTGCA GGCTCTGCCA TGTCCAAAGA AAAGAGCTTA 420
 TGACAGGACA TGCTATTCCA CCCAGCCAAT TGGATTCTCA GATTGATGAC TTCACTGGTT 480
 TCAGCAAAGA TGGGATGATG CAGAAACCTG GTAGCAATGC ACCTGTGGGA GGAAATGTTA 540
 CCAGCAATTT CTCTGGAGAT GACCTAGAAT GCAGAGGAAT AGCCTCCTCT CCCAAAAGCC 600
 AACAAGAAAT TAATGCTGAT ATAAAATGTC AAGTAGTGAA GGAAATCCGA TGCCTTGGAC 660
 AATATGAAAA AATCTTCGAA ATGCTTGAAG GAGTGCAAGG ACCTACTGCA GTCAGGAAAC 720
 GATTTTTTGA ATCCATCATC AAGGAAGCAG CAAGATGTAT GAGACGAGAC TTTGTTAAGC 780
 ACCTTAAGAA GAAACTGAAA CGTATGATTT GAGAATACTT GTCCCTGGAG GATTATCACA 840
 CCCCATAATG ATAATCTCAT TAATGATTGA GGAGAGAAAA GGATCAGATT GCTGTTTCT 900
 ACAATGGAGC AGGATATTGC TGAAGTCTCC TGGCATATGT TACCGAATCA ACTGGCCTTC 960
 CAGAGGCTAA GAAATTTCTG TTAGTAAAAG ATGTTCTTTT TCCCAAAGCG TTTTATTGTA 1020
 AAGGATAACT TGTGTTTGG TTATTTTGTG TTTCCACCTG TGCTGCTAGA TATTATTAAC 1080
 CCATTAGGTA AATACTATTA CAGTCGTGGT TTCTGCA

Seq ID NO: 302 Protein sequence:
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 | | | | |
 MTDKTEKVAV DPETVFKRPR ECDSPSYQKR QRMALLARKQ GAGDSLIAGS AMSKEKLMT 60
 GHAIPPSQLD SQIDDPFGPS KDRMMQKPGS NAPVGGNVT SFGDDLECR GIASSPKSQ 120
 EINADIKQV VKEIRCLGQY EKIFEMLEGV QGPTAVRKR FESIIEKAA RCMRRDPVKHL 180
 KKKLKRMI

Seq ID NO: 303 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 247-815

1 11 21 31 41 51
 | | | | |
 AGTGTTCGGC TGGGACAGGC ACGCTGTGGC TGGCTACTTC CCTTCCTTCC ATCCCCCTTG 60
 GGCCAAACAG GATCGGTGCT TCTGGTGAGA CGTCTCCCA TGCACATCAC TCCAGATGC 120
 CCTAGGGGGC ACATTTCCCA CAATCCCAAG AGGGCAGGTT TCTAGAAAGT GCCACCACTG 180
 GGGAGGGGCC ACAACTTCAC TGCCATTTTG TGAGGTGCGG CCGTCTCTCC TCCAGCAAGG 240
 GAAACAATGA CCGATAAAAC AGAGAAGGTG GCTGTAGATC CTGAAACTGT GTTTAAACGT 300
 CCCAGGGAAT GTGACAGTCC TTCGTATCAG AAAAGGCAGA GGATGGCCCT GTTGGCAAGG 360
 AAACAAGGAG CAGGAGACAG CCTTATTGCA GGCTCTGCCA TGTCCAAAGC AAAGAGCTTA 420
 TGACAGGACA TGCTATTCCA CCCAGCCAAT TGGATTCTCA GATTGATGAC TTCACTGGTT 480
 TCAGCAAAGA TAGGATGATG CAGAAACCTG GTAGCAATGC ACCTGTGGGA GGAAACGTTA 540
 CCAGCAGTTT CTCTGGAGAT GACCTAGAAT GCAGAGAAAC AGCCTCCTCT CCCAAAAGCC 600
 AACAAGAAAT TAATGCTGAT ATAAAACGTA AATTAGTGAA GGAACCTCGA TGCCTTGGAC 660
 AAAAAATATGA AAAAATCTTC GAAATGCTTG AAGGAGTGCA AGGACCTACT GCAGTCAGGA 720
 AACGATTTTT TGAATCCATC ATCAAGGAAG CAGCAAGATG TATGAGACGA GACTTTGTTA 780
 AGCACCTTAA GAAGAAACTG AAACGTATGA TTTGAGAATA CTTGTCCCTG GAGGATTATC 840
 ACACCCCAAA TGCATAATCT CGTTAATGAT TGAGGAGAGA AAAGGATCAG ATTGCTGTTT 900
 TCTACAATGG AGCAGGATAT TGCTGAAGTC TCCTGGCATA TGTACCGAA TCAACTGGCC 960
 TTCCAGAGGC TAAGAAATTT CTGTTAGTAA AAGATGTTCT TTTTCCCAA GCGTTTTATT 1020
 TGAAGGATA ACTTGTGTTT TGGTTATTT GTATTCCAC CTGTGCTGGT AGATATTATT 1080
 AACCATTAG GTAAATACTA TTACAGTCGT GGTTCCTGCA

Seq ID NO: 304 Protein sequence:
 Protein Accession #: Eos sequence

1	11	21	31	41	51	
MTDKTEKVVAV	DPETVFKRPR	ECDSFSYQKR	QRMALLARKQ	GAGDSLIIAGS	AMSKAKKLMT	60
GHAIPPSQLD	SQIDDFTFGS	KDRMMQKPGS	NAPVGGNVTS	SFSGDDLECR	ETASSPKSQQ	120
5	ENADIKRKL	VKELRCVGQK	YEKIFEMLEG	VQGPTAVRKR	FFESIIEKAA	180
	LKKKLRMI					

Seq ID NO: 305 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 87-689

1	11	21	31	41	51	
CGTGGAGGCA	GCTAGCGCGA	GGCTGGGGAG	CGCTGAGCCG	CGCGTCGTGC	CCTGCGCTGC	60
15	CCAGACTAGC	GAACAATACA	GTCAGGATGG	CTAAAGGTGA	CCCCAAGAAA	120
	AGATGTCCCG	TTATGCCTTC	TTTGTGCAGA	CATGCAGAGA	AGAACATAAG	180
	CAGAGGTCCC	TGTCAATTTT	GCGGAATTTT	CCAAGAAGTG	CTCTGAGAGG	240
	TGTCCGGGAA	AGAGAAATCT	AAATTTGATG	AAATGGCAAA	GGCAGATAAA	300
	ATCGGGAAT	GAAGGATTAT	GGACCAGCTA	AGGGAGGCAA	GAAGAAGAAG	360
20	CTCCCAAAAG	GCCACCGTCT	GGATTCTTCC	TGTTCTGTTC	AGAATTCCCG	420
	AAATCCACAA	CCCCGCGATC	TCTATTGGAG	ACGTGGCAAA	AAAGCTGGGT	480
	ATAATTTAAA	TGACAGTGAA	AAGCAGCCTT	ACATCACTAA	GGCGGCAAG	540
	AGTATGAGAA	GGAGCGCTCT	GACTATAAGT	CGAAAGGAAA	GTTTGATGGT	600
	CTGCTAAAGT	TGCCCGGAAA	AAGGTGGAAG	AGGAAGATGA	AGAGAGGAG	660
25	AGGAGGAGGA	GGAGGAGGAG	GATGAATAAA	GAAACTGTTT	ATCTGTCTCC	720
	TTAGAGTAGG	GGAGCGCCTG	AATTGCACAC	TCTCTTATTT	GAGAAGTGTC	780
	ATTAGGTTTA	ATTACAAAAT	TTGATCAGCA	TCATATTGTA	GTCTCTCAAA	840
	AATTGTCACT	GGTTTACATG	AAGTGGCCAT	GGGTGTCTGG	AGCACCTCGA	900
	AAGTTGTACA	TATTTCCAAA	CATTTTAAAA	ATGAAAAGGC	ACTCTCGTGT	960
30	CTGTGCACCT	TGCTGTTGGT	GTGACAAGGC	ATTTAAAGAT	GTTTCTGGCA	1020
	ATTTGTAAGG	TGGTGGTAAC	TATGGTTATT	GGCTAGAAAT	CCTGAGTTTT	1080
	TATCTATAGT	TTGTAAAAAG	AACAAAACAA	CCGAGACAAA	CCCTTGATGC	1140
	GCGTTGAGGC	TGTGGGGAAG	ATGCCCTTTG	GGAGAGGCTG	TAGCTCAGGG	1200
	GAGGCTGGAC	CTGTTGACTC	TGCAGGGGGC	ATCCATTAG	CTTCAGGTTG	1260
35	GTATATAGTG	ACATAGCATT	CTGCTGCCAT	CTTAGCTGTG	GACAAAGGGG	1320
	CATGAGAATA	TTTTTTTTTT	TAAGTGCCTG	AGTTTTTAAA	CTGTTTGTGT	1380
	TATAGAACTC	TTCAATGTCA	GCAAGCAAAA	GAGTCACTGC	ATCAATGAAA	1440
	CTCCTGTACT	TAAACACGAT	TGCAACCGTT	CTGTTATTTT	TTTTGTATGT	1500
	GAAATGTTTT	TGAAGTTAAA	TAAACAGTAT	TACATTTTAA	AAACTCTTCT	1560
40	AGTCAATTTT	TGACTCACAG	CAGTGAACAA	ACCCCACTC	CATTGTATTT	1620
	CTCCCTATAA	TTTGTGTGCT	TTCTTTTATT	ACTCAGTGGC	CAGCTCACTT	1680
	TGAAGGAGAG	GGCTACTTGA	AGCTACTGTG	TGATTTTGTG	TGTGTCTGAG	1740
	ATGAAGTCTG	GAGGAGTTAG	GAGAACGACA	TAGGCAAGGT	TCAGCAGCCT	1800
	AGGAAGGTGG	GATGATAGCA	CTGAGGCTAT	CTAGGTTTAA	CTTTTGTCCC	1860
45	CCTATTTTGT	GGGGCCAAAT	GCATTGCTAA	ACAGCAATTT	CAGAGTGAT	1920
	AAATTAAGGC	CTTATTTGTT	TTCTCTTTCA	CCCCTACCCC	CCGTGCTCCT	1980
	ACATTATTTG	TGGTGCCCAA	CATTGCGGGT	CTTGAGCCTG	CTGCTGGTCT	2040
	AGTGAGGGTA	TGTGGGATGG	GGTGGTGGGG	TAGGGGACGG	TATCCTTTTT	2100
	TTGGAAACAC	CAAAACACCC	AAGGAAGATG	ATAGGCTCCA	TCTTGGGCCA	2160
50	AGGCGAGGCT	AATGGAATCA	ACCATTTCTG	AGCACTAAAT	GTATCATGAA	2220
	GCCTGCTCAT	AAGTTTAGCT	CATTCACTGG	AAATGTAGAT	TGATGTTCAA	2280
	GAAGGAGCTT	GGTTTGTGTG	TCAGTGGTTA	TATTAGTGGG	TAGTGAACAA	2340
	GTTGGGGTGA	GGGGAGTAGC	CCACAGTAGC	AAGTGGTGAC	ACTAAATACC	2400
	CTGATGTGTA	TATACATCAT	TACTGTCCGT	AGCAATGAAG	GATACAGTAC	2460
55	GTGAGTGTG	CTATTGCCCA	GCATTAATAT	TTGGGTGTGT	ATGTTTGAGG	2520
	CGCAGGAGTG	TTTTTGTGCT	ATTAATTTTA	AGAGAAAGCA	GCTTTTCTCT	2580
	GTTGAGAAAC	TTGCATGTCT	GGAGGCGGTG	TCCTCTCCGC	CCTGTCCGGT	2640
	TAGGAGTTAT	GGTCACGGTG	ACAGCCTGAT	CTCTTATGTG	TTCAATAGCA	2700
	CATCAGAACT	GTTTGTCTCT	AATGTGTTCC	TCTAGTTCTA	GAAAATGACC	2760
60	AAAACCTCGT	TGTGAGGTTT	GCCCAGAGGC	ACTTGTTCCT	GAATTTCCCC	2820
	GCCATGTCTT	TGTCACTTGG	CATTCTAAGC	TAAAGCTTTA	GCTTCCCAAT	2880
	CTAGGCCAAG	ATTCCGGAGC	TGTTGCCAGC	CTCGTCAAA	ATGGAAGAGA	2940
	GGTCAAAGG	GAGTGATTGG	TTAAGTGGTG	CGCGTCTATC	TCATAACTAG	3000
	CAGGGAAGGG	CCAAGGATGG	AAAGGGGTAA	CTTTTGTGCT	TCCAAAGTAG	3060
65	GTGGGGGAGC	AGTTTAGCCA	GATGATCTTT	GATTAGGCAA	ACATTGAGTT	3120
	TGTCAAGTTG	AGGCCACTTG	GTCCATTAGC	TGGGGCAGCA	AGATCACTAC	3180
	CACACTGTGG	CAAGATTGCT	CTTCTAGTGG	AATAATGCCC	TAGTTTCTCT	3240
	AAGTGGCATG	ATGTTACCTA	AGGCTTAGGC	TTAGCTTGAT	TTCTGGGCCC	3300
	TTCTTAAGAT	GCCAACTGT	TGCTTTTTTT	TTTTTTTTTCC	CCCATTAAAA	3360
70	CTACTCCCTC	TAACCACTTC	ACCCCATTTT	TGAATGACAT	TTTATCTCTC	3420
	AGGCTGTGAT	GTAGTGACTA	TTGTCTGTGT	CTCCTGTGTG	TGTCTGTCTT	3480
	GTATTTGGGG	ACGTTGGATG	CATTCAATTT	CTGTAATAAA	G	

Seq ID NO: 306 Protein sequence:
Protein Accession #: NP_005333.1

1	11	21	31	41	51	
MAKGDPPKPK	GKMSAYAFV	QTCREEHKKK	NPEVPVNFPE	FSKKCSERWK	TMSGKEKSKP	60
80	DEMAKADKVR	YDREMKDYG	AKGKKKKKDP	NAPKRPPSGF	FLFCSEFRPK	120
	GDVAKKLGE	WNNLNDSEK	PYITKAALK	EKYEKDVADY	KSKGKFDGAK	180
	EEEEEEEEEE	EEEEEEEEEE				

Seq ID NO: 307 DNA sequence
Nucleic Acid Accession #: NM_022342
Coding sequence: 1..2178

	1	11	21	31	41	51	
	ATGGGTACTA	GGAAAAAAGT	TCATGCATT	GTCCTGTGCA	AACCCACCGA	TGACTTTGCT	60
5	CATGAAATGA	TCAGATACGG	AGATGACAAA	AGAAGCATTTG	ATATTCACCTT	AAAAAAGAC	120
	ATTCCGAGAG	GAGTTGTCAA	TAACCAACAG	ACAGACTGGT	CGTTTAAGTT	GGATGGAGTT	180
	TTCAACGATG	CCTCCAGGA	CTTGTTTAT	GAGACAGTTG	CAAAGGATGT	GGTTTCTCAG	240
	CCCTCGATG	GCTATAATGG	CACCATCATG	TGTTATGGGC	AGACGGGAGC	TGGCAAGACA	300
10	ACACCATGA	TGGGGGCAAC	TGAGAATTAC	AAGCACCAGG	GGATCCTCCC	TGCTGCCCTG	360
	AGCAGGTTT	TTAGGATGAT	CGAAGAACGC	CCACACATG	CCATCACTGT	GCGTGTTC	420
	ACTTGGA	TCTATAATGA	GAGCCTGTTT	GATCTCCTGT	CCACTCTGCC	CTATGTTGGA	480
	CCTCAGTCA	CACCAATGAC	CATCGTGGAA	AACCCCTCAAG	GAGTCTTCAT	TAAGGGCTTG	540
	CAGTTCCAC	TCACAAGTCA	GGAGGAGGAT	GCATTACGCC	TCCTTTTGA	GGGTGAGACC	600
15	ACAGGATTA	TAGCCTCCCA	CACATGAAC	AAAACTCTT	CCAGATCACA	CTGCAATTTT	660
	CCATCTACT	TAGAGGCCCA	TTCCCGGACC	TTATCAGAGG	AAAAGTACAT	CACCTCCAAA	720
	TTAAGTTGG	TGGATCTGGC	AGGCTCAGAG	AGGCTGGGGA	AGTCTGGGTC	TGAGGGCCAA	780
	TCCTGAAGG	AAGCCACCTA	CATCAACAAA	TCGCTCTCAT	TCCTGGAGCA	GGCCATCATT	840
	CCCTTGGGG	ACCAGAACCG	GGACCACATC	CCCTTTCGGC	AGTGCAAGCT	CACCCACGCT	900
20	TGAAGGACT	CGTTAGGGGG	AAACTGCAAT	ATGGTCCTCG	TGACAAACAT	CTATGGAGAA	960
	CTGCCAGT	TAGAAGAAAC	GCTATCTTCA	CTGAGATTG	CCAGCAGGAT	GAAGCTAGTC	1020
	CCACTGAGC	CTGCCATCAA	TGAAAAGTAT	GATGCTGAGA	GAATGGTCAA	GAACCTGGAG	1080
	AGGAAGTAC	CACACTCAA	GCAGGAGCTG	GCTATCCATG	ACAGCCTGAC	CAACCGCACC	1140
25	TTGTGACCT	ATGACCCCAT	GGATGAAATC	CAGATTGCTG	AGATCAACTC	CCAGGTGCGG	1200
	GGTACCTGG	AGGGGACACT	GGACGAGATC	GACATAATCA	GCCTTAGACA	GATCAAGGAG	1260
	TGTTCAACC	AGTTCGGGT	GGTCTGAGC	CAACAGGAAC	AGGAAGTGA	GTCCACTTTG	1320
	GCAGGAAGT	ACACCTCTGA	TGACAGGAAT	GACTTTGCG	CCATTCTCTG	TATCCAGAAG	1380
	CGGGGCTTG	TGGATGTTGA	TGGCCACCTA	GTGGGTGAGC	CTGAAGGACA	AAACTTTGGA	1440
30	TCGGAGTCG	CCCTTTCTC	TACCAACCT	GGGAAGAAAG	CCAAGTCCAA	GAAGACATTC	1500
	AAGAGCCAC	TAGAGCCCGA	CACCCACCC	TCCAACCCAG	TGGCCTTTGA	GGAGTTTAA	1560
	ATGAGCAAG	GTAGTGAGAT	CAACCGAAT	TTCAAAGAAA	ACAAATCCAT	CTTGAATGAA	1620
	GGAGGAAAA	GGGCCAGCGA	GACCACACAG	CACATCAATG	CCATCAAGCG	GGAGATTGAT	1680
	TGACCAAGG	AGGCCCTGAA	TTTCAGAAAG	TCACACGCGG	AGAAGCAAGG	CAAGTACGAA	1740
	ACAAGGGGC	TGATGATCAT	CGATGAGGAA	GAATTCCTGC	TGATCCTCAA	GCTCAAAGAC	1800
35	TCAAGAGC	AGTACCGCAG	CGAGTACCAG	GACCTGCGTG	ACCTCAGGGC	TGAGATCCAG	1860
	ATTGCCAGC	ACCTAGTCGA	TCAGTGTGCG	CACCGCTGCG	TCATGGAATT	TGACATCTGG	1920
	ACAATGAGT	CCTTTGTCT	CCCTGAGGAC	ATGCAGATGG	CACTGAAACC	AGGCGGCAGC	1980
	TCCGGCCAG	GCATGGTCCC	TGTGAACAGG	ATTGTGTCTC	TGGGAGAAGA	TGACCAGGAC	2040
40	AATTACAGC	AGCTGACGCA	GAGGGTGCTT	CCTGAGGGCC	CTGATTCAT	CTCCTTCTAC	2100
	ATGCCAAAG	TCAAGATAGA	GCAGAAGCAT	AATTACTTGA	AAACCATGAT	GGGCTCCAG	2160
	AGGCACATA	GAAATAG					

Seq ID NO: 308 Protein sequence:

Protein Accession #: NP_071737

	1	11	21	31	41	51	
	MGTRKKVHAF	VRVKPTDDFA	HEMIRYGDDK	RSIDIHLKKD	IRRGVVNNQQ	TDWSFKLDGV	60
	LHDASQDLVY	ETVAKDVVSQ	ALDGVNGTIM	CYGGTQAGKT	YTMGATENY	KHRGILPRAL	120
50	QQVFRMIEER	PTHATVVRVS	YLEIYNESLF	DLSTLPYVG	PSVTPMTIVE	NPQGVFIKGL	180
	SVHLTSQEED	AFSLLEFEGT	NRIIASHTMN	KNSRSRSHCIF	TIYLEAHSRT	LSEEEKYITSK	240
	INLVDLAGSE	RLGKSGSEQG	VLKEATYINK	SLSFLEQAI	ALGDQKRDHI	PFRQCKLTHA	300
	KLDLSLGNEN	MVLVTNIYGE	AAQLEETLSS	LRFASRMKLV	TTEPAINEKY	DAERMVKNLE	360
	KELALLKQEL	AHDSLTNRT	FVTYDPMDEI	QIAEINSQVR	RYLEGTILDEI	DIISLRQIKE	420
55	VFNQFRVVL	QQEQEVESYL	RRKYTLIDRN	DFAAISAIQK	AGLVDVDGHL	VGEPEGQNF	480
	LGVAFFSTKP	GKKAKSKKTF	KEPLRPDTPP	SKPVAFEEFK	NEQGSSEINRI	FKENKSILNE	540
	RRKRASETQ	HINAIKREID	VTKEALNFQK	SLREKQKQYE	NKGLMIIDEE	EPFLILKLD	600
	LKKQYRSEYQ	DLRLDLRAEQ	YQHLVDQCR	HRLLEMEFDIW	YNESFVIPED	MQMALKPGGS	660
	IRPGMVPVNR	IVSLGEDDQD	KFSQLQQRVL	PEGPDSISFY	NAKVKIEQKH	NVLKTMMLQ	720
60	QAHRK						

Seq ID NO: 309 DNA sequence

Nucleic Acid Accession #: CAT cluster

	1	11	21	31	41	51	
65	TTTTTTTTTT	TTTTTTTAA	TGCTGCTGT	CATGCTCTGT	CTACCAGGCT	GAATTTCCAA	60
	AAATTTCTGC	ATAGCAATTT	TAGCCAAAAC	TATATATGTT	CTGGGGAGGA	TAGGCATAGG	120
	CACATTGAAG	ACCAAAGGAA	AGAGTGAAGA	AGTGTAGTTG	GGTCATTGTG	AATGGATGTT	180
70	TAGATTGTCA	AGAAAAGTGG	GCCAGAGGCC	CCACCTCACA	CTAGGACGGC	AATGCTCTCT	240
	CATTAGTATC	TCAGGCACCA	TGGGTCTTAT	TTGGTGTCTAT	AAGAAACACC	CTCAACAAAG	300
	TAATGAACCC	TCAGCCTCCA	GCTTCTCTTC	TTCGGGATTC	TTCTTAGGGC	CTCCTTTTTC	360
	CTTTTATGTT	TCCAGTACCC	TGAATTTCTT	ATTCCCATCC	CCCATTAATA	TCTGCTTCAA	420
75	AGAAAAAACA	AGAAGGACAC	ATTCACCTTA	AGATCCAAAT	GAATGATAAG	AGCTTAAAC	480
	ATTATACCTA	TCAGTATTAT	TGCAATTTT	ATAGAAACCA	AAACCATATT	TCACCAAC	

Seq ID NO: 310 DNA sequence

Nucleic Acid Accession #: NM_018622.2

Coding sequence: 1-1140

	1	11	21	31	41	51	
80	ATGGCGTGGC	GAGGCTGGGC	GCAGAGAGGC	TGGGGCTGCG	GCCAGGCGTG	GGGTGCGTGG	60
	GTGGCGGGCC	GCAGCTGCCA	GGAGCTCACT	GCGGTCTTAA	CCCCGCGCGA	GCTCCTCGGA	120
85	CGCAGGTTTA	ACTTCTTTAT	TCAACAAAAA	TGCGGATTCA	GAAAGACACC	CAGGAAGGTT	180
	GAACCTCGAA	GATCAGACCC	AGGGACAAGT	GGTGAAGCAT	ACAAGAGAAG	TGCTTTGATT	240
	CCTCCTGTGG	AAGAAACAGT	CTTTTATCCT	TCTCCCTATC	CTATAAGGAG	TCTCATAAAA	300
	CCTTTATTTT	TACTGTGTTG	GTTTACAGGC	TGTGCATTG	GATCAGCTGC	TATTTGGCAA	360

TATGAATCAC TGAAATCCAG GGTCCAGAGT TATTTTGATG GTATAAAAGC TGATTGGTTG 420
 GATAGCATAA GACCACAAAA AGAAGGAGAC TTCAGAAAGG AGATTAACAA GTGGTGGAAAT 480
 AACCTAAGTG ATGGCCAGCG GACTGTGACA GGTATTATAG CTGCAATGT CCTTGTATTTC 540
 TGTATATGGA GAGTACCTTC TCTGCAGCGG ACAATGATCA GATATTTCAC ATCGAATCCA 600
 GCCTCAAAGG TCCTTTGTTC TCCAATGTTC CTGTCAACAT TCAGTCACTT CTCCTTATT 660
 CACATGGCAG CAAATATGTA TGTTTTGTGG AGCTTCTCTT CCAGCATAGT GAACATTCTG 720
 GGTCAAGAGC AGTTCAATGGC AGTGTAACCTA TCTGCAGGTG TTATTTCCAA TTTTGTTCAGT 780
 TACCTGGGTA AAGTTGCCAC AGGAAGATAT GGACCATCAC TTGGTGCATC TGGTGCATC 840
 ATGACAGTCC TCGCAGCTGT CTGCACTAAG ATCCCAGAAG GGAGGCTTGC CATTATTTTC 900
 CTTCCGATGT TCACGTTTAC AGCAGGGAAT GCCCTGAAAG CCATTATCGC CATGGATACA 960
 GCAGGAATGA TCCTGGGATG GAAATTTTTT GATCATGCGG CACATCTTGG GGGAGCTCTT 1020
 TTTGGAATAT GGTATGTTAC TTACGGTCAT GAACTGATTT GGAAGAACAG GGAGCCGCTA 1080
 GTGAAATCT GGCATGAAAT AAGGACTAAT GGCCCCAAAA AAGGAGGTGG CTCTAAGTAA

Seq ID NO: 311 Protein sequence:
 Protein Accession #: NP_061092.2

1 11 21 31 41 51
 MAWRGWAQRG WCGGQAWGAS VGGRSCEELT AVLTPPQLLG RRFNFFIQK CGFRKAPRKV 60
 EPRRSDPGTS GEAYIKRSALI PPVEETVFYP SPYPIRSLIK PLFFTUVGFTG CAFGSAAIWQ 120
 YESLKSRRVQS YFDGKADWL DSIRPQKEGD FRKEINKWNN NLSDGQRTVT GIIAANVLVF 180
 CLWRVPQLQR TMIRYFTSNP ASKVLCSPLM LSTFSHFSLF HMAANMYVLW SPSSSIVNIL 240
 GQEQFMAVYL SAGVISNFSV YLKVATGRY GPSLGAAGAI MTVLAAVCTK IPEGRILAIIF 300
 LPMFTFTAGN ALKAIAMDT AGMILGWKFF DHAHLGGLAL FGVYVYTYGH ELIWNKREPL 360
 VKIWHBIRTN GPKKGGGSK

Seq ID NO: 312 DNA sequence
 Nucleic Acid Accession #: NM_000625
 Coding sequence: 195..3656

1 11 21 31 41 51
 CTCTCGGCCA CCTTTGATGA GGGGACTGGG CAGTTCTAGA CAGTCCCGAA GTTCTCAAGG 60
 CACAGGTCTC TTCCTGGTTT GACTGTCTTT ACCCCGGGGA GGCAGTGCAG CCAGCTGCAA 120
 GCCCACAGT GAAGAACATC TGAGCTCAAA TCCAGATAAG TGACATAAGT GACCTGCTTT 180
 GTAAAGCCAT AGAGATGGCC TGTCTTGGGA AATTTCTGTT CAAGACCAAA TTCCACCAGT 240
 ATGCAATGAA TGGGGAAAAA GGCATCAACA ACAATGTGGA GAAAGCCCCC TGTGCCACCT 300
 CCAGTCCAGT GACACAGGAT GACCTTCAGT ATCACAACCT CAGCAAGCAG CAGAATGAGT 360
 CCCCAGCAGC CCTCGTGGAG ACGGGAAAGA AGTCTCCAGA ATCTCTGGTC AAGCTGGATG 420
 CAACCCCATT GTCTTCCCA CCGCATGTGA GGATCAAAAA CTGGGGCAGC GGGATGACTT 480
 TCCAAGACAC ACTTCCAT AAGGCCAAAG GGATTTTAACT TTGCAGGTCC AAATCTTGCC 540
 TGGGTCCAT TATGACTCCC AAAAGTTTGA CCAGAGGACC CAGGGACAAG CCTACCCCTC 600
 CAGATGAGCT TCTACCTCAA GCTATCGAAT TTGTCAACCA ATATTACGGC TCCTCAAAG 660
 AGCAAAAAAT AGGAGAACAT CTGGCCAGGG TGAAGCGGT AACAAAGGAG ATAGAAACAA 720
 CAGTAACCTA CCAACTGACG GGAGATGAGC TCATCTTCGC CACCAAGCAG GCCTGGCGCA 780
 ATGCCCCAGC CTGCATTGGG AGGATCCAGT GGTCCAACCT GCAGGTCTTC GATGCCCGCA 840
 GCTGTTCCAC TGCCCGGGA ATGTTTGAAC ACATCTGCAG ACACGTGCGT TACTCCACCA 900
 ACAATGGCAA CATCAGGTGC GCCATCACCG TGTTCCTCCA GCGGAGTGAT GGCAAGCAG 960
 ACTTCGGGT GTGGAAATGCT CAGCTCATCC GCTATGCTGG CTACCAGATG CCAGATGGCA 1020
 GCATCAGAGG GACCCCTGCC AACGTGGAAT TCATCTAGCT GTGCATCGAC CTGGGCTGGA 1080
 AGCCCAAGTA CGGCCGCTTC GATGTGGTCC CCCTGGTCTT GCAGGCCAAT GGCCGTGACC 1140
 CTGAGCTCTT CGAAATCCCA CCTGACCTTG TGCTTGAGGT GGCCATGGAA CATCCCAAAT 1200
 ACGATGGGT TCGGGAACAT GAGCTAAAGT GGTACGCCCT GCCTGCAATG GCCAACATGC 1260
 TGCTTGAGGT GGGCGGCTGC GAGTTCCAG GGTGCCCTT CAATGGCTGG TACATGGGCA 1320
 CAGAGATCGG AGTCCGGGAC TTCTGTGATG TCCAGCGCTA CAACATCCTG GAGGAAGTGG 1380
 GCAGGAGAAAT GGGCCTGGAA ACGCACAAAG TGGCCTCGCT CTGGAAGAGC CAGGCTGTGC 1440
 TTGAGATCAA CATTGCTGTG CTCCATAGTT TCCAGAAGCA GAATGTGACC ATCATGGACC 1500
 AACCATCGGC TGCAGAAATC TTCTGAAAGT ACATGCAGAA TGAATACCGG TCCCGTGGGG 1560
 GCTGCCCGGC AGACTGTGATT TGGCTGGTCC CTCCATGTC TGGGAGCATC ACCCCGTGT 1620
 TTCACCAGGA GATGCTGAAC TACGTCTGT CCCCTTTCTA CTACTATCAG GTAGAGGCCT 1680
 GGAAGAACCA TGTCTGGCAG GACGAGAAGC GGAGACCCAA GAGAAGAGAG ATTCCATTGA 1740
 AAGTCTTGGT CAAAGCTGTG CTCCTTGCCT GTATGCTGAT GCGCAAGACA ATGGCGTCCC 1800
 GAGTCAGAGT CACCATCTCT TTTGCGACAG AGACAGGAAA ATCAGAGGCG CTGGCCTGGG 1860
 ACCTGGGGGC CTTATTCAGC TGTGCTTCA ACCCAAGGT TGTCTGCATG GATAAGTACA 1920
 GGCTGAGCTG CTTGGAGGAG GAACGGCTGC TGTGGTGGT GACCAGTACG TTTGGCAATG 1980
 GAGACTGCCC TGGCAATGGA GAGAACTGA AGAAATCGCT CTTTATGCTG AAAGAGCTCA 2040
 ACAACAAAT CAGGTACGCT GTGTTTGGCC TCGGCTCCAG CATGTACCCT CGGTTCTGCG 2100
 CCTTTGCTCA TGCAATTGAT CAGAAGCTGT CCCACCTGGG GGCTCTCAG CTCACCCCGA 2160
 TGGGAGAAGG GGATGAGCTC AGTGGGCAGG AGGACGCCTT CCGCAGCTGG GCCGTGCAAA 2220
 CCTTCAAGGC AGCCTGTGAG ACCTTTGATG TCCGAGGCAA ACAGCAGATT CAGATCCCCA 2280
 AGCTCTACAC CTCCTAATGT ACCTGGGACC CGCACCACTA CAGGCTCGTG CAGGACTCAC 2340
 AGCCTTTGGA CCTCAGAAA GCCCTCAGCA GCATGCATGC CAAGAACGTG TTCACCATGA 2400
 GGCCTCAAATC TCGGCAGAA CTACAAAGTC CGATCCAGC CCGTGCCACC ATCCTGGTGG 2460
 AACTCTCCTG TGAGGATGGC CAAGGCCTGA ACTACCTGCC GGGGGAGCAC CTTGGGGTTT 2520
 GCCCAGGCAA CCAGCCGGCC CTGGTCCAAG GCATCCTGGA GCGAGTGGTG GATGGCCCCA 2580
 CACCCACCA GGCAGTGGCC CTGGAGGCC TGGATGAGAG TGGCAGTAC TGGGTCAATG 2640
 ACAAGAGGCT GCCCCCTGCT TCACTAGGCC AGGCCCTCAC CTACTTCTG GACATACCA 2700
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 GCCCCACATT CCTGGAGGTG CTAGAGGAGT TCCCGTCCCT GCGGGTGTCT GCTGGCTTCC 2880
 TGCTTTCCCA GCTCCCCATT CTGAAGCCCA GGTCTTACTC CATCAGCTCC CCCCGGATC 2940
 ACACGCCCA GAGATCCAC CTGACTGTGG CCGTGGTCC CACCATCACC CGAGATGGCC 3000
 AGGGTCCCTG GCACACGGC GTCTGCAGCA CATGGCTCAA CAGCCTGAAG CCCCAGACC 3060
 CAGTGCCTG CTTTGTGCGG AATGCCAGCG GCTTCCACCT CCCCAGGAT CCTTCCATC 3120

CTTGCATCCT CATCGGGCCT GGCACAGGCA TCGCGCCCTT CCGCAGTTTC TGGCAGCAAC 3180
 GGCTCCATGA CTCCCAGCAC AAGGGAGTGC GGGGAGGCCG CATGACCTTG GTGTTTGGGT 3240
 GCGCCGCCCC AGATGAGGAC CACATCTACC AGGAGGAGAT GCTGGAGATG GCCCAGAAAG 3300
 GGGTGTCTGCA TCGGGTGCAC ACAGCCTATT CCGCCTGTC TGGCAAGCCC AAGGTCTATG 3360
 5 TTCAGGACAT CCTGCGGCAG CAGCTGGCCA GCGAGGTGCT CCGTGTGCTC CACAAGGAGC 3420
 CAGGCCACCT CTATGTTTGC GGGGATGTGC GCATGGCCCG GGACGTGGCC CACACCCTGA 3480
 AGCAGCTGGT GGCCTGCCAAG CTGAAATTGA ATGAGGAGCA GGTCCGAGGAC TATTCTTTTC 3540
 AGCTCAAGAG CCAGAAGCGC TATCACGAAG ATATCTTTGG TGCTGTATTT CCTTACGAGG 3600
 CGAAGAAGGA CAGGGTGGCG GTGCAGCCCA GCAGCCTGGA GATGTCAGCG CTCTGAGGGC 3660
 10 CTACAGGAGG GGTAAAGCT GCCGGCACAG AACTTAAGGA TGGAGCCAGC TCTGCATTAT 3720
 CTGAGGTCAC AGGGCCTGGG GAGATGGAGG AAAGTGATAT CCCCCAGCCT CAAGTCTTAT 3780
 TTCTCAACG TTGCTCCCCA TCAAGCCCTT TACTTGACCT CCTAACAAAT AGCACCCCTG 3840
 ATTGATCGGA GCCTC

Seq ID NO: 313 Protein sequence:
 Protein Accession #: NP_000616

1 11 21 31 41 51
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 MACPWKFLFK TKFHQYAMNG EKGINNVEK APCATSSPVT QDDLQYHNLS KQNESPOPL 60
 VETGKKSPE LVKLDPPLS SPRHVRIKW GSGMTFQDTL HHKAKGILT RSKSCLGSIM 120
 TPKSLTRGPR DKPTPPDELL PQAIEFVNQY YGSLKEAKIE EHLARVEAVT KEIETTITYQ 180
 25 LTGDELIFAT KQAWRNAPRC IGRIQWSNLQ VFDARSCSTA REMFEHICRH VRYSTNNGNI 240
 RSAITVFPQR SDGKHDFRVW NAQLIRYAGY QMPDGSIRGD PANVEFTQLC IDLGWPKPYG 300
 RFDVPLVLQ ANGRDPLEFE IPPDLVLEVA MEHPKYEWFR ELELKWYALP AVANMLLEVG 360
 GLEFPFGCFN GWYMGTEIGV RDFCDVQRYN ILEEVGRRMG LETHKLASLW KDQAVVEINI 420
 AVLHSFQKQN VTIMDHSSAA ESFMKYMONE YRSRGGCPAD WIWLVPPMSG SITPVFHQEM 480
 30 LNVVLSPPFY YQVEAWKTHV WQDEKRRPKR REIPLKVLVK AVLFACMLMR KTMA SRVRVT 540
 ILFATETGKS EALAWDLGAL FSCAFNPKVV CMDKYRLSCL EEERLLLVT STFGNGDCPG 600
 NGEKLLKSLF MLKELNNKFR YAVFGLGSSM YPRFCAPAH IDQKLSHLGA SQTTPMGEED 660
 ELSGQEDAFR SWAGVTFKAA CTFDVRGKQ HIQIPKLYTS NVTWDPHYR LVQDSQPLDL 720
 35 SKALSSMHAK NVFTMRKLSR QNLQSPSSR ATILVELSCE DGQGLNLYLF EHLGVCPGNQ 780
 PALVQGILER VVDGPTPHQA VRLEALDESG SYWVSDKRLP PCSLSQALTY FLDITTPPTQ 840
 LLLQKLAQVA TESEPERQLE ALCQPSSEYSK WKFTNSPTFL EVLEEFPSLR VSGAFLLSQL 900
 PILKPRFYSI SSPRDHTPTE IHLTVAVVTY HTRDQGGPLH HGVCSTWLNS LKQDPVPCF 960
 VRNAGPHLP EDPSPHCILI GPGTGIAPFR SFWQORLHDS QHKGVRRGRM TLVFGCRRPD 1020
 EDHIYQEML EMAQKGVLHA VHTAYSRLPG KPKVYVQDIL RQQLASEVLR VHKPEPGHLY 1080
 40 VCGDVRMARD VAHTLKQLVA AKLKLNEBQV EDYFFQLKSQ KRYHEDIFGA VFPYEAKKDR 1140
 VAVQPSSELM SAL

Seq ID NO: 314 DNA sequence
 Nucleic Acid Accession #: XM_087254
 Coding sequence: 47..2332

1 11 21 31 41 51
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 50 AGAGTACGCT TTTACAGATA AAACCTGGTAC ACTGACAGAA AATGAGATGC AGTTTCGGGA 60
 ATGTTCAATT AATGGCATGA AATACCAAGA AATTAATGGT AGACTTGATC CCGAAGGACC 120
 AACACCAGAC TCTTCAGAAG GAAACTTATC TTATCTTAGT AGTTTATCCC ATCTTAACAA 180
 CTTATCCCAT CTTACAACCA GTTCTCTTT CAGAACCACT CCTGAAATG AAACCTGAACT 240
 AATTAAAGAA CATGATCTCT TCTTTAAAGC AGTCAGTCTC TGTACACTG TACAGATTAG 300
 CAATGTTCAA ACTGACTGCA CTGGTGATGG TCCCTGGCAA TCCCACTGG CACCATCGCA 360
 55 GTTGAGTAC TATGACTCTT CACCAGATGA AAAGGCTCTA GTAGAAGCTG CTGCAAGGAT 420
 TGTATTTGTG TTTATTGGCA ATTCTGAAGA AACTATGGAG GTTAAACTC TTGGAAGACT 480
 GGAACGGTAC AAACCTCTTC ATATTCTGGA ATTTGATTCA GATCGTAGGA GAATGAGTGT 540
 AATGTTTCAG GCACCTTCAG GTGAGAAGTT ATTATTGCT AAAGGAGCTG AGTCATCAAT 600
 TCTCCCTAAA TGTATAGGTT GAGAAATAGA AAAAACCGA ATTCATGTAG ATGAATTGTC 660
 60 TTTGAAAGGG CTAAGAACTC TGTGTATAGC ATATAGAAAA TTTACATCAA AAGAGTATGA 720
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 AGTATGGGTA CTTACTGGGG ATAAACATGA AACAGCTGTT AGTGTGAGTT TATCATGTGG 960
 65 CCATTTTCAT AGAACCATGA ACATCCTTGA ACTTATAAAC CAGAAATCAG ACAGCGAGTG 1020
 TGCTGAACAA TTGAGGCAGC TTGCCAGAAG AATTACAGAG GATCATGTGA TTCAGCATGG 1080
 GCTGGTAGTG GATGGGACCA GCCTATCTCT TGCATCAGG GAGCATGAAA AACTATTTAT 1140
 GGAAGTTTGC AGAAATTTGT CAGCTGTATT ATGCTGTCTG ATGGCTCCAC TGCAGAAAGC 1200
 70 AAAAGTAATA AGACTAATAA AAATATCACC TGAGAAACCT ATAACATTGG CTGTTGGTGA 1260
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 AGAAGGAAGA CAGGCTGCA GAAACAGTGA CTATGCAATA GCCAGATTGA AGTTCCCTCTC 1380
 CAAATTGCTT TTGTTTCATG GTCAATTTTA TTATATTAGA ATAGCTACCC TTGTACAGTA 1440
 TTTTTTTAT AAGAAATGTT GCTTTATCAC ACCCCAGTTT TTATATCAGT TCTACTGTTT 1500
 75 GTTTTCTCAG CAAACAGCGT GTACAGCGCT GTACCTGACT TTATACAATA TTTGTTTAC 1560
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	3	GAGTTATAT	GGCAAAACAA	CAGAAAGCAT	TAGTACAGAC	CCCTCCCAAC	ACCTCTAATT	2520
5	4	TGAATCTGAA	CATGTTAAAA	TTTGAGAATA	AAGAGACATT	TTTCATCTCT	TTGTCTGGTT	2580
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	11	ATTTATACCA	ATTCCTCTAA	CTGTGATGTA	ACACAGCGCT	TAAAGTTAGC	CATATAAATG	3000
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	20	CAATACAGTG	AGTTCTGCCA	ATGTCGCCAG	ACAAGGCATA	TTTCAGGTGT	GGCTGTGGAA	3540
	21	TGTAAAAATG	CTCAACTTGT	AGCAGTAAAT	GTTAGCAATG	AATTTAAATG	TAAAGATGAT	3600
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Seq ID NO: 315 Protein sequence:
Protein Accession #: XP_087254

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	MALETHFNTW	INHLYVTWGS	IFYFVFSFLY	GGILWPPLGS	QNMYPVFIQL	LSSGSAWPAI	660
	ILMVVTCLEF	DIKKVFPDRH	LHPSTBEKAQ	LTETNAGIKC	LDSMCCFPFG	EACASVGRM	720
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Seq ID NO: 316 DNA sequence
Nucleic Acid Accession #: NM_004473
Coding sequence: 661..1791

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Seq ID NO: 317 Protein sequence:
Protein Accession #: NP_004464

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	TCCTCCCTGT	TGACGAAGTC	TCTTTTCTTT	AGAGCATTTG	CATTCCCTGC	CTGGGGCGGG	4500
	CCCTCATGCT	CGTCTCTCTA	CCGAAACCTT	GCCTTTCTCG	ATTTTATCTT	TCGCACAGCA	4560
70	GTTCCGGATT	GGCTTGTGTG	TTTCACTTTT	AGGGAGAGTC	ATATTTTGAT	TATTGTATTT	4620
	ATTCCATATT	CATGTAAACA	AAATTTAGTT	TTTGTCTCTA	ATTGCACTCT	AAAAGGTTCA	4680
	GGGAACCGTT	ATTATAATTG	TATCAGAGGC	CTATAATGAA	GCTTTATACG	TGTAGCTATA	4740
	TCTATATATA	ATTCTGTACA	TAGCCTATAT	TTACAGTGAA	AATGTAAGCT	GTTTATTTTA	4800
	TATTAATAATA	AGCACTGTGC	TAATAACAGT	GCATATTCCT	TTCTATCATT	TTTGTACAGT	4860
75	TTGCTGTACT	AGAGATCTGG	TTTTGCTATT	AGACTGTAGG	AAGAGTAGCA	TTTCACTTCT	4920
	CTCTAGCTGG	TGGTTTACAG	GTGCCAGGTT	TTCTGGGTGT	CCAAAGGAAG	ACGTGTGGCA	4980
	ATAGTGGGCC	CTCCGACAGC	CCCTCTGCTC	GCCTCCCCAC	AGCCGCTCCA	GGGGTGGCTG	5040
	GAGACGGGTG	GGCGGCTGGA	GACCATGCAG	AGCGCCGTGA	GTTCTCAGGG	CTCCTGCTTT	5100
	CTGTCTCTGG	GTCACCTACT	GTTTCTGTCA	GGAGAGCAGC	GGGGCGAAGC	CCAGGCCCTC	5160
80	TTTCACTCCC	TCCATCAAGA	ATGGGGATCA	CAGAGACATT	CCTCCGAGCC	GGGGAGTTTC	5220
	TTTCTGCTCT	TCTCTTTT	GCTGTTGTTT	CTAAACAAGA	ATCAGTCTAT	CCACAGAGAG	5280
	TCCCACTGCC	TCAGGTTCTT	ATGGCTGGCC	ACTGCACAGA	GCTCTCCAGC	TCCAAGACCT	5340
	GTTGGTTCCA	AGCCCTGGAG	CCAAGTGCTG	CTTTTTGAGG	TGGCACTTTT	TCAATTTGCT	5400
	ATTCCACAC	CTCCACAGTT	CAGTGGCAGG	GCTCAGGATT	TGCTGGGTCT	GTTTTCCTTT	5460
	CTCACCGCAG	TCGTGCGACA	GTCTCTCTCT	CTCTCTCCCC	TCAAAGTCTG	CAACTTTAAG	5520
85	CAGCTCTTGC	TAATCAGTGT	CTCACACTGG	CGTAGAAGTT	TTTGTACTGT	AAAGAGACCT	5580
	ACCTCAGGTT	CTCGGTTGCT	GTGTGGTTTG	GTGTGTTCCC	GCAAAACCCC	TTTGTGCTGT	5640
	GGGGCTGTA	GCTCAGGTGG	CGTGGTGCAC	TGCTGTATC	AGTTGAATGG	TCAGCGTTGC	5700

ATGTCGTGAC CAAC TAGACA TTCTGTCGCC TTAGCATGTT TGCTGAACAC CTTGTGGAAG 5760
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5

Seq ID NO: 319 Protein sequence:
 Protein Accession #: NP_005679

10 1 11 21 31 41 51
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 VAHKKGELSM EDVWSLSKHE SSDVNCRRLE RLWQEELNEV GPDAASLRV VWIFCRTLRI 180
 LSIVCLMITQ LAGFSGPAPM VKHLEYTQA TESNLQYSL LVLGLLLEI VRSWSLALTW 240
 15 ALNYRTGVR LRGAILTMAFK KILKLNIKE KSLGELINIC SNDGQRMFEA AAVGSLLAG 300
 PVVAILGMIY NVIIILGPTGF LGSAPVILFY PAMMFASRLT AYFRKCVAA TDERVQKMNE 360
 VLTYYKFIKM YAWVKAFSQS VQKIREEERR ILEKAGYFQG ITVGVAPIV VIASVVTFSV 420
 HMTLGFDLTA AQAFVTVVTF NSMTFALKVT PFSVKSLSA SVAVDRFKSL FLMEEVHMIK 480
 NKPASPHIKI EMKNATLAW SSHSSIQNSP KLTPKMKKDK RASRGKKEKV RQLQRTHEQA 540
 20 VLAEQKHLL LDSDERPSP EEEGKHIHLG HRLQRTLHS IDLEIQEGKL VGICGSVSG 600
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 CCLRPDLAIL PSSDLTEIGE RGANLSSGQR QRISLARALY SDRSIYILDD PLSALDAHV 720
 NHIFNSAIRK HLKSKTVLFV THQLQYLVD DEVIFMKEGC ITERGTHEEL MNINGDYATI 780
 FNNLLLGSTP PVEINSKKET SGSQKKSQDK GPKTGSVKKE KAVKPEGQL VQLEEKQGS 840
 25 VPWSVGVYI QAAGGLAFL VIMALFMLNV GSTAFSTWWL SYWIKQSGN TTVTRGNETS 900
 VSDSMKDNPH MQYYASIAL SMAYMLILKA IRGVVFKGT LRASSRLHDE LFRILRSPM 960
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 LDDNQAPFFL FTCAMRWLA RLDLISIALI TTTGLMIVLM HGQIPPAYAG LAISYAVQLT 1140
 30 GLFQFTVRLA SETEARFTSV ERINHYIKTL SLEAPARIKN KAPSPDPQGE GEVTFENAEM 1200
 RYRENPLVL KKVSTFKPK EKIGIVGR TGSGKSSLMAL FRLVELSGG IKIDGVRISD 1260
 IGLADLRSL SIIPQEPVLF SGTVRSLNDP FNQYTEDQIW DALERTHME CIAQLPLKLE 1320
 SEVMENGDNF SVGERQLLCI ARALLRHCKI LILDEATAAM DTETDLIQE TIREAFADCT 1380
 35 MLTIAHRLHT VLGS DRIMVL AQGQVVEFDT PSVLLSNDSS RPYAMFAAAE NKVAVKG

Seq ID NO: 320 DNA sequence
 Nucleic Acid Accession #: AK022089.1
 Coding sequence: 181-1488

40 1 11 21 31 41 51
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 45 CCCACCCCC ACCCTCAGAT CACTTAAAGA TAAATTTCTT ATTCGTTTGC CCGACAGACC 180
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 50 GAGGCTACGT TTGGAGAGAA ACGATTTCTT CTGGGGAAGC CCAGTGATTA CTGCATCATA 420
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 CTTCAGTTC CTTTGTGGCG GACAGCTGAA GCCAAATTAG TGCAAAACAC AGAAAAATTG 600
 TGGGAGCTCA GCCCAGCAAA CTACATGAAG ACTTTACCAC CAGATAAACA AAAAAAGATA 660
 55 GTCAGGAAAA CTTTCGGGAA ACTGGCTAAA ATTAAGCAGG ACACAGTTTC TCATGATCGA 720
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 GTCAAGAGAA ATGGAATTGA AGACTGGAA ATTGAAAGT GTGAAGCTAA GTTCCATCTT 840
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 60 AGCGAAAGTG ATGGAATTGA ACAGCTGGAA GAACGACTGA AATATTACCG AATACTCATT 1020
 GATAAGCTCT CTGCTGAAAT AGAAAAAGAG GTAAAAAGTG TTTGCATTGA TATAAATGAA 1080
 GATGCGGAAG GGAAGCTGC AAGTGAAC TGAAAGCTCTA ATTTAGAGAG TGTAAAGTGT 1140
 GATTGGAGA AAAGCATGAA AGCTGGTTG AAAATTCAT CTCAATTTGAG TGGCATCCAG 1200
 AAAGAGATTA AATACAGTGA CTCATTGCTT CAGATGAAAG CAAAAGAATA TGAATCCTG 1260
 65 GCCAAGGAAT TCAATTCAT TCACATTAGC AACAAAGATG GGTGCCAGTT AAAGGAAAAC 1320
 AGAGCGAAGG AATCTGAGT TCCAGTAGC AATGGGGAGA TTCTCCCTT TACTCAAAGA 1380
 GTATTAGCA ATTACACAAA TGACACAGAC TCGGACACTG GTATCAGTTC TAACCACAGT 1440
 CAGGACTCCG AAACAACAGT AGGAGATGTG GTGCTGTGT CAACATAGTT CCAATGGCTC 1500
 CTTTCTGACC TGCTTTCATG TTTTAATGTT TGTTAATTT AATAGGAAAC CTCATTTTAA 1560
 70 ATATAACACT CAAAAAATG TAAATCATAT TGTAGTATTC AATAGTTAAT AAAAATCTGA 1620
 GAAATGTGT GTTTCG

Seq ID NO: 321 Protein sequence:
 Protein Accession #: NP_005438.1

75 1 11 21 31 41 51
 MAPFGRNLLK TRKKNRSPK DMDSEEKIV VWVCQEEKLV CGLTKRTTSA DVIQALLEEH 60
 EATFGEKRFL LGKPSDYCI EKWRGSEVL PPLTRILKLW KAWGDEQPNM QFVLVKADAF 120
 80 LPVPLWRTAE AKLVQNTKEK WELSPANMYK TLPPDKQKRI VRKTFRKLAK IKQDTVSHDR 180
 DNMETLVHLI ISQDHTIHQ VCRMKELDL IEKCEAKFHL DRVENDGENY VQDAYLMPFS 240
 SEVEQNLDLQ YEENQTLDEL SESDGIQLE ERLKYRILI DKLSAEIEKE VKSVCIDINE 300
 DAEGEAASEL ESSNLESVK DLEKSMKAGL KIHSHLSGIQ KEIKYSDSL QMKAKEYELL 360
 AKEFNLSLHIS NKDGCQLKEN RAKESEVPSS NGEIIPPFTQR VFSNYTNDTD SDTGISNHS 420
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Seq ID NO: 322 DNA sequence
 Nucleic Acid Accession #: NM_030920.1

Coding sequence: 317-1123

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	AGTTAGAGTC	CCAACCTCTG	GACTCCATTT	GCTATTCTCT	TCCTTCTCCC	CCACACCTAT	180
	CTGGTGGTGG	TAGTGGGCGT	TTATATTTGC	GTTCTCTTTC	ATTCATTTCT	AAATCTCTTA	240
	AAAAATTTGG	GTTGGGGGTA	TTGGGGAAGG	CAGGAAAGGG	AAAAGGAGAG	TAGTAGCTGA	300
10	AGAGCAAGAG	GAGGACATGG	AGATGAAGAA	GAAGATTAAAC	CTGGAGTTAA	GGAACAGATC	360
	CCCGGAGGAG	GATGACAGAT	TAGTCTTGA	TAATTGCGTG	TGTGTCAATG	GGGAAATTGA	420
	AGGCGCTGAAT	GATACTTTCA	AAGAACTAGA	ATTTCTGAGT	ATGGCTAATG	TGGAACCTAAG	480
	TTGCTGGGCC	CGGCTTCCCA	GCTTAAATAA	ACTTCGAAAA	TTGGAGCTTA	GTGATAATAT	540
	AATTTCTGGA	GCTTGGGAAG	TCCTGGCAGA	GAAATGTCCA	AATCTTACCT	ACCTCAATCT	600
15	GAGTGGAAAC	AAAATAAAG	ATCTCAGTAC	AGTAGAAGCT	CTGCAAAATC	TTAAAAATTT	660
	GAAAACTCTT	GACCTGTTTA	ACTGTGAGAT	CACAAACCTG	GAAGATTATA	GAGAAAGTAT	720
	TTTGTAACTA	TGCGACAGAT	TACATACCTT	AGATGGATTT	GATCAGGAGG	ATAATGAAGC	780
	GCGGACTCT	GAAGAGGAGG	ATGATGAGGA	TGGAGATGAA	GATGATGAAG	AGGAAGAGGA	840
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	TGAGGATGAG	GATGAAGATG	AAGATGAAGC	AGGTTCAAGG	TTGGGAGAGG	GAGAAGAGGA	960
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	GAAACGAGAT	GCTGAAGACG	ATGGAGAGGA	AGAAGATGAC	TAGATCATT	TAAGACCAGA	1140
	TTCTCTAATG	TTTCTGGGTG	TGCAATAGAG	TGATCACATC	TTTGTTCCTT	CATGTACGAT	1200
25	AGCTATCCCT	ACAGAAGATA	ATGTGTAAC	TTTTATAGGA	AAAGTGTGGT	TTTACTATTT	1260
	TTGCTTATC	ATTCCAAATA	AGAACTAGTC	TGTTAATGAT	CATATTGTAT	GTAGAGAAAA	1320
	ATTTTCATG	ACTCCCATG	TGGAATCCC	TAGCAATTTA	TTTAGACTTA	ATTTTTTAAA	1380
	TTCAAGCTTA	CTGTATTAGT	CATTTTATAG	CCATAATTAA	AACATGATCA	CTTTTAAACA	1440
	GGTGTAGTAT	GGTGTGATG	ATTCCTTAT	TATAGATTAA	CTGAAATTAC	AGTTTGTCTAT	1500
30	AATATAAAT	GACATAGTC	TCTTGAGTGG	TAAAGTGGTT	ATTTTTTTAG	AGGTGATCCA	1560
	GGAACTTTTA	GTTTGAAGGC	AGTTACCTTT	TTTTTTTTTT	TTTTTTTTTG	ACTAAGAGTG	1620
	TTTGGTTGCT	GTTTGTACAC	AAGTAACCTG	GAAATAGAAA	GCAGAAATAG	AAAGGTTCTA	1680
	TTCAAGCAAC	TAGTTCATGG	ATTTTGTGGA	GGTTCTATTC	AGTAATATGG	TTTATGGATT	1740
	TAGTGGTGAC	TGATAAGATT	TTATTTTGA	AGGAAAAATT	GCTTATACTA	AGTCCAGAGA	1800
35	CATGCAGGTG	AGCCCTTTTG	TCAGGCTGCA	AATCATGACA	TGCCGATGGT	TGTTTATTTT	1860
	GTTTTTAGGT	GTGCATTCTT	TTTCTTCTTA	GCAATTCCTT	TATGATCACC	TTCCCTTCTT	1920
	GTTTCACTCC	CTCCCGCTCT	CTCAAAAGGA	ACTTGGGAAA	CTTGTGAAAC	CCAGGAAAAAC	1980
	CTTTAGTCTT	ATACCTCAAC	TACGTTTCAG	TCCTGTCTGG	GTTTTAAATA	AGTGAAGTAG	2040
40	AAGAAATTGA	GTATTTTCTG	ACATAAGAAT	ATATTATCAA	TACAGTTTAA	TGCAGTAAAG	2100
	TCCTCTTACC	ATAAATGTTT	CTTGGTTGAC	AACATCTAAG	ACAAATATTAG	TGGGATGAAG	2160
	AAAGAAAAGC	AGGGGTGCTT	TTGGAAGCAG	TGTTAGTGTT	CCTCAAAAGT	CGGAACAATT	2220
	GCCTGTGAT	ATATTAATAA	GACATTAAAG	TCAAATTTTA	ATGTTGCGCT	CTCAAATGAT	2280
	TTGGATACCA	CTCTGCAAG	TATTTCTAAC	CTTTAATTCC	CAGTTTAAAA	ACAGATATAA	2340
45	TAATAGCATT	TAATTTGGAAT	ATACTAGGCA	GCTGGAAGAA	TATTTGAAAC	TAAATTGACA	2400
	TTAAATATAA	GATTTGTTTT	CAAGTGGATG	TCCATTAAAA	GTAGAAAAAT	ATTTGGGATA	2460
	AGTGAAGTGT	TGTTTCTCTA	CATGGCTACT	AAATAAAATA	TAATGAGTAT	ACAAGTATAT	2520
	CTCCTCTTTT	GCTATGGAGG	CTCCATGTTT	AAGGCAATGG	CTTTTTAAAT	CTTGGCTATC	2580
	TAAAAATTTT	TCCCTTTGTT	TTGAATATTT	GTAAGTTTTT	AAGAAGTTAG	TGTCAGCAAA	2640
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50	TACTGCTTCT	ACAAATGAAA	ATGATGACT	TGGTGTTTTA	AAGTAAAAAT	TATGATGTTA	2760
	CTTGTGGAGA	AACTAAAAAT	GTTGTACAAC	TGACCGAAAG	AAAACCTCTG	GGGATAAGTT	2820
	TAGTGAGGGG	ATTGGAATCC	CCAAAAAGAT	AACATTTTTC	TTCTGCTTTT	AAAACTGAA	2880
	ATTCCTGTGT	CTAGTCTCTA	ACAATTTCTA	TTACATACTA	TGCCAGATTA	CAAAATACTT	2940
	ATTTTAAAAA	TGAAATCTAT	ATATTGACTT	TCTTATCAAT	CATCTTACTG	TGCAATCAAA	3000
55	ATTAGAGTAC	TTTGGTTTGA	AAACAACACT	TAGAGCCTCC	AGATAACTTT	TAAGACTTAT	3060
	TTAGCTTTGT	GGGTGGTGGT	TTCTATGCAA	TAAAGTAAAG	TGGGTTTAT	ATTTTGTAGA	3120
	AGTTTTCGGT	CCTATTTTAA	TGCTCTTTGT	ATGGCAGTAT	GTATATATTG	TGTTAAGTTC	3180
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60	AGCCATGACA	GTGTTAAAAA	CAAAAC				

Seq ID NO: 323 Protein sequence:
Protein Accession #: NP_112182.1

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	PSLNKLRKLE	LSDNIISSGL	EVLAIEKCPNL	TYLNLSGNKI	KDLSTVEALQ	NLKNLKSLLD	120
	FNCEITNLED	YRESIFELLQ	QITVLDGFDQ	EDNEAPDSEE	EDDEDGDEDD	EEEEENEAGP	180
70	PEGEEEEEEE	EEEEDEDEDE	DEDEAGSELG	EGEEVGLSY	LMKEEIQDEE	DDDDVVEEGE	240
	EEEEEEEGGL	RGEKRRKRAE	DDGEEEDD				

Seq ID NO: 324 DNA sequence
Nucleic Acid Accession #: NM_003812
Coding sequence: 224..2722

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	GCTCTGCGCG	GCCACACCGA	GCGGCGCCCG	GGAGCTATGA	GCCATGAAGC	CGCCCGGCAG	240
	CAGCTGCGCG	CAGCCGCCCC	TGGCGGGCTG	CAGCCTTGCC	GGCGCTTCTT	GCGGCCCCCA	300
	ACGCGGCCCC	GCCGCTCGGG	TGCTGCGCAG	CGCCCCGGCC	CGCACGCGCG	CCTGCGCGCT	360
	GCTTCTGCTC	CTTCTCTGCG	TGCCTCCGCT	CGCCGCTCTG	TCCCGGCCCC	GCGCCTGGGG	420
85	GGCTGCTGCG	CCCAGCGCTC	CGCATTTGAA	TGAAACTGCA	GAAAAAATTT	TGGGAGTCTC	480
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Seq ID NO: 325 Protein sequence:
Protein Accession #: NP_003803

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INQDSESPYH VLDTKARHQK KHNKAVHLAQ ASFQIEAPGS KFILDILINN GLLSSDYVEI 180
HYENGKPYQS KGGECYHYHG SIRGVKDSKV ALSTCNGLHG MFEDDTFVYM IEPLELVHDE 240
KSTGRPHIIQ KTLAGGYSKQ MNKLTMERGD QWPFLESELQW LKRRKRAVNP SRGIFEEKY 300
LELMIVNDHK TYKKHRSSHA HTNPFASVSV NLVDSIYKEQ LNTRVVLVAV ETWTEKDQID 360
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Seq ID NO: 326 DNA sequence
Nucleic Acid Accession #: AK074418.1
Coding sequence: 244-1515

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CAATACCGAA GGGGCTGGGA AGAAATTATC TCCCTGTGGA ACCCTGGGG CTGGGCGGAG 1080
ACCGAATGGA GAGGGCGCTG GAGTGATGGG TCTCAGGAGT GGGAGGAAAC CTGTGATCCG 1140

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10	CCTGAAAATG	CCAGACAGTG	ACAGGCACCT	GAGCAGCCAT	TTCACCTCA	GAATGAAGGG	1680
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15	GGATAATTAT	GGGGTGTGAG	GTGCATTGCC	CTCTAAATCT	TTAAACAAGC	AATTGGCAGT	2040
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	TGCACACAGG	ATTTCCTTAA	TGGCTTAATA	AACTGTTATA	AAGAACTCCT	TGACTTGTCA	2220
20	GAATAAAATA	GCTGCCAGGG	GCTCTGCACA	ATGAGCCCTCT	TACCGTTAAA	AAAAAAAATA	2280
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Seq ID NO: 327 Protein sequence:
Protein Accession #: BAB85075.1

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	QYAGIFRFRF	WQCGQWVEVV	IDDRLPVQGD	KCLFVRPRHQ	NQEFWPCLE	KAYAKLLGSY	180
30	SDLHYGFLED	ALVDLTGGVI	TNIHLHSSPV	DLVKAVKTAT	KAGSLITCAT	PSGPTDTAQA	240
	MENGLVSLHA	YVTGTAEQIQ	YRRGWEEIIS	LWNPNWGWTG	EWGRWSDGS	QWEETCDPR	300
	KSQLHKKRED	GEFWMSCQDF	QQKFIAMPIC	SEIPITLDHG	NTLHEGWSQI	MFRKQVILGN	360
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	TGCCCTCACC	TCCAGCCCTG	GCGTGACCTT	TCCACCATTT	GAGGATGAGT	CCGAGGGGCT	240
	CCTAGGCACA	GAGGGGCCCC	TGGAGGAAGA	AGAGGATGGA	GAGGAGCTCA	TTGGAGATGG	300
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	TCTGGATGAT	GAGGACGTAG	AGGAGCTGAC	GGCCAGTCAG	AGGGAGGCAG	CAGAGCGGGC	420
50	CATGCGGCAG	CGTGACCGGG	AGGCTGGCGG	GGGCTGGGCG	CGCATGCGCC	GTGGGCTCCT	480
	GTATGACAGC	GATGAGGAGG	ACGAGGAGCG	CCCTGCCCGC	AAGCGCCGCC	AGGTGGAGCG	540
	GGCCACGGAG	GACGGCGAGG	AGGACGAGGA	GATGATCGAG	AGCATCGAGA	ACCTGGAGGA	600
	TCTCAAAGGC	CACCTCTGTG	GCGAGTGGGT	GAGCATGGCG	GGCCCCGGCG	TGGAGATCCA	660
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55	GGAGCGCATC	AGCGACATGT	GCAAAGAGAA	CCGTGAGAGC	CTGGTGGTGA	ACTATGAGGA	780
	CTTGGCAGCC	AGGGAGCAGC	TGCTGGCCTA	CTTCTGCTCT	GAGGCACCGG	CGGAGCTGCT	840
	GCAGATCTTT	GATGAGGCTG	CCCTGGAGGT	GGTACTGGCC	ATGTACCCCA	AGTACGACCG	900
	CATCACCAAC	CACATCCATG	TCCGCATCTC	CCACCTGCCT	CTGGTGGAGG	AGCTGCGCTC	960
	GCTGAGGCAG	CTGCATCTGA	ACCAGCTGAT	CCGACCCAGT	GGGGTGGTGA	CCAGCTGCAC	1020
60	TGGCGTCTCT	CCCCAGCTCA	GCATGGTCAA	GTACAACATG	AACAAGTGCA	ATTTCTGTCT	1080
	GGGTCTCTTC	TGCCAGTCCC	AGAACCAGGA	GGTGAACCA	GGCTCTGTCT	CTGAGTGCCA	1140
	GTGCGCCGCG	CCCTTTGAGG	TCAACATGGA	GGAGACCATC	TATCAGAACT	ACCAGCGTAT	1200
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	CAGAAACGAG	ATCCATGAGG	CCATGGAGCA	ACAGAGCATC	TCCATCTCGA	AGGCTGGCAT	1920
75	CGTCACTCCC	CTGACGGCTC	GCTGCAAGGT	CATTGCTGCC	GCCCAACCCA	TAGGAGGGCG	1980
	CTACGACCCC	TGGCTGACTT	TCTCTGAGAA	CGTGGACCTC	ACAGAGCCCA	TCATCTCACG	2040
	CTTTGACATC	CTGTGTGTGG	TGAGGGACAC	CGTGGACCCA	GTCCAGGACG	AGATGTGGGC	2100
	CCGCTTCTGT	GTGGGCGAGC	ACGTGACAGA	CCACCCGAGC	AACAAGGAGG	AGGAGGGGCT	2160
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80	CCAGGAGGTC	CTGAAGAAAGT	ACATCATCTA	CGCCAAGGAG	AGGGTCCACC	CGAAGCTCAA	2280
	CCAGATGGAC	CAGGACAAGG	TGGCCAAGAT	GTACAGTGAC	CTGAGGAAAG	AATCTATGGC	2340
	CACAGGCAGC	ATCCCACTTA	CGGTGCGGCA	CATCGAGTCC	ATGATCCGCA	TGGCGGAGGC	2400
	CCACGCGCGC	ATCCATCTGC	GGGACTATGT	GATCGAAGAC	GACGTCAACA	TGGCCATCCG	2460
	CGTGTGTGCT	GAGAGCTTCA	TAGACACACA	GAAAGTTCAGC	GTCTATGCGCA	GCATGCGCAA	2520
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	GAAGCAGTTA	GTGGCAGAGC	AGGTGACATA	TCAGCGCAAC	CGCTTTGGGG	CCCAGCAGGA	2640
	CACTATTGAG	GTCCCTGAGA	AGGACTTGGT	GGATAAGGCT	CGTCAGATCA	ACATCCACAA	2700

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 5 TGTTTGTTC TCCAAGCCTG CTTTGTGCTT CTCACCTTTG GGTGGGATGC CTGGCCAGTG 3000
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 GTAGCTGGGA TTACAGGCAC ATGCCACCAT GCCTGGCTAA TTTTGTATAT TTAGTAGAAA 2820
 CAGGGTTTCA CATGCTGGT CTGAACTCC TGACCTCAGG TGTTCACCT 2880
 ACCTCAGCT CCCAAGTGC TGGGGTTACA GGTGTGAGCC ATCGCGCTG GCCAGGACCT 2940
 TTGTTTCTTA TCTACATATT GGAAGATTG GTCTGTATG CCTTTGAGG TCTTTAGCT 3000
 CTAGTTCTC GACACTTAC CCTATATCAC AGCTAACTT YTCAGTCTA TCTATTCTT 3060
 ATGCTCCAGC CCTGGCAAT TTGCTCAAG ATGGGGGTTT GAAAATAACT TTAACGTACT 3120
 CAAGGAGTGT CTGGAGCACC TCCTAGTCTA AGTCTGCAAG CTCAGTTCT TGCCTAAAC 3180
 CATGCCAGTG GCCACCTTG GGTCTGAGCA GCTCTGGGCC TTTTGACCA AAGCCAGCCC 3240
 CTCGCCCTCT CTGTGGCATA GTCTTCTCTG CCCAGGACT GCAGGGCGGC TTCTCCAAG 3300
 GCTTCCAAG CTCAAAAGAA ATTTGGCTCC ATCCAAGAAG GCTCCAGCTC CCCTACTGGC 3360
 CCTGGCTTC AGGCCACAC CCCTGGGCCA GGTGTCTCA GGAGAATTCA 3420
 ATGGGCTCTA GAGAGACACA CAGAAAGTTT GGCATTGTG GAAATTTTCA AGRTGTATG 3480

TATGGYTACG GTATGGWGCA GGTGTGCTCTG GTCCYKGGGT GCAGGGAAGT GGGCTGCAGG 3540
 GAAGTGGATT GGAGGGGAGC TTGAGGAATA TAAGGAGCGG GGTGGGAGAC TCAGGCTATG 3600
 GACAAGGACA GCCCAAGGT TGGGAAGACC TGGCCTTAGT CGTCTCAGC CTAGGGCAGG 3660
 5 GCAGTGAAGA AAGCTCTCCC CGCTCCTGCT GTAATGACCC AGAGTAGCCT CCCAGGCGG 3720
 GCATCTTATG TGTGTCTTCA ACCATCTCTCA TGGTGGCACT TTTCTAGGCC TGTCTCCCAG 3780
 CATTGTGCAA GGCTCGGAAG AGAACCAGGA AGTGAAACTG GGTGAAACA GAAAGCTCAA 3840
 TGGATGGGCT AGGTTCCAG ATCATTAGGG CAGAGTTTG CAGTCTCTG GTTCACTGGG 3900
 AATCCACCA GCCACGAAT CATCTCCCTC TTTGAAGGAT TTTWATTCT ACTGGGTTTT 3960
 10 GGAACAACT CCTGCTGAGA CCCACAGCC AGAAACTGAA AGCAGCAGCT CCCCAAGCC 4020
 TGGAAATCC CTAAGAGAAG GCCTGGGGGA MAGGAATGG AGTGACAGG GACAGGTAGA 4080
 GAGAAGGGG CCCAATGGCC AGGAGTGAA GGAGGTGGC TTGCTGAGAG CAGTCTGCAC 4140
 ATGCTTCTGT CTGAGTGAG GAAGGTGTT CAGGGTCGAA ATTACACTTC TGTACCTGG 4200
 AGACGCTGTT TGTGGGAGCA CTGGGCTCAT GCCTGGCACA CAATAGGTCT GCAATAAAC 4260
 ATGGTTAAAT CCTGAAAAA AAAAAAAA

Seq ID NO: 333 Protein sequence
 Protein Accession #: NP_000011

1 11 21 31 41 51
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 20 MTLGSPRKGL LMLLMALVTQ GDPVKPSRGP LVTCTCESPH CKGPTCRGAW CTVVLVREEG 60
 RHPQEHRCG NLHRELRCGR PTEFVNHVCC DSHLCNHVNS LVLEATQPPS EQPGTDGQLA 120
 25 LILGPVLALL ALVALGVLLG WHVRRRQEQ RGLHSELGES SLILKASEQG DTMGLDLLDS 180
 DCTTSGSGSL PFLVQRTVAR QVALVECVGK GRYGEVVRGL WHGESVAVKI FSSRDEQSWF 240
 RETEIYNTVL LRHDNILGFI ASDMTSRNSS TQLWLITHYH EHGSLYDFLQ RQTLLEPHLAL 300
 RLAVSAACGL AHLHVEIFGT QGKPAIAHRD FKSRLVVKLS NLQCCIADLG LAVMHSQSGSD 360
 YLDIGNPRV GTKRYMAPEV LDEQIRTDCE ESYKWTDIWA FGLVLWEIAR RTIVNGIVED 420
 YRPPFYDVVP NDPSFEDMKK VVCVDQQTPT IPNRLAADPV LSLGAQMRE CWYPNPSARL 480
 30 TALRIKKTQ KISNSPEKPK VIQ

Seq ID NO: 334 DNA sequence
 Nucleic Acid Accession #: NM_004126.1
 Coding sequence: 108-329

1 11 21 31 41 51
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 35 GGACGAGCT CGTGGCCGCC TTCAGTTGTT TCGGACGCG CCGAGCTTCG CCGCTCTTCC 60
 AGCGGCTCCG CTGCCAGAGC TAGCCCGAGC CCGTTCTTGG GCGGAAATG CCTGCCCTTC 120
 40 ACATCGAAGA TTGCGCAGAG AAGGAAAAAC TGAAATGGA AGTTGAGCAG CTTGCGCAAAG 180
 AAGTGAAGTT GCAGAGACAA CAAGTGCTTA AATGTTCTGA AGAAATAAG AACTATATTG 240
 AAGAACGTTT TGGAGAGGAT CCTCTAGTAA AGGGAATCC AGAAGACAAG AACCCCTTTA 300
 AAGAAAAAGG CAGCTGTGTT ATTTTCATAA TAACCTGGGA GAAACTGCAT CCTAAGTGGA 360
 AGAAGTAGTT TGTTTTAGTT TTCCAGATA AAACCAACAT GCTTTTAAAG GAAGGAAGAA 420
 45 TGAAATTAA AGSAGACTTT CTTAAGCACC ATATAGATAG GGTATGTAT AAAAGCATAT 480
 GTGCTACTCA TCTTTGCTCA CTATGCAGTC TTTTAAAGA GAGCAGAGAG TATCAGATGT 540
 ACAATTATGG AAATAAGAAC ATTACTTGAG CATGACACT CTTCAGTAT ATTGCTTGAT 600
 GCTTCAAATA AAGTTTGTG TT

Seq ID NO: 335 Protein sequence
 Protein Accession #: NP_004117.1

1 11 21 31 41 51
 | | | | |
 55 MPALHIEDLP EKEKLMKEVE QLRKEVKLQR QQVSKCEBI KNYIERSGE DPLVKGIPED 60
 KNPFEKKGSC VIS

Seq ID NO: 336 DNA sequence
 Nucleic Acid Accession #: NM_005795
 Coding sequence: 555-1940

1 11 21 31 41 51
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 65 GCACGAGGGA ACAACCTCTC TCTCTSCAGC AGAGAGTGTC ACCTCCTGCT TTAGGACCAT 60
 CAAGCTCTGC TAACTGAATC TCATCTTAAT TGCAGGATCA CATTGCAAAG CTTTCACTCT 120
 TTCCACCTT GCTTGTGGGT AAATCTCTTC TGGGAATCT CAGAAAGTAA AGTTCCATCC 180
 70 TGAGAAATAT TCACAAAGAA TTCTCTTAAG AGCTGGACTG GGTCTTGACC CCTGGAATTT 240
 AAGAAATCTT TAAAGACAAT GTCAAATATG ATCCAAGAGA AAATGTGATT TGAGTCTGGA 300
 GACAATGTG CATATCGTCT AATAATAAAA ACCCATATA GCCTATAGAA AACAATATTT 360
 GAATAATAAA AACCCATACT AGCCTATAGA AAACAATATT TGAAAGATTG CTACCACTAA 420
 AAAGAAACT ACTACAACCT GACAAGACTG CTGCAAACTT CAATTGGTCA CCACAACCTG 480
 ACAAGGTGTC TATAAAACAA GATTGCTACA ACTTCTAGTT TATGTTATAC AGCATATTTT 540
 75 ATTTGGGCTT AATGATGGAG AAAAAGTGTA CCTGTATT TCTGGTCTC TTGCCPTTTT 600
 TTATGATTCT TGTACAGCA GAATTAGAAG AGAGTCCTGA GGACTCAATT CAGTTGGGAG 660
 TTACTAGAAA TAAATCATG ACAGCTCAAT ATGAATGTTA CCAAAGATT ATGCAAGACC 720
 CCATTCAACA AGCAGAAGCC GTTACTGCA ACAGAACCTG GGATGGATGG CTGCTGTTGA 780
 ACGATGTGTC AGCAGGAAC GAATCAATGC AGCTCTGCCC TGATTACTTT CAGGACTTTG 840
 80 ATCCATCAGA AAAAGTTACA AAGATCTGTG ACCAAGATGG AAAGTGGTTT AGACATCCAG 900
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 AGACTGCACT AAATTGTTT TACCTGACCA TAATTGGACA CGGATTGTCT ATTGCATCAC 1020
 TGCTTATCTC GCTTGGCATA TTCTTTTATT TCAAGAGCCT AAGTTGCCAA AGGATTACCT 1080
 85 TACAAAAA TCTGTTCTT TCAATTGTTT GTAACCTCTG TGAACAATC ATTCACCTCA 1140
 CTGCAGTGGC CAACAACAG GCCTTAGTAG CCACAAATCC TGTTAGTTGC AAGTGTCCC 1200
 AGTTTATTCA TCTTACCTG ATGGGCTGTA ATTACTTTTG GATGCTCTGT GAAGGCATTT 1260
 ACCTACACAC ACTCATTTGT GTGGCCGTGT TGCAGAGAA GCAACATTTA ATGTGGTATT 1320
 ATTTTCTTGG CTGGGATTT CCACTGATTC CTGCTGTAT ACATGCCATT GCTAGAAGCT 1380

TATATTACAA TGACAAATTGC TGGATCAGTT CTGATACCCA TCTCCTCTAC ATTATCCATG 1440
 GCCCAATTGT TGCTGCTTTA CTGGTGAATC TTTTTCCTT GTTAAATATT GTACGCGTTC 1500
 TCATCACCAG GTTAAAGATT ACACACCAAG CGGAATCCAA TCTGTACATG AAAGCTGTGA 1560
 GAGCTACTCT TATCTTGGTG CCATTGCTTG GCATTGAATT TGTGCTGATT CCATGGCGAC 1620
 CTGAAGGAAA GATTGCAGAG GAGGTATATG ACTACATCAT GCACATCCTT ATGCACTTCC 1680
 AGGGTCTTTT GGTCTCTACC ATTTTCTGCT TCTTTAATGG AGAGGTTCAG GCAATTCTGA 1740
 GAAGAAACTG GAATCAATAC AAAATCCAAT TTGGAACAG CTTTCCCAAC TCAGAAAGCTC 1800
 TTCGTAGTGC GTCTTACACA GTGTCAACAA TCAGTGATGG TCCAGGTTAT AGTCATGACT 1860
 GTCTAGTGA ACACTTAAAT GGAAGAACGA TCCATGATAT TGAATATGTT CTCTTAAAC 1920
 CAGAAATTTT ATATAATTGA AAATAGAAGG ATGGTTGTCT CACTGTTTGG TGCTTCTCCT 1980
 AACTCAAGGA CTGGACCCA TGAATCTGTA GCCAGAAGAC TTCAATATTA AATGACTTTG 2040
 GGGAAATGCT TAAAGAGAG CCTTCACATG AAATAGTAG TGTGTTGATA AGAGTGTAA 2100
 ATCCAGCTCT ATGTGGGAAA AAAGAAATCC TGGTTGTAA TGTGTTGTCAG TAAATACTCC 2160
 CACTATGCTT GATGTGACGC TACTAACCTG ACATCACCAG GTGTGGAATT GGAGAAAAGC 2220
 ACAATCAACT TTCTGAGCT GGTGTAAGCC AGTTCACGCA CACCATGATG GAATTCAAAC 2280
 AAATGGCTGT AAACCTAAC ATACATGTTG GGCATGATTC TACCCTTATT CSCCCCAAGA 2340
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 TCCCATCTTG ATTGGGGCAG TTGACTTTTT TTTTTCCTCA GAGTGCCGTA GTCTTTTGTG 2460
 TAACTACCTT CTCAATGGA CAATACCAGA AGTGAATTAT CCTGCTGGC TTTCTTTCT 2520
 CTATGAAAAG CAATGAGTA CAATTGTTAT GATCTACTCA TTTGCTGACA CATCAGTTAT 2580
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 TTCTATATCA TTAGGAAAAC ATCTTAGTTG ATGCTACAAA ACACCTTGTC AACCTCTTCC 2700
 TGTCTTACCA AACAGTGGGA GGGAAATCCT AGCTGTAAT ATAAATTTTG CCCTTCCATT 2760
 TCTACTGTAT AAACAAATTA GCAATCATT TATATAAAGA AAATCAATGA AGGATTTCTT 2820
 ATTTTCTTGG AATTTGTAA AAAGAAATG TGAATAATGA GCTTGTAAT ACTCCATTAT 2880
 TTTATTTTAT AGTCTCAAT CAAATACATA CAACCTATGT AATTTTAAAC GCAATATAT 2940
 AATGCAACAA TGTGTGTATG TTAATATCTG ATACTGTATC TGGGCTGATT TTTTAAATAA 3000
 AATAGAGTCT GGAATGCT

Seq ID NO: 337 protein sequence
 Protein Accession #: NP_005786.1

1 11 21 31 41 51
 MEKCKTLYPL VLLPFFMILV TAELESPED SIQLGVTRNK IMTAQYECYQ KIMQDPIQQA 60
 EGVVYCNRTWD GWLWCNDVAA GTESMQLCPD YFQDFDPSEK VTKICDQDGN WFRHPASNRT 120
 WTNVTQCNVN THEKVKTALN LPYLTIIGHG LSIASLLISL GIFFYFKSL SQRITLHKNL 180
 FFSFVNCNSV TIIHLTAVAN NQALVATNPV SCKVQFIHL YLMGCNFWM LCEGIYHLTL 240
 IVVAVFAEKQ HLMWYFELGW GFPLIPACIH AIARSLYND NCWISSDTHL LYIIHGPICA 300
 ALLVNLFPFL NIVRVLTIKL KVTHQAESNL YMKAVRATLI LVPLLGIEFV LIPWRPEGKI 360
 AEEVYDYIMH ILMHFQQLLV STIFCFNGE VQAILRRNWN QYKIQGNFS SNSEALRSAS 420
 YTVSTISDGP GYSHDCPSEH LNKSIHDIE NVLLKPEPLY N

Seq ID NO: 338 DNA sequence
 Nucleic Acid Accession #: NM_001795
 Coding sequence: 25-2379

1 11 21 31 41 51
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 GCCTGCCTGG GCCTGCTGGC AGTGGCAGCA GTGGCAGCAG CAGGTGCTAA CCCTGCCCAA 120
 CGGGACACCC ACAGCCTGCT GCCCACCCAC CGGCGCCAAA AGAGAGATTG GATTTGGAAC 180
 CAGATGCACA TTGATGAAGA GAAAAACACC TCACTTCCCC ATCATGTAGG CAAGATCAAG 240
 TCAAGCGTGA GTGCAAGAA TGCCAAGTAC CTGCTCAAAG GAGAATATGT GGGCAAGGTC 300
 TTCGGGCTGC ATGCAGAGAC AGGAGACGTG TTCGCCATTG AGAGGCTGGA CCGGGAGAAT 360
 ATCTCAGATG ACCACCTCAC TGTGTCTATT GTGGACAAGG ACACCTGGTG AAACTGGAG 420
 ACTCCTTCCA GCTTCACCAT CAAAGTTTAT GACGTGAACG ACAACTGGCC TGTGTTCAAG 480
 CATCGGTTGT TCAATGCGTC CGTGCCTGAG TCGTCGGCTG TGGGGACCTC AGTCATCTCT 540
 GTGACAGCAG TGGATGCAGA CGACCCCACT GTGGGAGACC ACGCTCTGT CATGTACCAA 600
 ATCTGTAAGG GGAAGAGATA TTTTGCCATC GATAATTCTG GACGTATTAT CACAATAACG 660
 AAAAGCTTGG ACCGAGAGAA GCAGGCCAGG TATGAGATCG TGGTGAAGC GCGAGATGCC 720
 CAGGGCCTCC GGGGGGACTC GGGCAGGCC ACCGTGCTGG TCACTCTGCA AGACATCAAT 780
 GACAACCTCC CCTTCTTAC CAGACCAAG TACACATTG TCGTGCCTGA AGACACCGT 840
 GTGGGCACCT CTGTGGGCTG TCTGTTTGTG GAGGACCCAG ATGAGCCCA GAACCGGATG 900
 ACCAAGTACA GCATCTTGGG GGGCGACTAC CAGGACGCTT TCACCATGTA GACAAACCC 960
 GCCCACAAAG AGGCATCAT CAAGCCCATG AAGCCTCTGG ATTATGAATA CATCCAGCAA 1020
 TACAGCTTCA TCGTCGAGGC CACAGACCCC ACCATCGACC TCCGATACAT GAGCCCTCCC 1080
 GCGGGAACA GAGCCCAAGT CATTATCAAC ATCACAGATG TGGACGAGCC CCCATTTTT 1140
 CAGCAGCCTT TCTACCACT CCAGCTGAAG GAAAACCAAG AGAAGCCTCT GATTGGCACA 1200
 GTGCTGGCCA TGGACCTTGA TGGCGGTAGG CATAGCATG GATACTCCAT CCGCAGGACC 1260
 AGTGACAAGG GCCAGTTCTT CCGAGTCACA AAAAAGGGGG ACATTATCAA TGAGAAAGAA 1320
 CTGGACAGAG AAGTCTACCC CTGGTATAAC CTGACTGTGG AGGCCAAAGA ACTGGATTCC 1380
 ACTGGAACCC CCACAGGAAA AGAATCCATT GTGCAAGTCC ACATTGAAGT TTTGGATGAG 1440
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 CATGGCCAGC TGGTCTGCA GATCTCGCA ATAGACAAGG ACATAACACC ACGAAACGTG 1560
 AAGTTCAAAT TCACCTTGAA TACTGAGAAC AACTTTACCC TCACGGATAA TCACGATAAC 1620
 ACGCCAAACA TCACAGTCAA GTATGGCGAG TTTGACCGGG AGCATACCAA GGTCCACTTC 1680
 CTACCGGTGG TCACTCTAGA CAATGGGATG CCAAGTCGCA CGGGCACCAG CACGTGACCC 1740
 GTGGCCGTGT CAAAGTGCAA CGAGCAGGGC GAGTTTCACT TCTGCGAGGA TATGGCCGCC 1800
 CAGTGGGGCG TACAGTGGTA GGCATCTTAC TCTGATCCTT CCGATCACA 1860
 GTGATCACCC TGTCTATCTT CTGCGGCGG CGGCTCCGGA AGCAGGCCCG CGCGCACGGC 1920
 AAGAGCGTGC CGGAGATCCA CGAGCAGCTG GTCACTACG ACGAGGAGGG CGGCGCGGAG 1980
 ATGGACACCA CCGCTACGTA TGTGTGCGTG CTCAACTCGG TCGCGCGCGG CGGGCGCAAG 2040
 CCCCAGCGGC CCGCGCTGGA CGCCCGGCTT TCCCTCTATG CGCAGGTGCA GAAGCCACCG 2100
 AGGCACGCGC CTGGGGCACA CGGAGGGCCC GGGGAGATGG CAGCCATGAT CGAGGTGAAG 2160
 AAGGACGAGG CGGACACGCA CGGCGACGGC CCCCCTACG ACACGTGCA CATCTACGGC 2220
 TACGAGGGCT CCGAGTCCAT AGCCGAGTCC CTCAGTCCCC TGGGCACCGA CTCATCCGAC 2280

	TCTGACGTGG	ATTAGCATTT	CCTTAAACGAC	TGGGGACCCA	GGTTTAAAGAT	GCTGGCTGAG	2340
	CTGTACGGCT	CGGACCCCGG	GGAGGAGCTG	CTGTATTAGG	CGGCCGAGGT	CACTCTGGGC	2400
	CTGGGGACCC	AAACCCCTCG	CAGCCAGGC	CAGTCAGACT	CCAGGCACCA	CAGCCCTCAA	2460
5	AAATGGCAGT	GACTCCCGAG	CCCAGCACCC	CTTCTCTGTG	GGTCCCAGAG	ACCTCATCAG	2520
	CCTTGGGATA	GCAAACTCCA	GGTTCCTGAA	ATATCCAGGA	ATATATGTCA	GTGATGACTA	2580
	TTCTCAATAG	CTGGCAATAT	CAGGCTGGTG	TTCTGTCTGG	GCTCAGACAT	CCACATAACC	2640
	CTGTACCCCA	CAGACCGCCG	TCTAACTCAA	AGACTTCTCT	TGGCTCCCA	AGGCTGCAA	2700
	GCAAAACAGA	GCTGTTTAA	CTGCTGCAGG	GTCTTTTCT	AGGGTCCCTG	AACGCCCTGG	2760
10	TAAGGCTGGT	GAGGTCTGGG	TGCCTATCTG	CCTGGAGGCA	AAGGCCTGGA	CAGCTTGACT	2820
	TGTGGGGCAG	GATTCTCTGC	AGCCCATTC	CAAGGAGAG	TGACCATCAT	GCCCTCTCTC	2880
	GGGAGCCCTA	GCCCTGCTCC	AACTCCATAC	TCCACTCCAA	GTGCCCCACC	ACTCCCCAAC	2940
	CCCTCTCCAG	GCCTGTCAAG	AGGGAGGAAG	GGGCCCCATG	GCAGCTCCTG	ACCTTGGGTC	3000
	CTGAAGTGAC	CTCACTGGCC	TGCCATGCCA	GTAACCTGTG	TGTACTGAGC	ACTGAACCAC	3060
15	ATTGAGGGAA	ATGCTTATTA	AACCTTGAAG	CAACTGTGAA	TTCATTCTGG	AGGGGCGAGT	3120
	GAGATCAGGA	GTGACAGATC	ACAGGGTGAG	GGCCACCTCC	ACACCCACCC	CCTCTGGAGA	3180
	AGGCCTGGAA	GAGCTGAGAC	CTTGCTTTGA	GACTCCTCAG	CACCCCTCCA	GTTTTCCTCG	3240
	AGAAGGGGCA	GATGTTCCCG	GAGATCAGAA	GACGTCTCCC	CTTCTCTGCC	TCACCTGGTC	3300
	GCCATTCAT	GCTCTCTTTC	TTTTCTCTGT	CTACTCTCTA	TCCCTTGGTT	TAGAGGAACC	3360
20	CAAGATGTGG	CCTTTAGCAA	AACTGACAAT	GTCCAAACCC	ACTCATGACT	GCATGACGGA	3420
	CCGAGCATG	TGCTTTTACA	CCTCGCTGTT	GTCCATCTCT	AGGGAACTGA	CCCTCAGGCA	3480
	CACCTTGCG	AAGGAAGGCC	CTGCCCTGCC	CAACCTCTGT	GGTCACCCAT	GCATCATTC	3540
	ACTGGAACGT	TTCATGCAA	ACACACCTTG	GAGAAGTGGC	ATCAGTCAAC	AGAGAGGGGC	3600
	AGGGAAGGAG	ACACCAAGCT	CACCCCTCGT	CATGGACCGA	GGTTCCCACT	CTGGCAAAGC	3660
	CCCTCACACT	GCAAGGGATT	GTAGATAACA	CTGACTTGT	TGTTTTAACC	AATAACTAGC	3720
25	TTCTTATAAT	GATTTTTTTA	CTAATGATAC	TTACAAGTTT	CTAGCTCTCA	CAGACATATA	3780
	GAATAAGGCT	TTTTGCATAA	TAAGCAGGTT	GTTATTTAGG	TTAACAATAT	TAATTCAGGT	3840
	TTTTTAGTTG	GAAAAACAAT	TCCTGTAAAC	TTCTATTTTC	TATAATTGTA	GTAATTGCTC	3900
	TACAGATAAT	GTCTATATAT	TGGCCAAACT	GGTGCATGAC	AAGTACTGTA	TTTTTTTATA	3960
30	CCTAAATAAA	GAAAAATCTT	TAGCCTGGGC	AACAAAAAAA			

Seq ID NO: 339 Protein sequence

Protein Accession #: NP_001786

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	VIVDKDTGEN	LETPSSFTIK	VHDVNDNWPV	PTHRLFNASV	PSSAVGTSV	ISVTAVDADD	180
	PTVGDHASVM	YQILKGEYF	AIDNSGRIIT	ITKSLDREKQ	ARYEIVVEAR	DAQGLRGDSG	240
40	TATVLTQLQD	INDNFFFTQ	TKYTFVVPED	TRVGTSVGS	FVEDPDEPQN	RMTKYSILRG	300
	DYQDAFTIET	NPAHNELI	PMKPLDYEYI	QYQSFIVEAT	DPTIDLRYMS	PPAGNRAQVI	360
	INITDVDEPP	IFQQPFYHFQ	LKENQKKPLI	GTVLAMPDPA	ARHSIGYSIR	RTSDKGQFFR	420
	VTKKGDIYNE	KELDREVYPW	YNLTVEAKEL	DSTGTPGKE	SIVQVHIEVL	DENDNAPEFA	480
	KPYQPKVCEN	AVHGLVLQI	SAIDKDIPTP	NVKFKFTLNT	ENNFPLTDNH	DNTANITVKY	540
45	GQFDREHTKV	HFLPVVISDN	GMPSTGTST	LTVAVCKCNE	QGEFTFCEDM	AAQVGVSIQA	600
	VVAILLCILT	ITVITLLIFL	RRRLRKQARA	HGKSVPEIHE	QLVTYDEEGG	GEMDTTSYDV	660
	SVLNSVRRRG	AKPPPRALDA	RPSLYAQVQK	PPRHAPGAHG	PGGEMAAMIE	VKKDEADHDE	720
	DGPPYDTLHI	YGYEGSESIA	ESLSSLGTD	SDSDVDYDFL	NDWGRPFKML	AELYGSDPRE	780
50	ELLY						

Seq ID NO: 340 DNA sequence

Nucleic Acid Accession #: NM_003088

Coding sequence: 112-1593

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60	AACGGCAGAG	CCGAGGCGGT	GCAGATCCAG	TTCGCGCTCA	TCAACTGCGG	CAACAAGTAC	180
	CTGACGGCGG	AGGCGTTCCG	GTTCAAGGTG	AACGCGTCCG	CCAGCAGCCT	GAAGAAGAAG	240
	CAGATCTGGA	CGCTGGTGAC	GCCCCGTGAC	GAGGCGGGCA	GCGCGGCGGT	GTGCGTCCGC	300
	AGCCACCTGG	GCCGTACCT	GCGGCGGAC	AAGGACGGCA	ACGTGACCTG	CGAGCGCGAG	360
	GTGCGCGGTC	CGACTGCGCG	TTTCTCATC	GTGGCGCAGC	ACGACGGTCG	CTGGTCTGCTG	420
65	CAGTCCGAGG	AGGACCGGCG	CTACTTCGGC	GGCACCGAGG	ACCGCTGTCT	CTGCTTCGCG	480
	CAGACGGTGT	CCCCCGCCGA	GAAGTGGAGC	GTGCACATCG	CCATGCACCC	TCAGGTCAAC	540
	ATCTACAGTG	TCACCCGTAA	GCGCTACGCG	CACCTGAGCG	CGCGGCGGGC	CGACGAGATC	600
	GCCGTGGACC	GCGACGTGTC	CTGGGGCGTC	GACTCGCTCA	TCACCTCTCG	CTTCCAGGAC	660
	CAGCGCTACA	GCGTGCAGAC	CCCGGACCAC	CGCTTCTGCG	GCCACGACGG	GCGCCTGGTG	720
70	GCGCGCCCGG	AGCGGGCCAC	TGGCTACACG	CTGGAGTTCC	GCTCCGGCAA	GGTGGCCTTC	780
	CGCGACTGCG	AGGGCGCTTA	CCTGGCGCGG	TCGGGGCCCA	GCGGCACTGT	CAAGGCGGGC	840
	AAGGCCACCA	AGGTGGGCAA	GGACGAGCTC	TTTGCTCTGG	AGCAGAGCTG	CGCCAGGTC	900
	GTGCTGCAGG	CGGCCAACGA	GAGGAACGTG	TCCACGCGCC	AGGGTATGGA	CCTGTCTGCC	960
75	AATCAGGAGG	AGGACCGGCG	CCAGGAGACC	TTCAGCTGG	AGATCGACCG	GCACACCAAA	1020
	AAGTGTGCCT	TCCGTACCCA	CACGGGCAAG	TACTGGACGC	TGACGGCCAC	CGGGGGCGTG	1080
	CAGTCCACCG	CCTCCAGCAA	GAATGCCAGC	TGCTACTTTG	ACATCGAGTG	GCGTGACCGG	1140
	CGCATCACAC	TGAGGGCGTC	CAATGGCAAG	TTTGTGACCT	CCAAGAAGAA	TGGGCGAGCTG	1200
	GCCGCTCCGG	TGGAGACAGC	AGGGGACTCA	GAGCTCTTCC	TCTGAAGCT	CATCAACCGC	1260
80	CCCATCATCG	TGTTCCGCGG	GGAGCATGGC	TTCATCGGCT	GCCGCAAGGT	CACGGGCACC	1320
	CTGGACGCCA	ACCGCTCCAG	CTATGACGTC	TTCAGCTGG	AGTTCAACGA	TGGCGCCTAC	1380
	AACATCAAG	ACTCCACAGG	CAAATACTGG	ACGGTGGGCA	GTGACTCCGC	GGTCACCAGC	1440
	AGCGGCGACA	CTCCTGTGGA	CTTCTTCTTC	GAGTTCGTGG	ACTATAACAA	GGTGGCCATC	1500
	AAGGTGGGCG	GCGGCTACTT	GAAGGGCGAC	CACGACGGCG	TCTGAAGGCG	CTCGGCGGAA	1560
	ACCGTGGACC	CGGCTCGCT	CTGGGAGTAC	TAGGGCCGGC	CGTCTCTTCC	CGGCCCTTGC	1620
85	CCACATGGCG	GCTCTGCGCA	ACCTTCCCTG	CTAACCCCTT	CTCGGCCAGG	TGGGCTCCAG	1680
	GGCGGGAGGC	AAGCCCCCTT	GCCTTTCAAA	CTGGAAACCC	CAGAGAAAC	GGTGCCCCCA	1740
	CCTGTGCGCC	CTATGGACTC	CCCACTCTCC	CCTCGGCCCG	GGTTCCTTAC	TCCCTCGGG	1800

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 CGGGGCGAGT CTGGCACCTC TTCTTCTGA CCTCAGACGG CTCTGAGCCT TATTTCTCTG 1920
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 CTCCACAGTG GGAGAGGCTC AGCCTGGCTC CCTTCCCTGG AGCGGCAGGG CGTGACGGCC 2220
 ACAGGGTCTG CCGCTGCAC GTTCTGCCAA GGTGTGGTG GCGGGCGGT AGGGGTGTGG 2280
 GGGCGCTCTT CCTCCTGTCT CTTCCTTTC ACCCTAGCCT GACTGGAAGC AGAAAAATGAC 2340
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 CCCCTCTT CCCTCCTTCC CGTCCAGCCC CAGCCTGGG CCTGGGCTGC CGACACCTGG 2520
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 TCCCAACTCA GCATCTCACT CTGGGTGTCT TGGTCTTTTA TTTTGTGTA GTGTCAATTG 2700
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 AGTCTGC

Seq ID NO: 341 Protein sequence
 Protein Accession #: NP_003079

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 CLRSHLGRYL AADKDNVTCR EREVPGPDCR FLIVAHDDGR WSLQSEAHRR YFGGTEDRLS 120
 CFAQTVSPAE KWSVHIAMHP QVNIYSVTRK RYAHLSARPA DEIAVDRDVP WGVDSLITLA 180
 FQDQRYVQT ADHRFLRHDG RLVARPEPAT GYTLEFRSGK VAFRDCGRY LAPSGPSGTL 240
 KAGKATKVGK DELFALEQSC AQVVLQAANE RNVSTRQGM LSAQDEETD QETFOLEIDR 300
 DTKKCAFRTH TGYWTLTAT GGVQSTASSK NASCYFDIEW RDRRITLRAS NGKFVTSKKN 360
 GQLAASVETA GDSLFMLMKL INRPIIVFRG EHGFIGCRKV TGTLDANRSS YDVQLEFND 420
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 SAETVDPASL WEY

Seq ID NO: 342 DNA sequence
 Nucleic Acid Accession #: FGENESH predicted
 Coding sequence:660..1705

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 CTGAGCGCGG ACAGATCCAA GTTGGGAGCA GCTCTGCGTG CGGGGCCCTCA GAGAATGAGG 240
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 TGGACTTCAG TCCACCTGGG ACCGAGGTGA GTGCGCTCTG CCGGGGACAG CTCCCGATCT 900
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 TAGACGACTT GGGAGGCTTT GCCTGCGAAT GTGCTACGGG CTTCGAGCTG GGAAGGACG 1080
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 CCAGGCGCCC GCGGCCACT GCAACAGGCC CCGTGCGCGA GAGAACATGG CCAATCAGGG 1200
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 TCTGCTTTCA CGAAAGCCCC TCTTCCAGC CAAGGAAGGA GTCTATGGGC CCGCGGGGCC 1560
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Seq ID NO: 343 Protein sequence
 Protein Accession #: FGENESH predicted

1 11 21 31 41 51
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 GLGKPAVEGG DRAPDTALRP RAGQIQVGSS SACGASENEA GVRPVPPLAG ALARAGRRT 180
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 RGTPEGHRNR ARSKEMRCH LRANGYLCKY QPEVLCAPAP PGAASNLVSR APFQLHSAAL 360
 DFPSPGTEVS ALRCGQLPIS VTCIADEIGA RWDKLSGDVL CPCPGRYLRA GKCAELPNCL 420
 DDLGGFACBC ATGPFLKDG RSCVTSGEQG PTLGGTGVP RRPATATSP VPQRTWPIRV 480
 DEKLGETPLV PEQDNSVTSI PEIPRWGSQS TMSLQMSLQ AESKATITPS GSVISKFNST 540
 TSSATPQAFD SSSAVVFIFV STAVVVLVIL TMTVLGLVKL CFHESPSSQP RKESMGPPGL 600
 ESDPEPALG SSSAHCTNNG VKVGDCLDRD RAEGALLAES PLGSSDA

Seq ID NO: 344 DNA sequence
Nucleic Acid Accession #: NM_012072
Coding sequence: 149-2107

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CGTGGGGACC	GCTGCTACA	CGGCCCACTC	GGGCAAGCTG	AGCGCTCGCG	AGGCCCAGAA	300
CCACTGCAAC	CAGAACGGGG	GCAACCTGGC	CACTGTGAAG	AGCAAGGAGG	AGGCCCAGCA	360
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Seq ID NO: 345 Protein sequence
 Protein Accession #: NP_036204

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Seq ID NO: 347 Protein sequence
 Protein Accession #: CAA83435

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Seq ID NO: 348 DNA sequence
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CGGTCTCTGC	TGCACCTGTG	CCGTCCCCAG	AGCTACAGGC	CCCATCTGGT	CCTAAGTCCC	540
TGCTGCCCTT	CCCCTTCCCA	CAGTGTCCAT	TCTTCTCTCC	ATTTCAGGATG	CCCACGGCTG	600
GAGCTGCCTC	TCTCATCCAC	TTTCCAATAA	A			

Seq ID NO: 349 Protein sequence:
Protein Accession #: NP_002629

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1	11	21	31	41	51	
MRASSFLIVV	VFLIAGTLVL	EAAVTGVPVK	GQDTVKGRVP	FNGQDPVKQ	VSVKQDKVK	60
AQEPVKGPPV	TKPGSCPIIL	IRCAMLNPPN	RCLKDITDCPG	IKKCEGSGC	MACFVPO	

Seq ID NO: 350 DNA sequence
Nucleic Acid Accession #: NM_007183
Coding sequence: 75-2468

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1	11	21	31	41	51	
GAATTCCGGA	CAGGACGTGA	AGATAGTTGG	GTTTGGAGGC	GGCCGCCAGG	CCCAGGCCCG	60
GTGGACCTGC	CGCCATGCAG	GACGTAAGT	TCCTGCTGTC	GGCCCTGCAG	CCTGAGGCCG	120
GCGTGTGCTC	CCTGGCGCTG	CCCTCTGACC	TGCAGCTGGA	CCGCCGGGGC	GCCGAGGGGC	180
CGGAGGCCGA	CGCGCTGCGG	GCAGCCCGCG	TCCAGGAGCA	GGTCCGCGCC	CGCTCTTTCG	240
AGCTGGGACA	GCAGCCGCGG	CACAACGGGG	CCGCTGAGCC	CGAGCCTGAG	GCCGAGACTG	300
CCAGAGGCAC	ATCCAGGGGG	CAGTACCACA	CCCTGCAGGC	TGGCTTCAGC	TCTCGCTCTC	360
AGGGCTCTAG	TGGGACAAAG	ACCTCGGGCT	TCCGCCCCAT	CGCCAGGCCG	GCCTACAGCC	420
CAGCCTCTCT	GTCTCTCCCG	TCCGCCCTGG	ATCTGAGCTG	CAGTCCGAGG	CTGAGTTTCA	480
CCCACAATGG	GGGACAGCGC	TTTGGGGCCG	CTGGGTACGG	GGGTGCCCAG	CCCACCCCTC	540
CCATGCCCAC	CAGGCCCGTG	TCCTTCCATG	AGCGCGGTGG	GGTTGGGAGC	CGGGCCGACT	600
ATGACACACT	CTCCCTGCGC	TCGCTGCGGC	TGGGGCCCGG	GGGCCTGGAC	GACCGCTACA	660
GCCTGTGTCT	TGAGCAGCTG	GAGCCCGCGG	CCACCTCCAC	CTACAGGGCC	TTTGCGTAGC	720
AGCGCCAGGC	CAGCTCCAGC	TCCAGCCGGG	CAGGGGGGCT	GGACTGGCCC	GAGGCCACTG	780
AGGTTTCCCC	GAGCCGAGAC	ATCCGTGCCC	CTGCCGTGCG	GACCCTGCAG	CGATTCCAGA	840
GCAGCCACCG	GAGCCGCGGG	GTAGGCGGGG	CAGTGCCGGG	GGCCGTCTCT	GAGCCAGTGG	900
CTCGAGCGCC	ATCTGTGCGC	AGCCTCAGCC	TCAGCCTGGG	TGACTCGGGC	CACCTGCCCG	960
ACGTGCATGG	GTTCAACAGC	TACGGTAGCC	ACCGAACCTT	GCAGAGACTC	AGCAGCGGTT	1020
TTGATGACAT	TGACCTGCCC	TCAGCAGTCA	AGTACCTCAT	GGCTTCAGAC	CCCAACCTGC	1080
AGGTGCTGGG	AGCGGCCCTAC	ATCCAGCACA	AGTGTACAGC	CGATGCAGCC	GCCAAGGAAG	1140
AGGCCCGCAG	CCTTCAGGCC	GTGCCTAGGC	TGGTGAAGCT	CTTCAACCCAC	GCCAACCCAG	1200
AAGTGCAGCG	CCATGCCACA	GGTGCCATGC	GCAACCTCAT	CTACGACAAC	GCTGACAACA	1260
AGCTGGCCCT	GCTGGCGGAG	AACGGGATCT	TCGAGCTGCT	GCGGACACTG	CGGGAGCAGG	1320
ATGATGAGCT	TCGCAAAAT	GTCACAGGGA	TCCTGTGGAA	CCTTTCATCC	AGCGACCAAC	1380
TGAAGGACCG	CCTGGCCAGA	GACACGCTGG	AGCAGCTCAC	GGACCTGGTG	TTGAGCCCCC	1440
TGTCCGGGGC	TGGGGGTCCC	CCCCCTCATC	AGCAGAACGC	CTCGGAGCGC	GAGATCTTCT	1500
ACAACGCCAC	CGGCTTCTCT	AGGAACCTCA	GCTCAGCCTC	TCAGGCCACT	CGCCAGAAAG	1560
TGCGGGAGTG	CCAGGGGCTG	GTGGACGCCC	TGGTCACCTC	TATCAACCCAC	GCCCTGGAGC	1620
CGGGCAAAATG	CGAGGACAAG	AGCGTGGAGA	ACGCGGTGTG	CGTCTGCGG	AACCTGTCTC	1680
ACCGCCTCTA	CGACGAGATG	CCGCCGTCCG	CGCTGCAGCG	GCTGGAGGGT	CGCGGCCGCA	1740
GGGACCTGGC	GGGGGCGCGC	CCGGGAGAGG	TCGTGGGCTG	CTTCACGCCG	CAGAGCCGGC	1800
GGCTGCGCGA	GCTGCCCTCT	GCCGCCGATG	CGCTCACCTT	CGCGAGGTTG	TCCAAGGACC	1860
CCAAGGGCCT	CGAGTGGCTG	TGGAGCCCCC	AGATCGTGGG	GCTGTACAAC	CGGCTGCTGC	1920
AGCGCTGCGA	GCTCAACCGG	CACACGACGG	AGGCGGCGCG	CGGGGCGCTG	CAGAACATCA	1980
CGGCAGGCGA	CGCAGGTGGG	GCGGGGGTGC	TGAGCCCGCT	GGCCCTGGAG	CAGGAGCGTA	2040
TTCTGAACCC	CCTGTAGAC	CGTGTGAGGA	CCGCCGACCA	CCACAGCTG	CGCTCACTGA	2100
CTGGCCTCAT	CCGAAACCTG	TCTCGGAACG	CTAGGAACAA	GGACGAGATG	TCCACGAAGG	2160
TGGTGAGCCA	CCTGATCGAG	AAGCTGCCAG	GCAGCGTGGG	TGAGAAGTCG	CCCCAGCCG	2220
AGGTGCTGGT	CAACATCATA	GCTGTGCTCA	ACAACCTGGT	GGTGGCCAGC	CCCATCGCTG	2280
CCCGAGACCT	GCTGTATTIT	GACGGACTCC	GAAAGCTCAT	CTTCATCAAG	AAGAAGCGGG	2340
ACAGCCCCGA	CAGTGAAGAG	TCCTCCCGGG	CAGCATCCAG	CTCCTGGGCC	AACCTGTGGC	2400
AGTACAACAA	GCTCCACCGT	GACTTTCGGG	CGAAGGGCTA	TCGGAAGGAG	GACTTCTCTG	2460
GCCCCATAGT	GAAGCCTTCT	GGAGGAGAAG	GTGACGTGGC	CCAGCGTCCA	AGGGACAGAC	2520
TCAGTCTCAG	GCTGCTTGGC	AGCCAGCCTT	GGAGGAGAAG	GCTAATGACG	GAGGGGCCCC	2580
TCGCTGGGGC	CCCTGTGTGC	ATCTTTGAGG	GTCCTGGGCC	ACCAGGAGGG	GCAGGGTCTT	2640
ATAGCTGGGG	ACTTGGCTTC	CGCAGGGCAG	GGGGTGGGGC	AGGGCTCAAG	GCTGTCTCTG	2700
TGTATGGGGT	GGTGACCCAG	TCACATTGGC	AGAGGTGGGG	GTTGGCTGTG	GCCTGGCAGT	2760
ATCTTGGGAT	AGCCAGCACT	GGGAATAAAG	ATGGCCATGA	ACAGTCACAA	AAAAAAAAAA	2820
AAAAGGAATT	C					

Seq ID NO: 351 Protein sequence
Protein Accession #: NP_009114.1

85
1 11 21 31 41 51

	MQDGNFLLSA	LQPEAGVCSL	ALPSDLQLDR	RGAEGPEAER	LRAARVQEQV	RARLLQLGQQ	60
	PRHNGAAEPE	PEAETARGTS	RGQYHTLQAG	FSSRSQGLSG	DKTSGFRPIA	KPAYSPASWS	120
5	SRSAYDLSCS	RRLSAHNGG	SAFGAAGYGG	AQPTPPMPTR	PVSFHERGGV	GSRADYDTLS	180
	LRSLRLGPGG	LDDRYSLVSE	QLEPAATSTY	RAFAYERQAS	SSSSRAGGLD	WPEATEVSPS	240
	RTIRAPAVRT	LQRFQSSHRS	RGVGGAVPGA	VLEPVARAPS	VRSLSLSLAD	SGHLPDVHGF	300
	NSYGSHTRLQ	RLSSGDDID	LPSAVKYLMA	SDPNLQVLGA	AYIQHKCYSD	AAAKKQARSL	360
	QAVPRLVKLF	NHANQEVQRH	ATGAMRNLIY	DNADNKLALV	EENGIFELLR	TLREQDDDEL	420
10	KNVTGILWNL	SSSDHLKDR	ARDTLEQLTD	LVLSPLSGAG	GPPLIQNAS	EAEIFYNATG	480
	FLRNLSSASQ	ATRQKMRECH	GLVDALVTSI	NHALDAGKCE	DKSVENAVCV	LRNLSYRLYD	540
	EMPPSALQRL	EGRRGRDLAG	APPGEVVGC	TPQSRRLREL	PLAADALTFA	EVSKDPKGLE	600
	WLWSPQIVGL	YNRLLRCEL	NRHTTEAAAG	ALQNTITAGDR	RWAGVLSRLA	LEQERILNPL	660
	LDVRVTADHH	QLRSLTGLIR	NLSRNARNKD	EMSTKVVSHL	IEKLPGSVGE	KSPPAEVLVN	720
15	IIVLVNLLV	ASPLAARDLL	YFDGLRKLIF	IKKKRDSPTS	EKSSRAASSL	LANLWQYNKL	780
	HRDFRAKGYR	KEDFLGP					

Seq ID NO: 352 DNA sequence
Nucleic Acid Accession #: M31469
Coding sequence: 1-651

	1	11	21	31	41	51	
25	ATGGCTGCGC	AGGGAGAGCC	CCAGGTCCAG	TTCAAACCTG	TATTGGTTGG	TGATGGTGGT	60
	ACTGGAAGAA	CGACCTTCGT	GAAACGTCAT	TTGACTGGTG	AATTTGAGAA	GAAGTATGTA	120
	GCCACCTTGG	GTGTTGAGGT	TCATCCCCTA	GTGTTCCACA	CCAACAGAGG	ACCTATTAAG	180
	TTCAATGTAT	GGGACACAGC	CGGCCAGGAG	AAATTCGGTG	GACTGAGAGA	TGGCTATTAT	240
	ATCCAAGCCC	AGTGTGCCAT	CATAATGTTT	GATGTAACAT	CGAGAGTTAC	TTACAAGAAT	300
30	GTGCTAACT	GGCATAGAGA	TCTGGTACGA	GTGTGTGAAA	ACATCCCCAT	TGTGTTGTGT	360
	GGCAACAAAG	TGGATATTAA	GGACAGGAAA	GTGAAGCGCA	AATCCATTGT	CTTCCACCGA	420
	AAGAAGAAAT	TTCACTACTA	CGACATTTCT	GCCAAAAGTA	ACTACAACCT	TGAAAAGCCC	480
	TTCTCTGGC	TTGCTAGGAA	GCTCATTGGA	GACCCCTAAT	TGGAATTTGT	TGCCATGCCT	540
	GCTCTCGCC	CACCAGAAAT	TGTCATGGAC	CCAGCTTTGG	CAGCACAGTA	TGAGCACGAC	600
35	TTAGAGGTTG	CTCAGACAAC	TGCTCTCCCG	GATGAGGATG	ATGACCTGTG	A	

Seq ID NO: 353 Protein sequence
Protein Accession #: AAA36546

	1	11	21	31	41	51	
40	MAAQGEPOVQ	FKLVLVGDGG	TGKTTFVKRH	LTGEFEKKYV	ATLGVEVHPL	VFHTNRGPIK	60
	FNWVDTAGQE	KFGGLRDGYI	IQAQCAIIMF	DVTSRVITYKN	VPNWHRDVLR	VCENIPIVLC	120
	GNKVDIKDRK	VKAISIVFHR	KKNLQYYDIS	AKSNYNFEKP	PLWLARKLIG	DPNLEFVAMP	180
45	ALAPEVVMVD	PALAAQYEH	LEVAQTALP	DEDDDL			

Seq ID NO: 354 DNA sequence
Nucleic Acid Accession #: NM_002820
Coding sequence: 304-831

	1	11	21	31	41	51	
55	CCGGTTCCGA	AAGAAGCTGA	CTTCAGAGGG	GGAAACTTTC	TTCTTTTAGG	AGGCGGTTAG	60
	CCCTGTTCCA	CGAACCCAGG	AGAACTGCTG	GCCAGATTAA	TTAGACATTG	CTATGGGAGA	120
	CGTGTAACA	CACACTATTAT	CATTGATGCA	TATATAAAAC	CATTTTATT	TCGCTATTAT	180
	TTCAGAGGAA	GCGCCTCTGA	TTTGTTCCTT	TTTTCCTTT	TTGCTCTTTC	TGGCTGTGTG	240
	GTTTGGAGAA	AGCACAGTTG	GAGTAGCCGG	TTGCTAAATA	AGTCCCAGAG	GCGAGCGGAG	300
	ACGATGCAGC	GGAGACTGGT	TCAGCAGTGG	AGCGTCGCGG	TGTTCTGCT	GAGCTACGCG	360
60	GTGCCCTCCT	GCGGCGCTC	GGTGGAGGGT	CTCAGCCGCC	GCCTCAAAAG	AGCTGTGTCT	420
	GAACATCAGC	TCCTCCATGA	CAAGGGGAAG	TCCATCCAAG	ATTTACGCGG	ACGATTCTTC	480
	CTTCACCATC	TGATCGCAGA	AATCCACACA	GCTGAAATCA	GAGCTACCTC	GGAGGTGTCC	540
	CCTAACTCCA	AGCCCTCTCC	CAACACAAAG	AACCACCCCG	TCCGATTGGG	GTCTGATGAT	600
	GAGGGCAGAT	ACCTAACTCA	GGAAACTAAC	AAGGTGGAGA	CGTACAAGA	GCAGCCGCTC	660
65	AAGACACCTG	GGAGAGAAAA	GAAAGGCAAG	CCCGGGAAAC	GCAAGGAGCA	GGAAAAGAAA	720
	AAACGGCGAA	CTCGCTCTGC	TCTGGTAGAC	TCTGGAGTGA	CTGGGAGTGG	GCTAGAAGGG	780
	GACCACCTGT	CTGACACCTC	CACAACGTCG	CTGGAGCTCG	ATTCACGTA	ACAGGCTTCT	840
	CTGGCCCGTA	GCCTCAGCGG	GGTGCTCTCA	GCTGGGTTTT	GGAGCCTCCC	TTCTGCCTTG	900
	GCTTGGACAA	ACCTAGAATT	TTCTCCCTTT	ATGTATCTCT	ATCGATTGTG	TAGCAATTGA	960
70	CAGAGAATAA	CTCAGAATAT	TGTCTGCCTT	AAAGCAGTAC	CCCCCTACCA	CACACACCCC	1020
	TGTCTCCAG	CACCATAGAG	AGGCGCTAGA	GCCCATTCCT	CTTCTCCAC	CGTCACCCAA	1080
	CATCAATCCT	TTACCACTCT	ACCAATAAAT	TTCATATTCA	AGCTTCAGAA	GCTAGTGACC	1140
	ATCTTCATAA	TTTGCTGGAG	AAGTGTATTT	CTTCCCTTCA	CTCTCACACC	TGGGCAAACT	1200
	TTCTTCAGTG	TTTTCATT	CTTACGTTCT	TTCACTTCAA	GGGAGAAATAT	AGAAGCATTT	1260
75	GATATTATCT	ACAAACACTG	CAGAACAGCA	TCATGTCATA	AACGATTCTG	AGCCATTAC	1320
	ACTTTTATT	TAATTAATG	TATTTAATTA	AATCTCAAT	TTATTTAAT	GTAAGAAGT	1380
	TAAATATGT	TTTAAACACA	TGCTTAAAT	TTGTTTAAAT	AAATTTAACT	CTGTTTCTCA	1440
	CCAGCTCATA	CAAAATAAAT	GGTTCTGAA	AATGTTTAA	TATTAACCTA	CAAGGATATA	1500
	GGTTTTCTC	ATGTATCTTT	TTGTTCTATT	GCAAGATGAA	ATAATTTTTC	TAGGGTAATG	1560
80	CCGTAGGAAA	AATAAACTT	CACATTTAAA	AAAAA			

Seq ID NO: 355 Protein sequence
Protein Accession #: NM_002820

	1	11	21	31	41	51	
85	MORRLVQQWS	VAVFLLSYAV	PSCGRSVEGL	SRRLKRAVSE	HQLLHDKGKS	IQDLRRRFFL	60
	HHLIAEIHIA	EIRATSEVSP	NSKPSPTKN	HPVRFGSDDE	GRYLTQETNK	VETYKEQPLK	120

TPGKKKKGKPF GKRKEQEKKK RRTRSAWLDS GVTGSGLEGD HLSDTSTTSL ELDSDR

Seq ID NO: 356 DNA sequence

Nucleic Acid Accession #: NM_017522

Coding sequence: 1-2100

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1	11	21	31	41	51	
ATGGGCTCC	CCGAGCCGGG	CCCTCTCCGG	CTTCTGGCGC	TGCTGCTGCT	GCTGCTGCTG	60
CTGCTGCTGC	TGCGGCTCCA	GCATCTTGCG	GCGGCAGCGG	CTGATCCGCT	GCTCGGCGGC	120
CAAGGGCCGG	CCAAAGGATG	CGAAAAGGAC	CAATTCCAGT	GCCGGAAACGA	GCGCTGCATC	180
CCCTCTGTGT	GGAGATGCGA	CGAGGACGAT	GACTGTCTAG	ACCACAGCGA	CGAGGACGAC	240
TGCCCCAAGA	AGACCTGTGC	AGACAGTGAC	TTCACTGTGT	ACAAAGGCCA	CTGCATCCAC	300
GAACGGTGGG	AGTGTAGCGG	CGAGGAGGAG	TGTCCTGATG	GCTCCGATGA	GTCCGAGGCC	360
ACTTGACCCA	AGCAGGTGTG	TCCTGCAGAG	AAGCTGAGCT	GTGGACCCAC	CAGCCACAAG	420
TGTGTACCTG	CCTCGTGGCG	CTGCGACGGG	GAGAAGGACT	GCGAGGGTGG	AGCGGATGAG	480
GCCGGCTGTG	CTAGCTCACT	GGGCACCTGC	CGTGGGACG	AGTTCAGTG	TGGGATGGG	540
ACATGTGTCC	TTGCAATCAA	GCATGCAAC	CAGGAGCAGG	ACTGTCCAGA	TGGGAGTGAT	600
GAAGCTGGCT	GCCTACAGGG	GCTGAACGAG	TGTCTGCACA	ACAATGGCGG	CTGCTCACAC	660
ATCTGCACTG	CTAGCTCACT	TGGCTTTGAA	TGCACGTGCC	CAGCAGGCTT	CCAGCTCCTG	720
GACCAGAAGA	CTTGTGGCGA	CATTGATGAG	TGCAAGGACC	CAGATGCCTG	CAGCCAGATC	780
TGTGTCAATT	ACAAGGGCTA	TTTAAAGTGT	GAGTGTACC	CTGGCTGCGA	GATGGACCTA	840
CTGACAAGA	TCTATAGCGG	TGCTGTGGC	AAGAGCCAT	CCCTAATCTT	CACCAACCGC	900
ACGAGTGGCG	AGGATCGACC	TGTGAAGCGG	AATATTAC	GCCTCATCCC	CATGCTCAAG	960
AATGTCGTGG	CACATAGATGT	GGAAGTTGCC	ACCAATCGCA	TCTACTGGTG	TGACCTCTCC	1020
TACCGTAAGA	TCTATAGGAC	CTACATGGAC	AAGGCCAGTG	ACCCGAAAGA	GCGGGAGGTC	1080
CTCATTGACG	AGCAGTTGCA	CTCTCCAGAG	GGCTTGGCAG	TGGACTGGGT	CCACAAGCAC	1140
ATCTACTGGA	CTGACTCGGG	CAATAAGACC	ATCTCAGTGG	CCACAGTTGA	TGGTGGCCGC	1200
CGACGCACTC	TCTTCAAGTG	TAACCTCAGT	GAACCCCGGG	CCATCGCTGT	TGACCCCTCG	1260
CGAGGGTTCA	TGTATTGGTC	TGACTGGGGG	GACCAGGCCA	AGATTGAGAA	ATCTGGGCTC	1320
AACGGTGTGG	ACCGGCAAAAC	ACTGGTGTCA	GACAATATTG	AATGGCCCAA	CGGAATCACC	1380
CTGATCTGCG	TGAACTCAGG	CTTGTACTGG	GTAGACTCCA	AGCTACACCA	ACTGTCCAGC	1440
ATTGACTTCA	GTGGAGGCAA	CAGAAAGACG	CTGATCTCCT	CACTGACTTT	CCTGAGCCAC	1500
CCTTTTGGGA	TAGCTGTGTT	TGAGGACAAG	GTGTTCTGGA	CAGACCTGGA	GAACGAGGCC	1560
ATTTTTCAGT	CAAACTCGCT	CAATGGCCTG	GAAATCTCCA	TCCTGGCTGA	GAACCTCAAC	1620
AACCCACATG	ACATTGTCTAT	CTTCCATGAG	CTGAAGCAGC	CAAGAGCTCC	AGATGCCTGT	1680
GAGCTGAGTG	TCCAGCCTAA	TGGAGGCTGT	GAATACCTGT	GCCTTCCTGC	TCCTCAGATC	1740
TCCAGCCACT	CTCCCAAGTA	CACATGTGCC	TGTCCTGACA	CAATGTGGCT	GGGTCCAGAC	1800
ATGAAGAGGT	GCTACCGAGA	TGCAAAAGAA	GACAGTAAGA	TGGGCTCAAC	AGTCACTGCC	1860
GCTGTTATCG	GGATCATCGT	GCCCATAGTG	GTGATAGCCC	TCCTGTGCAT	GAGTGGATAC	1920
CTGATCTGGA	GAACTCAGAG	GCGGAAGAAC	ACCAAAAGCA	TGAATTTTGA	CAACCCAGTC	1980
TACAGGAAAA	CAACAGAAGA	AGAAGATGAA	GATGAGCTCC	ATATAGGGAG	AACTGCTCAG	2040
ATTGGCCATG	TCTATCCTGC	ACGAGTGGCA	TTAAGCCTTG	AAGATGATGG	ACTACCCTGA	2100
GGATGGGATC	ACCCCTTCG	TGCCTCATGG	AATTCAGTCC	CATGCACTAC	ACTCCGATG	2160
GTGTATGACT	GGATGAATGG	GTTTCTATAT	ATGGGTCTGT	GTGAGTGTAT	GTGTGTGTGT	2220
GATTTTTTTT	TTTAAATTTA	TGTTGCGGAA	AGGTAACCCAC	AAAGTTATGA	TGAACTGCAA	2280
ACATCCAAAG	GATGTGAGAG	TTTTTCTATG	TATAATGTTT	TATACACTTT	TAACTGGTTT	2340
GCACTACCCA	TGAGGAATTC	GTGGAATGGC	TACTGCTGAC	TAACATGATG	CACATAACCA	2400
AATGGGGGCC	AATGGCACAG	TACCTTACTC	ATCATTAAAA	AACTATATTT	ACAGAAGATG	2460
TTTGGTTGCT	GGGGGGCTTT	TTTAGGTTTT	GGGCATTGT	TTTTTGTAAG	TAAGATGATT	2520
ATGCTTTGTG	GCTATCCATC	AACATAAGT				

Seq ID NO: 357 Protein sequence

Protein Accession #: NP_059992

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1	11	21	31	41	51	
MGLPEPGPLR	LLALLLLLLL	LLLLRLQHLA	AAAADPLLGG	QGPKECEKD	QFQCRNERCI	60
PSVWRCEDD	DCLDHSDEDD	CPKKTCDSD	FTCDNGHCIH	ERWKCDEEE	CPDGSDESEA	120
TCTKQVCPAE	KLSCGPTSHK	CVPASWRCDG	EKDCGGGADE	AGCATSLGTC	RGDEFQCGDG	180
TCVLAIKHCN	QEQDCPDGSD	EAGCLQGLNE	CLHNNGGCSH	ICTDLKIGFE	CTCPAGFQLL	240
DQKTCGDIDE	CKDPDCAGSI	CVNYKYFKC	ECYPGCEMDL	LTNCKAAAG	KSPSLIFTNR	300
TSAEDRPVKR	NYSRLPLMLK	NVVALDVEVA	TNRIYWCDLS	YRKIYSAYMD	KASDPKEREV	360
LIDEQLHSPE	GLAVDWVHKH	IYWTDSGNKT	ISVATVDGGR	RRTLFNRNLS	EPRAIADVPL	420
RGFMYSWDWG	DQAKIEKSGL	NGVDRQTLVS	DNIEWPNGIT	LDLLSQRLYW	VDSKLHLQSS	480
IDFSGGNRKT	LISSTDFLSH	PFGIAVPEDK	VFWTDLNEA	IFSANRLNGL	EISILAENLN	540
NPHDIVIFHE	LKQPRAPDAC	ELSVQPNNGC	EYLCLPAPQI	SSHSPKYTCA	CPDTMWLPGD	600
MKRCYRDANE	DSKMGSTVTA	AVIGIIIVIV	VIALLCMSGY	LIWRNWKRN	TKSMNFDNEV	660
YRKTTEEDE	DELHIGRTAQ	IGHVYPARVA	LSLEDDGLP			

Seq ID NO: 358 DNA sequence

Nucleic Acid Accession #: M27826

Coding sequence: <1-503

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1	11	21	31	41	51	
AGCCCAAGAA	ACATCTCACC	AATTTCAAAT	CTGATCTATT	CGGCTTAGCG	ACTGAAGATT	60
GACGCTGCCC	GATCGCCTCG	GAAGTCCCT	GGACCATCAC	AGAAGCCGAG	CTTCGGGTAA	120
CTCTCACAGT	GGAGGGTAAG	TCCATCCCCT	GTTTAAATCGA	TACGGGGGCT	ACCCACTCCA	180
CGTTGCCCTC	TTTTCAAGGG	CCTGTTTCCC	TTGCCCCCAT	AACTGTTGTG	GGTATTGACG	240
GCCAAAGCTTC	AAAACCCCTG	AAAACCTCCC	CACCTCTGGT	CCAACCTTGA	CAACACTCTT	300
TTATGCACTC	TTTTTTAGTT	ATCCCCACCT	GCCCCACTTC	CTTATTAGGC	CGAAATATTT	360
TAACCAAAAT	ATCTGCTTCC	CTGACTATTC	CTGGAGTACA	GCTACATCTC	ATTGCTGCC	420
TTCTTCCCAA	TCCAAAGCCT	CCTTTGTGTC	CTCTAACATC	CCCAATATAT	CAGCCCTTAC	480
CACAAGACCT	CCCTTCAGCT	TAATCTCTCC	CACCTTAGGT	TCCACGCGG	CCCCTAATCC	540
CACTTGAAGC	AGCCCTGAGA	AACATCGCCC	ATTCTCTCTC	CATACCAACC	CCCAAAATTT	600
TTGCGCGCTC	CAACACTTCA	ACACTATTTT	GTTTTATTGT	TCTTATTAAT	ATCAGAAGGC	660

AGGAATGTCA GGCCTCTGAG CCCAGGCCAG GCCATCGCAT CCCCTGTGAC TTGCAAGTAT 720
 ACATCCAGAT GGCCTGAAGT AACTGAAGAT CCACAAAAGA AGTAAAAACA GCCTTAACCTG 780
 ATGACATTCC ACCATTGTGA TTTGTTCTCG CCCACCCCTA ACTGATCAAT GTACTTTGTA 840
 ATCTCCCCCA CCTTAAAGAA GGTTCCTTTGT AATTCTCCCC ACCCTTGAGA ATGTACTTTG 900
 TGAGATCCAC CCCTGCCAC CAGAGAACAA CCCCCTTTGA TTGTAATTTT TTATTACCTT 960
 CCCAATCCT ATAAACAGC CCCACCCCTA TCTTCCTTCA CTGACTCTCT TTTCGGACTC 1020
 AGCCACGGC ACCCAGGTGA AATAAACAGC TTTATTGCTC AC

Seq ID NO: 359 Protein sequence
 Protein Accession #: AAA65999

1 11 21 31 41 51
 PKKHLTNFKS DLFLGATEDW RCPIASEVPW TITEAELRVT LTVEGKSIPC LIDTGATHST 60
 LPSFQGPVSL APIITVVGIDG QASXPLKTPP LWCQLGQHSF MHSFLVIPTC PLPLLRNLI 120
 TKLSASLTIP GVQLHLIAL LPNPKPLCP LTSPQYQPLP QDLPSA

Seq ID NO: 360 DNA sequence
 Nucleic Acid Accession #: NM_001854
 Coding sequence: 162-5582

1 11 21 31 41 51
 AACCATCAAA TTTAGAAGAA AAAGCCCTTT GACTTTTTC CCCTCTCCCT CCCCAATGGC 60
 TGTGTAGCAA ACATCCCTGG CGATACCTTG GAAAGGACGA AGTTGGTCTG CAGTCGCAAT 120
 TTCGTGGGTT GAGTTCACAG TTGTGAGTGC GGGGCTCGGA GATGGAGCCG TGGTCTCTA 180
 GGTGGAAAC GAAACGGTGG CTCCTGGGATT TCACCGTAAC AACCTTCGCA TTGACCTTCC 240
 TCTTCCAAGC TAGAGAGGTC AGAGGAGCTG CTCCAGTTGA TGTACTAAAA GCACATAGATT 300
 TTCACAAATC TCCAGAGGGA ATATCAAAAA CAACGGGATT TTGCACAAAC AGAAAGAATT 360
 CTAAAGGCTC AGATACTGCT TACAGAGTTT CAAAGCAAGC ACAACTCAGT GCCCAACAA 420
 AACAGTTATT TCCAGGTGGA ACTTTCCTCAG AAGACTTTTC AATACTATT ACAGTAAAAAC 480
 CAAAAAAGG AATTGAGTCT TTCTTTTAT CTATATATAA TGAGCATGGT ATTCAGCAAA 540
 TTGGTGTGTA GGTGGGAGA TCACCTGTTT TTCTGTTTGA AGACCACACT GGAAAACTCG 600
 CCCAGAAGA CTATCCCTC TCCAGAACTG TTAACATCGC TGACGGGAAG TGGCATCGGG 660
 TAGCAATCAG CGTGGAGAGA AAAACTGTGA CAATGATTGT TGATTGTAAG AAGAAAAACA 720
 CGAAACCACT TGATAGAAGT GAGAGAGCAA TTGTGTATAC CAATGGAATC ACGGTTTTTG 780
 GAACAAGGAT TTTGGATGAA GAAGTTTTTG AGGGGACAT TCAGCAGTTT TTGATCACAG 840
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Seq ID NO: 361 Protein sequence
Protein Accession #: NP_001845

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Seq ID NO: 363 Protein sequence

Protein Accession #: NP_003098

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EVFLAQGTLR PDLIESASLV ASGKAELIKT HHNDTELIRK LREEGVIEP LKDFHKDEVR 420
ILGRELGLPE ELVSRHPFPG PGLAIRVICA EEPYICKDFP ETNNILKIVA DFSASVKKPH 480
TLLQVRKACT TEEDQEKLMQ ITSLSHSLNAF LLPIKTVGVQ GDCRSYSYVC GISSKDEPDW 540
ESLIFLARLI PRMCHNVNRV VYIFGPPVKE PPTDVTPTFL TTGVLSLRLQ ADPEAHNLR 600
ESGYAGKISQ MPVILTPLHF DRDPLQKQPS QRSVVIRTP ITSDFM TGIP ATPGNEIPVE 660
VVLKVMTEIK KIPGISRMY DLTSKPPGTT EWE

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Seq ID NO: 366 DNA sequence
Nucleic Acid Accession #: NM_004219
Coding sequence: 46-654

40
45
50
55

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1 11 21 31 41 51
GCGGCTCAG ATGAATGCGG CTGTTAAGAC CTGCAATAAT CCAGAAATGGC TACTCTGATC 60
TATGTTGATA AGGAAAAATGG AGAACCCAGGC ACCCGTGTGG TTGCTAAGGA TGGGCTGAAG 120
CTGGGGCTCG GACCTTCAAT CAAAGCCTTA GATGGGAGAT CTCAAGTTTC AACACCCAGT 180
TTTGGCAAAA CGTTCGATGC CCCACCAGCC TTACTTAAAG CTACTAGAAA GGCTTTGGGA 240
ACTGTCAACA GAGCTACAGA AAAGTCTGTA AAGACCAAGG GACCCCTCAA ACAAAAACAG 300
CCAAGCTTTT CTGCCAAAAA GATGACTGAG AAGACTGTTA AAGCAAAAAG CTCTGTTCCT 360
GCCTCAGATG ATGCTATCC AGAAATAGAA AAATCTTTC CCTTCAATCC TCTAGACTTT 420
GAGAGTTTGG ACCTGCCTGA AGAGACCAG ATTGCGCACC TCCCTTGAG TGGAGTGCTC 480
CTCATGATCC TTGACGAGGA GAGAGAGCTT GAAAAGCTGT TTCAGCTGGG CCCCCCTTCA 540
CCTGTGAAGA TGCCCTCTCC ACCATGGGAA TCCAATCTGT TGCACTGCC TTCAAGCATT 600
CTGTGACCC TGGATGTTGA ATTGCCACCT GTTTGCTGTG ACATAGATAT TTAAATTTCT 660
TAGTGCTTCA GAGTTGTGT GTATTGTAT TAATAAAGCA TTCTTCAACA GAAAAAANA 720
AAAAAANA

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Seq ID NO: 367 Protein sequence
Protein Accession #: NP_004210

60
65

```

1 11 21 31 41 51
MATLIYVDKE NGEPGTRVVA KDGLKLGSGP SIKALDGRSQ VSTPRFGKTF DAPPALPKAT 60
RKALGTVNRA TEKSVKTKGP LKQKQPSFSA KKMTEKTVKA KSSVPSDDA YPEIEKFFPF 120
NPLDFESFDL PEEHQIAHLP LSGVPLMILD EERELEKLQ LGPPSPVKMP SPPWESNLLQ 180
SPSSILSLD VELPPVCCDI DI

```

Seq ID NO: 368 DNA sequence
Nucleic Acid Accession #: NM_000597
Coding sequence: 118-1104

70
75
80
85

```

1 11 21 31 41 51
ATTGCGGGCG AGGGAGGAGG AAGAAGCGGA GGAGGCGGCT CCGCTCGCA GGGCCGTGCA 60
CCTGCCCGCC CGCCGCTCG CTGCTCGCC CGCCGCGCG CGCTGCGGAC CGCCAGCATG 120
CTGCCGAGAG TGGGCTGCC CGCGTGGCG CTGCGCGCG CGCCGCTGCT GCGCTGCTG 180
CGCTGCTCG TCGTCTACT GGGCGCGAGT GCGCGCGCG CGCGGGCGCG CGCGGAGGTG 240
CTGTTCCGCT GCCCGCCCTG CACACCCGAG CGCCTGGCG CCTGCGGGCC CCGCGCGGTT 300
GCGCGCGCG CGCGGTGGC CGCAGTGGCC GGAGGCGCCC GCATGCCATG CGCGGAGCTC 360
GTCCGGGAGC CGGGCTGCG CTGCTGCTCG GTGTGCGCCC GGCTGGAGGG CGAGGCGTGC 420
GGCGTCTACA CCCCCTGCTG CGGCCAGGG CTGCGCTGCT ATCCCCACCC GGGCTCCGAG 480
CTGCCCTTGC AGGCGCTGTT CATGGGCGAG GGCACCTGTG AGAAGCGCG GAGCGCGGAG 540
TATGGCGCCA GCCCGGAGCA GGTTCAGAC AATGGCGATG ACCACTCAGA AGGAGGCGCT 600
GTGGAGAACC ACGTGGACAG CACCATGAAC ATGTTGGGCG GGGGAGGCAG TGCTGGCCGG 660
AAGCCCCCTA AGTCGGGTAT GAAGGAGCTG GCCGTGTTCC GGGAGAAGGT CACTGAGCAG 720
CACCGGCAGA TGGCAAGGG TGGCAAGCAT CACCTTGGCC TGAGGAGGCC CAAGAAGCTG 780
CGACCACCCC CTGCCAGGAC TCCCTGCCAA CAGGAAGTGG ACCAGGTCTT GGAGCGGATC 840

```

TCCACCATGC GCCTTCGGGA TGAGCGGGGC CCTCTGGAGC ACCTCTACTC CCTGCACATC 900
 CCCAAGCTGTG ACAAGCATGG CCTGTACAAC CTCAAACAGT GCAAGATGTC TCTGAACGGG 960
 CAGCGTGGGG AGTGCTGGTG TGTGAACCCC AACACCGGGA AGCTGATCCA GGGAGCCCCC 1020
 ACCATCCGGG GGGACCCCGA GTGTCACTCT TTCTACAATG AGCAGCAGGA GGCTTGCGGG 1080
 GTGCACACCC AGCGGATGCA GTAGACCGCA GCCAGCGGGT GCCTGGCGCC CCTGCCCCCC 1140
 GCCCCTCTCC AAACACCGGC AGAAAAACGGA GAGTGCCTTG GTGGTGGGTG CTGGAGGATT 1200
 TTCCAGTTCT GACACACGTA TTTATATTG GAAAGAGACC AGCACCGAGC TCGGCACCTC 1260
 CCCGGCCTCT CTCTCCAG CTGCAGATGC CACACCTGCT CCTTCTTGCT TTCCCCGGGG 1320
 GAGGAAGGGG GTTGTGGTCG GGGAGCTGGG GTACAGGTTT GGGGAGGGGG AAGAGAAATT 1380
 TTTATTTTGT AACCCCTGTG TCCTTTTGC ATAAGATTAA AGGAAGGAAA AGT

Seq ID NO: 369 Protein sequence
 Protein Accession #: NP_000588

1 11 21 31 41 51
 MLPRVGC PAL PLPPPLPLPL LPLLLLLLGA SGGGGGARAE VLFRCPPCTP ERLAACGPPP 60
 VAPPAVA AVV AGGARMPCAE LVREPGCGCC SVCARLEGEA CGVYTPRCQ GLRCYPHPGS 120
 ELPLQALVMG EGTCCKRRDA EYGASPEQVA DNGDDHSEGG LVENHVDSTM NMLGGGGSAG 180
 RKPLKSGMKE LAVFREKYTE QHRQMGKGGK HHLGLEEPKK LRPPPARTPC QQELDQVLER 240
 ISTMLPDER GPLLEHLYSLH IPNCDKHGLY NLKQCKMSLN GQRGECWCVN PNTGKLIQGA 300
 PTIRGDPECH LFYNEQQEAC GVHTQRMQ

Seq ID NO: 370 DNA sequence
 Nucleic Acid Accession #: NM_004264
 Coding sequence: 6-440

1 11 21 31 41 51
 GGAACATGGC GGATCGGCTC ACGCAGCTTC AGGACGCTGT GAATTCGCTT GCAGATCAGT 60
 TTTGTAATGC CATTGGAGTA TTGCAGCAAT GTGGTCCTCC TGCCTCTTTC AATAATATTC 120
 AGACAGCAAT TAACAAGAC CAGCCAGCTA ACCCTACAGA AGAGTATGCC CAGCTTTTGT 180
 CAGCACTGAT TGACAGAAC GCAAAAGACA TTGATGTTT GATAGATTCC TTACCCAGTG 240
 AAGAATCTAC AGCTGCTTTA CAGGCTGCTA GCTTGATATA GCTAGAAGAA GAAAACCATG 300
 AAGCTGCTAC ATGTGTGGAG GATGTTGTTT ATCGAGGAGA CATGCTTCTG GAGAAGATAC 360
 AAAGCGCACT TGCTGATATT GCACAGTCAC AGCTGAAGAC AAGAAGTGGT ACCCATAGCC 420
 AGTCTCTTCC AGACTCATAG CATCAGTGGG TACCATGTGG CTGAGAAAAG AACTGTTTGA 480
 GTGCCATTAA GAATTTCTGCA TCAGACTTAG ATACAAGCCT TACCAACAAAT TACAGAAACA 540
 TTAAACACTA TGACACATTA CCTTTTATAG TATTTTAAAT AGTCTTCTAT TTTCACTCTT 600
 GATAAGCTTA TAAATCATGA TTGAATCAGC TTTAAAGCAT CATACCATCA TTTTATAACT 660
 GAGTGAATTA ATTAAGGCAT GTAATACATT AATGAACATA ATATAAGGAA ACATATGTAA 720
 AATTCTGTTA TGACATAATT TATGCTCTCA TTTTGTGTGA TTGGCCAGTA CTTTACAAT 780
 C

Seq ID NO: 371 Protein sequence
 Protein Accession #: NP_004255

1 11 21 31 41 51
 MADRLTQLQD AVNSLADQFC NAIGVLQQCG PPASFNNIQT AINKDQPNP TEEYAQLFAA 60
 LIARTAKDID VLIDSLPSEE STAALQAASL YKLEENHEA ATCVEDVVYR GDMLEKIQS 120
 ALADIAQSQL KTRSGTHSQS LPDS

Seq ID NO: 372 DNA sequence
 Nucleic Acid Accession #: AJ271091
 Coding sequence: 1-1113

1 11 21 31 41 51
 ATGGAGAATC AGGTGTTGAC GCCGCATGTC TACTGGGCTC AGCGACACCG CGAGCTATAT 60
 CTGCGCGTGG AGCTGAGTGA CGTACAGAAC CCTGCCATCA GCATCACTGA AAACGTGCTG 120
 CATTTCAAAG CTCAGGAGCA TGGTGCCAAA GGAGACAATG TCTATGAATT TCACCTGGAG 180
 TTCTTAGACC TTGTGAAACC AGAGCCTGTT TACAAACTGA CCCAGAGGCA GGTAAACATT 240
 ACAGTACAGA AGAAAGTGAG TCAGTGGTGG GAGAGACTCA CAAAGCAGGA AAAGCGACCA 300
 CTGTTTTTGG CTCCTGACTT TGATCGTTGG CTGGATGAAT CTGATGCGGA AATGGAGCTC 360
 AGAGCTAAGG AAGAAGAGCG CCTAAATAAA CTCCGACTGG AAAGCGAAGG CTCTCCTGAA 420
 ACTCTTACAA ACTTAAGGAA AGGATACCTG TTTATGTATA ATCTTGTCGA ATTCTTGGGA 480
 TTCTCCTGGA TCTTTGTCAA CCTGACTGTG CGATTCTGTA TCTTGGGAAA AGAGTCCTTT 540
 TATGACACAT TCCATACTGT GGTGACATG ATGTATTTCT GCCAGATGCT GGCAGTTGTG 600
 GAAACTATCA ATGCAGCAAT TGGAGTCACT ACGTCACCGG TGCTGCCTTC TCTGATCCAG 660
 CTTCTTGGA GAAATTTTAT TTTGTTTATC ATCTTTGGCA CCATGGAAGA AATGCAGAAC 720
 AAAGCTGTGG TTTTCTTTGT GTTTTATTTG TGGAGTGCAA TTGAAATTT CAGGTACTCT 780
 TTCTACATGC TCAGCTGCAT TGACATGGAT TGAAGGTGC TCACATGGCT TCGTTACACT 840
 CTGTGGATTG CTTCTATATC ACTGGGATGT TTGGCGGAAG CTGTCTCAGT GATTCACTCC 900
 ATTCCAATAT TCAATGAGAC CGGACGATTC AGTTTCACAT TGCCATATCC AGTGAAATC 960
 AAAGTTAGAT TTTCTTTTCT TCTTCAGATT TATCTTATAA TGATATTTTT AGGTTTATAC 1020
 ATAAATTTTC GTCACTTTTA TAAACAGCGC AGACTGAAAA TGAGGGCAGG CGCAGTGGCT 1080
 CATGCCTGTG ATCCACGCGC TTTGGGAGGC TGA

Seq ID NO: 373 Protein sequence
 Protein Accession #: CAB69070

1 11 21 31 41 51
 MENQVLTPHV YWAQRHRELY LRVELSDVQN PAISITENVL HFKAQGHGAK GDNVYEFHLE 60
 FLDLVKPEPV YKLQRQVNI TVQKVSQWW ERLTKQEKRP LFLAPDFDRW LDESDAEMEL 120
 RAKEERLNK LRLESEGSPE TLTLNLRGYL FMYNLVQFLG FSWIFVNLTV RFCILKESF 180

YDTFHTVADM MYFCQMLAVV ETINAAIGVT TSPVLPSLIQ LLGRNFILFI IFGTMEEMQN 240
 KAVVFPFVYL WSAIEIFRYS FYMLTICIDMD WKVLTWLRYT LWIPLYPLGC LAEAVSVIQS 300
 IPIFNETGRF SFTLPYPVKI KVRFSFPLQI YLIMIFLGLY INFRHLYKQR RLKMRAGAVA 360
 HACDPSALGG

Seq ID NO: 374 DNA sequence
 Nucleic Acid Accession #: NM_016395
 Coding sequence: 1-1113

1 11 21 31 41 51
 | | | | |
 ATGGAGAATC AGGTGTTGAC GCCGCATGTC TACTGGGCTC AGCGACACCG CGAGCTATAT 60
 CTGCGCGTGG AGCTGAGTGA CGTACAGAAC CCTGCCATCA GCATCACTGA AAACGTGCTG 120
 CATTTCAAAG CTCAGAGACA TGGTGCCAAA GGAGACAATG TCTATGAATT TCACCTGGAG 180
 TTCTTAGACC TTGTGAAACC AGAGCCTGTT TACAACTGA CCCAGAGGCA GGTAACATT 240
 ACAGTACAGA AGAAAGTGAG TCAGTGGTGG GAGAGACTCA CAAAGCAGGA AAAGCGACCA 300
 CTGTTTTTGG CTCCTGACTT TGATCGTTGG CTGGATGAAT CTGATGCGGA AATGGAGCTC 360
 AGAGCTAAGG AAGAAGAGCG CCTAAATAAA CTCCGACTGG AAAGCGAAGG CTCTCCTGAA 420
 ACTCTTACAA ACTTAAGGAA AGGATACCTG TTTATGTATA ATCTTGTGCA ATTCTTGGGA 480
 TTCTCCTGGA TCTTTGTCAA CCTGACTGTG CGATTCTGTA TCTTGGGAAA AGAGTCCTTT 540
 TATGACACAT TCCATCTGTG GGCTGACATG ATGTATTTCT GCCAGATGCT GGCAGTTGTG 600
 GAAACTATCA ATGCAGCAAT TGGAGTCACT ACGTACCCGG TGCTGCCTTC TCTGATCCAG 660
 CTTCTTGGA GAAATTTTAT TTTGTTTATC ATCTTTGGCA CCATGGAAGA AATGCAGAAC 720
 AAAGCTGTGG TTTTCTTTGT GTTTTATTTG TGGAGTGCAA TTGAAATTTT CAGGTACTCT 780
 TTCTACATGC TGACGTGCAT TGACATGGAT TGGAAAGGTG TCACATGGCT TCGTTACACT 840
 CTGTGGAATC CCTTATATCC ACTGGGATGT TTGGCGGAAG CTGTCTCAGT GATTCACTCC 900
 ATTCCAATAT TCAATGAGAC CGGACGATTC AGTTTCACAT TGCCATATCC AGTGAAATC 960
 AAAGTTAGAT SFTTCTTTT TCTTCAGATT TATCTTATAA TGATATTTTT AGGTTTATAC 1020
 ATAAATTTTC GTCACCTTTA TAAACAGCGC AGACTGAAAA TGAGGGCAGG CGCAGTGGCT 1080
 CATGCCTGTG ATCCACGCGC TTTGGGAGGC TGA

Seq ID NO: 375 Protein sequence
 Protein Accession #: NP_057479

1 11 21 31 41 51
 | | | | |
 MENQVLTPHV YWAQRHRELY LRVELSDVQN PAISITENVL HFKAQGHGAK GDNVVEFHLE 60
 FLDLVKPEPV YKLTRQVNI TVQKVKVQWW ERLTKQEKRP LFLAPDFDRW LDESDAEMEL 120
 RAKEERLNK LRLESEGSPE TLNLRKGYL FMYNLVQFLG FSWIFVNLTV RFCILGKESF 180
 YDTFHTVADM MYFCQMLAVV ETINAAIGVT TSPVLPSLIQ LLGRNFILFI IFGTMEEMQN 240
 KAVVFPFVYL WSAIEIFRYS FYMLTICIDMD WKVLTWLRYT LWIPLYPLGC LVEAVSVIQS 300
 IPIFNETGRF SFTLPYPVKI KVRFSFPLQI YLIMIFLGLY INFRHLYKQR RRRYGKKRKR 360
 STKKKDLDF LPV

Seq ID NO: 376 DNA sequence
 Nucleic Acid Accession #: NM_005987
 Coding sequence: 1-270

1 11 21 31 41 51
 | | | | |
 ATGAATCTC AGCAGCAGAA GCAGCCTTGC ACCCCACCCC CTCAGCCTCA GCAGCAGCAG 60
 GTGAAACAAC CTTGCCAGCC TCCACCCAG GAACCATGCA TCCCCAAAAC CAAGGAGCCC 120
 TGCCAAACCA AGGTGCCTGA GCCTGCCAC CCCAAAGTGC CTGAGCCCTG CCAGCCCAAG 180
 ATTCAGAGC CCGCCAGGCC CAAGGTGCCT GAGCCCTGCC CTTCACCGGT CACTCCAGCA 240
 CCAGCCAGC AGAAGACCAA GCAGAAGTAA

Seq ID NO: 377 Protein sequence
 Protein Accession #: NP_005978

1 11 21 31 41 51
 | | | | |
 MNSQQKQPC TPPPQPPQQQ VKQPCPPPPQ EPCIPKTKEP CQPKVPEPCH PKVPEPCQPK 60
 IPEPCQKVP EPCPSTVTPA PAQKTKQK

Seq ID NO: 378 DNA sequence
 Nucleic Acid Accession #: NM_002105
 Coding sequence: 74-505

1 11 21 31 41 51
 | | | | |
 ACAGCAGTTA CACTGCGGCG GCGCTCTGTT CTAGTGTGTT AGCCGTCGTG CTTACCCGGT 60
 CTACCTCGCT AGCATGTCGG GCCGCGGCAA GACTGGCGGC AAGGCCCGCG CCAAGGCCAA 120
 GTCGCGCTCG TCGCGCGCGC GCCTCCAGTT CCCAGTGGGC CGTGTACACC GGCTGCTGCG 180
 GAAGGGCCAC TACGCGGAGC GCGTTGGCGC CGGCGCGCCA GTGTACTTGG CGGCAGTGCT 240
 GGAGTACCTC ACCGCTGAGA TCCTGGAGCT GCGGGGCAAT GCGGCCCGCG ACAACAAGAA 300
 GACGCGAATC ATCCCCGCC ACCTGCAGCT GGCCATCCGC AAGCAGGAGG AGCTCAACAA 360
 GCTGTGCGGC GCGGTGACGA TCGCCAGGG AGGCGTCTTG CCCAACATCC AGGCGGTGCT 420
 GCTGCCCAAG AAGACCAGCG CCACCGTGGG GCCGAAGGCG CCTTCGGGCG GCAAGAAGGC 480
 CACCCAGGCC TCCAGGAGT ACTAAGAGGG CCCGCGCCGC GCGCGGCCGC CCCAGCTCCC 540
 CATGCCACCA CAAAGGCCCT TTTAAGGGCC ACCACCGCCC TCATGGAAAG AGCTGAGCCG 600
 CTTCAAGACT CGGGGCAAGC GGGCGCGGCG TCCCTTCCCC TCCCTCCCC TCGCCGCGCT 660
 TCGCGCGCGC GCCTCGAGTC CCCGCGCGCC CCCGCTCCCG TCCCGCACCG CCGTCCGCGT 720
 CGGCTCGGG CCGCTCGGTC CCGCGTCCG CCTCCGGTA GGGTTCGGGC CTTCCGGATG 780
 CGGCTTGGGC GCTCTTCGGG GACCTCCGTG GCGCGGAAGA CCCGAGCTG CCGGGGGGAG 840

GCCGGCGGCG CCGCACCTGC CCGCCTCGGC GTTCGTGACT CAGCCGCCCC ATCCCGAGTC 900
 GCTAAGGGGC TGGGGGAGG CCGCAGCACC TTCTGGAAGA CTGGCCCTTC CGCTCTGACG 960
 CAGGGCCGAG GTGGGCGATC CAGGCCGAGA GCCGGCGGCC CTGAAGGTGA GTGAGGCCCT 1020
 CGGCAGCTGC AGCCGGGGTG TCTGGTACCC CCCCAGCGTG GTGCTTAGCC CAGGACTTTC 1080
 5 AGACGGCCGC TGGCCGGGAG GCTTTGGTGG GAGAGACGCG ATCCCGGATT TCGGTCTGGC 1140
 GCCCTTCTG CGGCCGGGAC CAGGCCCTTT CACATCAGCT CTCCCTCCAT CTTTATTTCAT 1200
 AGGTCTGCGC TGGGGCCGGG ACGAAGCACT TGGTAACAGG CACATCTTCC TCCCGAGTGA 1260
 CTGCCTCCTA GGAGGACATT TAGGGGAGGG CAGAGGCCCTG CAGTTTGGCT TCACGGCTGG 1320
 10 CTATGTGGAC AGCAAGAGTC GTTTTGCGGA ACGCGACTGG CAGCCAGGCC TGTCCGGGCC 1380
 CCGACGCGC CCAATTTCCT TTCCAGCAAA CTCAACTCGG CAATCCAAGC ACCTAGATAC 1440
 CAGCACAGT CGGTTAATCC CTGTCTGGAC TGAGCCTCCG TTGGCTTCTG AACTGGAATT 1500
 CTGCAGCTAA CCCTTCCACG ACTAGAACCT TAGGCATTGG GGAGTTTATG ATGGACTAAT 1560
 TTTATTAAG GATTGTTTTT TTTT

Seq ID NO: 379 Protein sequence
 Protein Accession #: NP_002096

1 11 21 31 41 51
 | | | | | |
 20 MSGRGKTGGK ARAKAKSRSS RAGLQFPVGR VHRLLRKGHY AERVGAGAPV YLAADVLEYLT 60
 AEILELAGNA ARDNKKTRII PRHLQLAIRN DEBLNKLGG VTIAQGGVLP NIQAVLLPKK 120
 TSATVGPAP SGGKATQAS QEY

Seq ID NO: 380 DNA sequence
 Nucleic Acid Accession #: AL136942
 Coding sequence: 184-864

1 11 21 31 41 51
 | | | | | |
 30 ACGGTCGCG CAGAAGCTCG GAGCTCTCGG GGTATCGAGG AGGCAGGCC GCGGGCGCAC 60
 GGGCGAGCGG GCGGGGAGCG AGGAGCGCGG AGCAGCGCGC CGGCGGGCTC 120
 CAGGCGAGGC GGTGAGCGCT CCGTAAACT TGCGCGCGCG CTGCGCCAC TCGCGCCGGA 180
 GCGATGAAGA TGGTCGCGCC CTGGACGCGG TTCTACTCCA ACAGCTGCTG CTTGTGCTGC 240
 35 CATGTCCGCA CCGGACCCAT CCTGCTCGGC GTCTGATATC TGATCATCAA TGCTGTGGTA 300
 CTGTTGATTT TATTGAGTGC CTGGCTGAT CCGGATCAGT ATAACCTTTC AAGTCTGAA 360
 CTGGGAGGTG ACTTTGAGTT CATGGATGAT GCCAACATGT GCATTGCCAT TCGGATTTCCT 420
 CTTCTCATGA TCCTGATATG TGCTATGGCT ACTTACGGAG CGTACAAGCA ACGCGCAGCC 480
 40 TGGATCATCC CATCTCTCTG TTACCATGATC TTTGACTTTG CCTGGAACAT GTTGGTTGCA 540
 ATCACTGTGC TTATTTATCC AAACCTCATT CAGGAATACA TACGCAACT GCCTCCTAAT 600
 TTTCCCTACA GAGATGATGT CATGTCAAGT AATCCTACCT GTTGGTCTCT TATTATTCTT 660
 CTGTTTATTA GCATTATCTT GACTTTTAAG GGTACTTGA TTAGCTGTGT TTGGAATGTC 720
 TACCGATACA TCAATGATG GAACCTCTCT GATGTCCTGG TTTATGTTAC CAGCAATGAC 780
 ACTACGGTGC TGCTACCCCT GTATGATGAT GCCACTGTGA ATGGTGCTGC CAAGGAGCCA 840
 45 CCGCCACCTT ACGTGTCTGC CTAAGCCTTC AAGTGGGCGG AGCTGAGGCG AGCAGCTTGA 900
 CTTTGACAGC ATCTGAGCAA TAGTCTCTGT ATTTCACTTT TGCCATGAGC CTCTCTGAGC 960
 TGTGTTGTTG CTGAAATGCT AGTTTTTAAA ATTTAGATGT TAGATTGAAA ACTGTAGTTT 1020
 TCAACATATG CTTTGCTAGA ACACCTGTGAT AGATTAACTG TAGAATCTCT CCTGTACGAT 1080
 TGGGGATATA ACGGGCTTCA CTAACCTTCC CTAGGCATTG AAACCTTCCC CAAATCTGAT 1140
 50 GGACATAGAA GATCTGCTTT GTACCTGCTG GGCCCCAAG TTGGGCAATT TTCTCTCTGT 1200
 TCCCTCTCTT TTGAAATGT AAAATAAAAC CAAAATAGA CAACCTTTTC TTCAGCCATT 1260
 CCAGCATAGA GAACAAACC TTATGGAAAC AGGAATGTCA ATTGTGTAAT CATTGTTCTA 1320
 ATTAGGTAAA TAGAAGTCTT TATGATGTG TTACAAGAAT TTCCCCACA ACATCCTTTA 1380
 TGAAGTAAAT TCAATGACAG TTTGTGTTG GTGGTAAAGG ATTTCTCTCA TGGCCTGAAT 1440
 55 TAAGACCAT AGAAGACACC AGGCCGTGGG AGCAGTGACC ATCTACTGAC TGTTCTTGTTG 1500
 GATCTTGTTG CTAGGGACAT GGGGTGACAT GCCTCGTATG TGTAGAGGG TGGAAATGGAT 1560
 GTGTTTGGCG CTGCATGGGA TCTGGTCCCC CTCTCTCTCT GGATTCACAT CCCCACCCAG 1620
 GGCCCGCTTT TACTAAGTGT TCTGCCCTAG ATTGGTTCAA GGAGGTCATC CAACTGACTT 1680
 60 TATCAAGTGG AATTGGGATA TAATTGATAT ACTTCTGCTT AACCAACTGG AAAAGGGTTT 1740
 TCTTTTCCCT GCAAGCTACA TCCTACTGCT TTGAACCTCC AAGTATGTCT AGTCACCTTT 1800
 TAAATGTAA ACATTTCAG AAAAATGAGG ATTGCCTTCC TTGATGCGC TTTTACCTT 1860
 GACTACCTGA ATGCAAGGG ATTCTTATAT ATTCAATATG TACAAGTCA GCAACTCTCC 1920
 TGTGTTTCA TTATTGAATG TGCTGTAAAT TAAGTCGTTT GCAATTAAA CAAGGTTTGC 1980
 CCACATCCAA AAAAAAAAAA AAAAA

Seq ID NO: 381 Protein sequence
 Protein Accession #: CAB66876

1 11 21 31 41 51
 | | | | | |
 70 MKMVPWTRF YSNCCCLCCH VRTGILLGV WYLIINAVVL LILLSALADP DQYNFSSSEL 60
 GGDFFEMDDA NMCIAIAISL LMILICAMAT YGAYKQRAAW IIPFFCYQIF DFALNMLVAI 120
 TVLIYPNSIQ EYIRQLPPNF PYRDDVMSVN PTCLVLIILL PISIIILTFKG YLISCVWNCY 180
 RYINGRNSSD VLVVTSNDT TVLLPPYDDA TVNGAAKEPP PPYVSA

Seq ID NO: 382 DNA sequence
 Nucleic Acid Accession #: NM_002510
 Coding sequence: 92-1774

1 11 21 31 41 51
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 80 CAGATGCCAG AAGAACACTG TTGCTCTTGG TGGACGGGCC CAGAGGAATT CAGAGTTAAA 60
 CCTTGAGTGC CTGCGTCCGT GAGAATTCAG CATGGAATGT CTCTACTATT TCCTGGGATT 120
 TCTGCTCCTG GCTGCAAGAT TGCCACTTGA TGCCGCCAAA CGATTTTCATG ATGTGCTGGG 180
 85 CAATGAAAGA CTTCTGCTT ACATGAGGGA GCACAATCAA TTAATGGCT GGTCTTCTGA 240
 TGAATATGAC TGGAAATGAA AACTCTACCC AGTGTGGAAG CGGGAGACA TGAGTGGAA 300
 AAACCTCTGG AAGGGAGGCC GTGTGCAGGC GGTCTTGACC AGTGACTCAC CAGCCTCTGT 360

	GGGCTCAAAT	ATAACATTTC	CGGTGAACCT	GATATTCCCT	AGATGCCAAA	AGGAAGATGC	420
	CAATGGCAAC	ATAGTCTATG	AGAAGAACTG	CAGAAATGAG	GCTGGTTTAT	CTGCTGATCC	480
	ATATGTTTAC	AACGTGGACG	CATGGTCAGA	GGACAGTGAC	GGGGAAAATG	GCACCGGCCA	540
5	AAGCCATCAT	AACGTCTTCC	CTGATGGGAA	ACCTTTTCCT	CACCACCCCG	GATGGAGAAG	600
	ATGGAATTC	ATCTACGTCT	TCCACACACT	TGGTCAGTAT	TTCAGAAAT	TGGGACGATG	660
	TTCACTGAGA	GTTTCTGTGA	ACACAGCCAA	TGTGACACTT	GGGCCCTCAAC	TCATGGAAGT	720
	GACTGTCTAC	AGAAGACATG	GACGGGCATA	TGTTCCCATC	GCACAAGTGA	AAGATGTGTA	780
	CGTGGTAACA	GATCAGATTC	CTGTGTTTGT	GACTATGTTT	CAGAAGAAGC	ATCGAAATTC	840
	ATCCGACGAA	ACCTTCTCTA	AAGATCTCCC	CATTATGTTT	GATGTCCTGA	TTCATGATCC	900
10	TAGCCACTTC	CTCAATTATT	CTACCATTAA	CTACAAGTGG	AGCTTCGGGG	ATAATACTGG	960
	CCTGTTTGT	TCCACCAATC	ATACTGTGAA	TCACACGTAT	GTGCTCAATG	GAACCTTCAG	1020
	CCTTAACCTC	ACTGTGAAAG	CTGCAGCACC	AGGACCTTGT	CCGCCACCGC	CACCACCACC	1080
	CAGACCTTCA	AAACCCACCC	CTTCTTTAGG	ACCTGCTGGT	GACAACCCCC	TGGAGCTGAG	1140
15	TAGGATTCCT	CCTGAAAAC	GCCAGATTAA	CAGATATGGC	CACCTTCAAG	CCACCATCAC	1200
	AAATGTAGAG	GGAAATCTTAG	AGGTTAACAT	CATCCAGATG	ACAGACGTCC	TGATGCCGGT	1260
	GCCATGGCCT	GAAGCTCCC	TAATAGACTT	TGTCGTGACC	TGCCAAGGGA	GCAITCCCAC	1320
	GGAGGTCTGT	ACCATCATTT	CTGACCCAC	CTGCGAGATC	ACCCAGAAAC	CAGTCTGCAG	1380
	CCCTGTGGAT	GTGGATGAGA	TGTGTCTGCT	GACTGTGAGA	CGAACCTTCA	ATGGGTCTGG	1440
20	GACGTACTGT	GTGAACCTCA	CCCTGGGGGA	TGACACAAGC	CTGGCTCTCA	CGAGCACCTT	1500
	GATTTCGTGT	CCTGACAGAG	ACCCAGCCTC	GCCTTTAAGG	ATGGCAAAAC	GTGCCCTGAT	1560
	CTCCGTTGGC	TGCTTGCCCA	TATTTGTGAC	TGTGATCTCC	CTCTTGGTGT	ACAAAAACA	1620
	CAAGGAATAC	AAACCAATAG	AAAATAGTCC	TGGGAATGTG	GTGAGAAGCA	AAGGCCTGAG	1680
	TGCTTTTCTC	AACCGTGCAA	AAGCCGTGTT	CTTCCCGGGA	AACCCAGAAA	AGGATCCGCT	1740
25	ACTCAAAAC	CAAGAATTTA	AAGGAGTTTC	TTAAATTTTC	ACCTTGTTC	TGAAGCTCAC	1800
	TTTTCACTGC	CATTGATGTG	AGATGTGCTG	GAGTGGCTAT	TAACCTTTT	TTCCTAAAGA	1860
	TTATTGTTAA	ATAGATATTG	TGGTTTGGGG	AAGTTGAATT	TTTTATAGT	TAAATGTCAT	1920
	TTTAGAGATG	GGGAGAGGGA	TTATACTGCA	GGCAGCTTCA	GCCATGTTGT	GAAACTGATA	1980
	AAAGCAACTT	AGCAAGGCTT	CTTTTCATTA	TTTTTTATGT	TTCACCTATA	AAGTCTTAGG	2040
30	TAACTAGTAG	GATAGTAAGC	CTGTGCTCCG	AGAGTAAGGA	GAGAAGCTAC	TATTGATTAG	2100
	AGCCTAACCC	AGGTTAACTG	CAAGAAGAGG	CGGGATACCT	TCAGCTTCC	ATGTAACCTG	2160
	ATGCATAAAG	CCAATGTAGT	CCAGTTTCTA	AGATCATGTT	CCAAGCTAAC	TGAATCCCAC	2220
	TTCAATACAC	ACTCATGGAAC	TCCTGATGGA	ACAATAACAG	GCCCAAGCCT	GTGGTATGAT	2280
	GTGCACACTT	GCTAGACTCA	GAAAAAATAC	TACTCTCATA	AATGGGTGGG	AGTATTTTGG	2340
35	TGACAACCTA	CTTTGCTTGG	CTGAGTGAAG	GAATGATATT	CATATATTCA	TTTATTCAT	2400
	GGACATTTAG	TTAGTGCCTT	TTATATACCA	GGCATGATGC	TGAGTGACAC	CTCTGTGTAT	2460
	ATTTCCAAAT	TTTTGTATAG	TCGCTGCACA	TATTTGAAAT	CATATATTAA	GACTTTCCAA	2520
	AGATGAGGTC	CCTGGTTTTT	CATGGCAACT	TGATCAGTAA	GGATTTCAAC	TCTGTTTGTA	2580
	ACTAAACCA	TCTACTATAT	GTTAGACATG	ACATTCTTTT	TCTCTCCTTC	CTGAAAAATA	2640
40	AAGTGTGGGA	AGAGACAAAA	AAAAAATA				

Seq ID NO: 383 Protein sequence
Protein Accession #: NP_002501

45	1	11	21	31	41	51	
	MECLYYFLGF	LLLAARLPLD	AAKRFHDLVG	NERPSAYMRE	HNQLNGWSSD	ENDWNEKLYP	60
	VWKRGRMRWK	NSWKGGRVQA	VLTSDSPALV	GSNITFAVNL	IFPRCQKEDA	NGNIVYEKNC	120
	RNEAGLSADP	VYVNTAWSE	DSGNGTGTG	SHNVFPDGK	PPPHHPGWRR	WNFIYVFHTL	180
50	QYFQKLGR	SVRVSVNTAN	VTGPGQLMVE	TVYRRHGRAY	VPDIAQKDVY	VVDQIPVVFV	240
	TMFQKNDENS	SDFTFLKDLF	IMFDVLHDP	SHFLNYSTIN	YKWSFGDNTG	LFVSTNHTVN	300
	HTYVLNGTFS	LNLTVKAAAP	GPCPPPPPPP	RPSKPTPSLG	PAGDNPLELS	RIPDENCQIN	360
	RYGHFQATIT	IVEGILEVNI	IQMTDVLMPV	PWPESSLIDF	VVTCQGS IPT	EVCTIISDPT	420
	CEITQNTVCS	PVDVDEMCAL	TVRRTFNGSG	TYCVNLTLGD	DTSLALTSTL	ISVPRDRDPAS	480
55	PLRMANSALI	SVGCLAIFVT	VISLLVYKXH	KEYNPIENSP	GNVVRSGKLS	VFLNRAKAVF	540
	FPGNQEKDPL	LKNQEFKGV					

Seq ID NO: 384 DNA sequence
Nucleic Acid Accession #: NM_001134
Coding sequence: 48-1877

60	1	11	21	31	41	51	
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65	AATATGGAAT	AGCTTCCATA	TTGGATTCTT	ACCAATGTAC	TGCAGAGATA	AGTTTAGCTG	180
	ACCTGGCTAC	CATATTTTTC	GCCAGTTTTC	TTCAGAAAGC	CACCTACAAG	GAAGTAAGCA	240
	AAATGGTGAA	AGATGCATTG	ACTGCAATTG	AGAAACCCAC	TGGAGATGAA	CAGTCTTCAG	300
	GGTGTTTAA	AAACCGCTA	CCTGCTTTTC	TGGAAGAACT	TTGCCATGAG	AAAGAAATTT	360
70	TGGAGAAGTA	CGGACATTCA	GACTGCTGCA	GCCAAAGTGA	AGAGGGAAGA	CATAACTGTT	420
	TTCTTGACCA	CAAAAAGCCC	ACTCCAGCAT	CGATCCCACT	TTTCCAAGTT	CCAGAACCTG	480
	TCACAAGCTG	TGAAGCATAT	GAAGAAGACA	GGGAGACATT	CATGAACAAA	TCATTTATG	540
	AGATAGCAAG	AAGGCATCCC	TTCTGTATG	CACCTACAAT	TCITCTTTGG	GCTGCTCGCT	600
	ATGACAAAAT	AATTCATCT	TGCTGCAAG	CTGAAAATGC	AGTTGAATGC	TTCCAAACAA	660
75	AGGCAGCAAC	AGTTTACAAA	GAATTAAGAG	AAAGCAGCTT	GTTAAATCAA	CATGCATGTG	720
	CAGTAATGAA	AAATTTTGGG	ACCCGAACTT	TCCAAGCCAT	AACCTGTACT	AAACTGAGTC	780
	AGAAGTTTAC	CAAGTTTAAT	TTTACTGAAA	TCCAGAAACT	AGTCTGGAT	GTGGCCCATG	840
	TACATGAGCA	CTGTGTCAGA	GGAGATGTGC	TGGATTGTCT	GCAGGATGGG	GAAAAATCA	900
	TGTCCTACAT	ATGTTCTCAA	CAAGACACTC	TGTCAAACAA	AATAACAGAA	TGCTGCAAC	960
80	TGACCAAGCT	GGAACTGGGT	CAATGTATAA	TTTCATGCAGA	AAATGATGAA	AAACCTGAAG	1020
	GTCTATCTCC	AAATCTAAAC	AGGTTTITAG	GAGATAGAGA	TTTAAACCAA	TTTCTTCAG	1080
	GGGAAAAAAA	TATCTTCTTG	GCAAGTTTTC	TTTCATGAATA	TTCAAGAAGA	CATCCTCAGC	1140
	TTGCTGTCTC	AGTAATTTCTA	AGAGTTGCTA	AAGGATACCA	GGAGTTATTG	GAGAAGTGT	1200
85	TCCAGACTGA	AAACCTCTT	GAAATGCCAAG	ATAAAGGAGA	AGAAGAATTA	CAGAAATACA	1260
	TCCAGGAGAG	CCAAGCATTC	GCAAGCGGAA	GCTGCGGCCT	CTTCCAGAAA	CTAGGAGAAT	1320
	ATTACTTACA	AAATGCGTTT	CTGTTGCTT	ACACAAAGAA	AGCCCCCAG	CTGACCTCGT	1380
	CGGAGCTGAT	GGCCATCACC	AGAAAAATGG	CAGCCACAGC	AGCCACTTGT	TGCCAACTCA	1440
	GTGAGGACAA	ACTATTGGCC	TGTGGCGAGG	GAGCGGCTGA	CATTATTATC	GGACACTTAT	1500

GTATCAGACA TGAAATGACT CCAGTAAACC CTGGTGTGG CCAGTGTGCG ACTTCTTCAT 1560
 ATGCCAACAG GAGGCCATGC TTCAGCAGCT TGGTGGTGGG TGAACATAT GTCCCTCCTG 1620
 CATTCTCTGA TGACAAGTTC ATTTTCCATA AGGATCTGTG CCAAGCTCAG GGTGTAGCGC 1680
 TGCAAAACGAT GAAGCAAGAG TTTCTCATTA ACCTGTGAA GCAAAAGCCA CAAATAACAG 1740
 AGGAACAAC TGAAGCTGTC ATTGCAGATT TCTCAGGCCT GTTGGAGAAA TGCTGCCAAG 1800
 GCCAGGAACA GGAAGTCTGC TTTGCTGAAG AGGACAAAA ACTGATTTC AAAACTCGTG 1860
 CTGCTTTGGG TCTCTTAAAT ACTTCAGGGG AAGAGAAGAC AAAACGAGTC TTTCATTCGG 1920
 TGTGAACTTT TCTCTTAAAT TTTAACTGAT TTAACACTTT TTGTGAATTA ATGAAATGAT 1980
 AAAGACTTTT ATGTGAGATT TCCTTATCAC AGAAATAAAA TATCTCCAAA TG

Seq ID NO: 385 Protein sequence
 Protein Accession #: NP_001125

1 11 21 31 41 51
 MKWVESIFLI FLNFTESRT LHRNEYGIAS ILDSYQCTAE ISLADLATIF PAQFVQEATY 60
 KEVSKMVKDA LTAIEKPTGD EQSSGCLLENQ LPAFLEELCH EKEILEKYGH SDCCSQSEEG 120
 RHNCFLAHKK PTPASIPLEFQ VPEPVTSCBA YEEDRETFMN KFIYBIARRH PFLYAPTILL 180
 WAARYDKIIP SCCKAENAVE CFQTKAATVT KELRESSLLN QHACAVMKNP GTRTFQAITV 240
 TKLSQKPTKV NFTEIQKLVL DVAHVHEHCC RGDVLDCLQD GEKIMSYICS QQDTLSNKIT 300
 ECKKLITLER QQCIIHAEND EKPEGLSPNL NRPLGDRDFN QFSSGEGNIF LASFVHEYSR 360
 RHPQLAVSVI LRVAQGYQEL LEKCFQTEPN LECQDKGEE LQKYIQESQA LAKRSCGLFQ 420
 KLGEYYLQNA FLVAYTKKAP QLTSSSELMAI TRKMAATAAT CCQLSEDKLL ACGEGAADII 480
 IGHLCIRHEM FTVNPGVGQC CTSSYANRRP CFSSLVVDET YVPPAFSDDK FIFHKDLCOA 540
 QGVALQTMKQ EFLINLVKQK PQITEEQLEA VIADFSGLLE KCCQGGQEV CPABEGQKLI 600
 SKTRAAALGV

Seq ID NO: 386 DNA sequence
 Nucleic Acid Accession #: NM_002205.1
 Coding sequence: 1..3149

1 11 21 31 41 51
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 GGCTTCAACT TAGACGCGGA GGCCCGACCA GTACTCTCGG GGCCCGCGG CTCTCTCTTC 180
 GGATTCTCAG TGGAGTTTAA CCGGCCGGGA ACAGACGGGG TCAGTGTGCT GGTGGGAGCA 240
 CCAAGGCTA ATACCAGCCA GCCAGGAGTG CTGAGGGGTG GTGCTGTCTA CTTCTGTCTC 300
 TGGGGTGCCA GCCCACACA GTGCACCCCT ATTGAATTG ACAGCAAAGG CTCTCGGCTC 360
 CTGGAGTCTC CACTGTCCAG CTCAGAGGGA GAGGAGCCTG TGGAGTACAA GTCTTGCAG 420
 TGGTTCGGGG CAACAGTTTG AGCCCATGGC TCCTCCATCT TGGCATGCGC TCCACTGTAC 480
 AGCTGGCGCA CAGAGAAGGA GCCACTGAGC GACCCCGTGG GCACCTGCTA CTCTCCACA 540
 GATAACTTCA CCCGAATTCT GGAGTATGCA CCTGCGCGCT CAGATTTTCA CTGGGCAGCA 600
 GGACAGGGTT ACTGCGCAAG AGGCTTCAGT GCCAGATTCA CCAAGACTGG CCGTGTGGTT 660
 TTAGTGGGAC CAGGAAGCTA TTTCTGGCAA GGCCAGATCC TGTCTGCCAC TCAGGAGCAG 720
 ATTGCAGAAT CTTATTACCC CGAGTACCTG ATCAACCTGG TTCAGGGGCA GCTGCAGACT 780
 CGCCAGGCCA GTTCCAGCCA TGATGACAGC TACCTAGGAT ACTCTGTGGC TGTGGGTGAA 840
 TTCAGTGGTG ATGACACAGA AGACTTTGTT GCTGGTGTGC CCAAGGGGAA CCTCACTTAC 900
 GGCTATGTCA CCATCCTTAA TGGCTCAGAC ATTGATCCCC TCTACAATT CTCAGGGGAA 960
 CAGATGGCTC CTACTTTTGG CTATGTCAGT GCCGCCACAG ACGTCAATGG GGACGGGCTG 1020
 GATGACTTGC TGGTGGGGGC ACCCTGTCTC ATGGATCGGA CCCTGACGG GCGGCTCAG 1080
 GAGGTGGGCA GGGTCTACGT CTACCTGCAG CACCCAGCCG GCATAGAGCC CACGCCACC 1140
 CTTACCTCA CTGGCCCTCA TGAGTTTGGC CGATTGGGCA GCTCCTGTAC CCCCCTGGGG 1200
 GACCTGGACC AGGATGGCTA CAATGATGTG GCCATCGGGG CTCCCTTTGG TGGGGAGACC 1260
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 CGAGGAGGCC GAGACCTGGA TGGCAATGGA TATCCTGATC TGATTGTGGG GTCCCTTTGGT 1440
 GTGGACAAGG CTGTGGTATA CAGGGGCGCG CCCATCGTGT CCGCTAGTGC CTCCCTCACC 1500
 ATCTTCCCGC CCATGTTCAA CCAAGAGGAG CGGAGCTGCA GCTTAGAGGG GAACCTGTG 1560
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 GGTTCACAG TGGAACTTCA GCTGGACTGG CAGAAGCAGA AGGGAGGGGT ACGGCGGGCA 1680
 CTGTTCCCTG GTTCCAGCCA GGCACCCCTG ACCCAGACCC TGCTCATCCA GAATGGGGCT 1740
 CGAGAGGATT GCAGAGAGAT GAAGATCTAC CTCAGGAACG AGTCAGAATT TCGAGACAAA 1800
 CTCTCGCGCA TTCACATCGC TCTCAACTTC TCCTTGGACC CCCAAGCCCC AGTGGACAGC 1860
 CACGGCCTCA GGCCAGCCCT ACATTATCAG AGCAAGAGCC GGATAGAGGA CAAGGCTCAG 1920
 ATCTTGCTGG ACTGTGGAGA AGACAACATC TGTGTGCTG ACCTGCAGCT GGAAGTGTIT 1980
 GGGGAGCAGA ACCATGTGTA CCTGGGTGAC AAGAATGCCC TGAACCTCAC TTTCCATGCC 2040
 CAGAAATGTG GTGAGGGTGG CGCCTATGAG GCTGAGCTTC GGGTCACCGC CCCTCCAGAG 2100
 GCTGAGTACT CAGGACTCGT CAGACACCCA GGGAACTTCT CCAGCCTGAG CTGTGACTAC 2160
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 GCCAGTCTGT GGGGTGGCCT TCGGTTTACA GTCCCTCATC TCGGGGACAC TAAGAAAACC 2280
 ATCCAGTTTG ACTTCCAGAT CCTCAGCAAG AATCTCAACA ACTCGCAAAG CGACGTGGIT 2340
 TCCTTTCCGC TCTCCGTGGA GGCTCAGGCC CAGGTCAACC TGAACGGTGT CTCCAAGCCT 2400
 GAGGCAGTGC TATCCCTAG AAGCGACTGG CATCCCGAG ACCAGCTCA GAAGGAGGAG 2460
 GACCTGGGAC CTGCTGTCCA CCAATGCTAT GAGCTCATCA ACCAAGGCCC CAGCTCCATT 2520
 AGCCAGGGTG TGCTGGAAC TCACTGTCCC CAGGCTCTGG AAGGTGAGCA GCTCCTATAT 2580
 GTGACAGAG TACCGTGGC CAACCTGACC ACCAATCACC CCATTAAACC AAAGGGCCTG 2640
 GAGTTGGATC CCGAGGGTTC CCTGCACCAC CAGCAAAAC GGGAACTCC AAGCCGAGC 2700
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 TGTGAGCTCG GGGCTGGCCA CCAACAAGAG AGCCAAAGTC TGCAAGTGCA TTTCGAGTC 2820
 TGGGCCAAGA CTTTCTTGA GCGGGAGCAC CAGCCATTTA GCCTGCAAGT TGAGGCTGTG 2880
 TACAAAGCCC TGAAGATGCC CTACCGAATC CTGCTCGGC AGCTGCCCCA AAAAGAGCGT 2940
 CAGGTGGCCA CAGCTGTGCA ATGACCAAG GCAAGAGGCA GCTATGGCGT CCACTGTGG 3000
 ATCATCATCC TAGCCATCCT GTTTGGCCTC CTGCTCTAG GTCTACTCAT CTACATCCTC 3060
 TACAAGCTTG GATTCTTCAA ACGCTCCCTC CCATATGGCA CCGCCATGGA AAAAGCTCAG 3120
 CTCAGCCTC CAGCCACCTC TGATGCTGTA

Seq ID NO: 387 Protein sequence
Protein Accession #: NP_002196.1

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5      1      11      21      31      41      51
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GFSVEFYRPG TDGVSVLVGA PKANTSQPGV LQGGAVVLCF WGASPTQCTP IEFDSKGSRL 120
LESSLSSEEG EEPVEYKSLQ WFGATVRAHG SSILACAPLY SWRTEKEPLS DPVGTCTYST 180
10    DNFTRILEYA PCRSDFSWAA GQGYCQGGFS AEFTKTGRVV LGPGSYFVQ GQILSATQEQ 240
      IAESYYPEYL INLVQQLQQT RQASSIYDDS YLGYSVAVGE PSGDDTEDFV AGVPKGNLTY 300
      GYVTILNGSD IRSLYNFSGE QMASYFGYAV AATDVNGDGL DDLLVGAPLL MDRTPDGRPQ 360
      EVGRVYVYLQ HPAGIEPTPT LTLTGHDEFG RFGSSLTPLG DLDQDGYNDV AIGAPFGGET 420
      QQGVVVFVPG GPGLGSKSPS QVLQPLWAAS HTPDFFGSAL RGRDLGNG YPDLIVGSFG 480
15    VDKAVVYRGR PIVSASASLT IFPAMFNPEE RSCSLEGNPV ACINLSFCLN ASGKHVADSI 540
      GFTVELQLDW QKQKGGVRRR LFLASRQATL TQTLIIQNGA REDCREMKIY LRNESEFRDK 600
      LSPIHIALNF SLDPQAPVDS HGLRPALHYQ SKSRIEDKAQ ILLDCGEDNI CVPDLQLEVP 660
      GEQNHVYLG D KALNLTTHA QNVGEGGAYE AELRVTAPE AEYSGLVHRP GNPSLSLSDY 720
      PAVNQSRLLV CDLGNPMKAG ASLWGLRFT VPHLRDTKKT IQDFQILSK NLNNSQSDVV 780
20    SFRLSVEAQA QVTLNGVSKP EAVLFPVSDW HPRDQPKKEE DLGPAVHHVY ELINQGPSSI 840
      SQGVLELSCP QALBGGQQLLY VTRVTGLNCT TNHPINPKGL ELDPGSLHH QKREAPSR 900
      SASSGFQILK CPEAECFRLR QELGPLHQQE SSQLQHFVRV WAKTFLQREH QPFSLQCEAV 960
      YKALKMPYRI LPRQLPQKER QVATAVQWTK AEGSYGVPLW IILAILPGL LLLGLLIYIL 1020
25    YKLGFFKRSL PYGTAMEKAQ LKPPATSDA

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Seq ID NO: 388 DNA sequence
Nucleic Acid Accession #: NM_002425
Coding sequence: 26..1453

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35    TGCCACAGCA TACCTAGAAA AGTACTACAA CCTCGAAAAG GATGTGAAAC AGTTTAGAAG 180
      AAAGGACAGT AATCTCATTT TTAATAAAATG CCAAGGAATG CAGAAGTTCC TTGGTTTGG 240
      GGTGACAGGG AAGCTAGACA CTGACACTCT GGAGGTGATG CGCAAGCCCA GGTGTGGAGT 300
      TCCTGACGTT GGTCACTTCA GCTCCTTTCC TGGCATGCCG AAGTGGAGGA AAACCCACCT 360
      TACATACAGG ATTGTGAATT ATACACCAGA TTTGCCAAGA GATGCTGTTG ATTCTGCCAT 420
40    TGAGAAAGCT CTGAAAGTCT GGAAGAGAGT GACTCCACTC ACATTCTCCA GGCTGTATGA 480
      AGGAGAGGCT GATATAATGA TCTCTTTCCG AGTTAAAGAA CATGGAGACT TTTACTCTTT 540
      TGATGGCCCA GGACACATCT TGGCTCATGC CTACCCACCT GGACCTGGGC TTTATGGAGA 600
      TATTCACTTT GATGATGATG AAAAATGGAC AGAAGATGCA TCAGGCACCA ATTTATTCTC 660
      CGTTGCTGCT CATGAACCTG GCCACTCCCT GGGGCTCTTT CACTCAGCCA ACACCTGAAGC 720
45    TTTGATGTAC CCATCTTACG ACTCATTCAC AGAGCTCGCC CAGTTCCGCC TTTCCGCAAG 780
      TGATGTGAAT GGCATTCACT CTCTCTACGG ACCTCCCCTC GCCTCTACTG AGGAACCCCT 840
      GGTGCCCCCA AAATCTGTTC CTTGCGGATC TGAGATGCCA GCCAAGTGTG ATCTGCTTTT 900
      GCTCTCGAT GGCATGATCT CTCTGAGGGG AGAATATCTG TTTCTTAAAG ACAGATATTT 960
50    TTGGCGAAGA TCCCACTGGA ACCCTGAACC TGAATTTTCA TTGATTCTG CATTTTGGCC 1020
      CTCTCTTCCA TCATATTTGG ATGCTGCATA TGAAGTTAAC AGCAGGACA CCGTTTTTAT 1080
      TTTTAAAGGA ATGAGATTCT GGGCCATCAG AGGAAATGAG GTACAGCAG GTTATCCAAG 1140
      AGGCATCCAT ACCCTGGGTT TTCCTCCAAC CATAAGGAAA ATTGATGCAG CTGTTCTTGA 1200
      CAAGGAAAAG AAGAAAACAT ACTTCTTTGC AGCGGACAAA TACTGGAGAT TTGATGAAAA 1260
      TAGCCAGTCC ATGGAGCAAG GCTTCCCTAG ACTAATAGCT GATGACTTTC CAGGAGTTGA 1320
      GCCTAAGGTT GATGCTGTAT TACAGGCATT TGGATTTTTC TACTTCTTCA GTGGATCATC 1380
55    ACAGTTTGAG TTTGACCCCA ATGCCAGGAT GGTGACACAC ATATTAAAGA GTACAGCTG 1440
      GTTACATTGC TAGGCGAGAT AGGGGGAAGA CAGATATGGG TGTTTTAAAT AAATCTAATA 1500
      ATTATTATC TAATGTATTA TGAGCCAAAA TGGTTAATTT TTCCTGCATG TTCTGTGACT 1560
      GAAGAAGATG AGCCTTGCAG ATATCTGCAT GTGTCATGAA GAATGTTTCT GGAATTTCTC 1620
      ACTTGCTTTT GAATTGCACT GAACAGAATT AAGAAATACT CATGTGCAAT AGGTGAGAGA 1680
60    ATGTATTTTC ATAGATGTGT TATTACTTCC TCAATAAAAA GTTTTATTTT GGGCTGTGTC 1740
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Seq ID NO: 389 Protein sequence
Protein Accession #: NP_002416

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KIQGMQKFLG LEVTGKLDTD TLEVMRKPRC GVPDVGHFSS FPGMPKWRKT HLTIRIVNYT 120
70    PDLPRDAVDS AIEKALKVWE EVTPLTF SRL YEGEADIMIS FAVKEHGDFY SFDGPGHSLA 180
      HAYPPGPLY GDIHFDDEK WTEDASGTNL FLVAHELGH SLGLFHSANT EALMYPLVNS 240
      PTELAQFRLS QDDVNGIQSL YGPPASTEE PLVPTKSVPS GSEMPAKCDP ALSFDAISTL 300
      RGEYLFKDR YFWRRSHWNP EPEFHLISAF WPSLPSYLD AYEVSNRDTV FIFKGNFPA 360
      IRGNEVQAGY PRGHTLGGP PTKRIDAAV SDKEKKTYF PAADKYWRFD ENSQSMEQGF 420
75    PRLIADDFPG VEPKVDVAVLQ AFGFFYFFSG SSQFEFDPNA RMVTHILKSN SWLHC

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Seq ID NO: 390 DNA sequence
Nucleic Acid Accession #: NM_002421.2
Coding sequence: 1..1409

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CCAGCGACTC TAGAAACACA AGAGCAAGAT GTGGACTTAG TCCAGAAATA CCTGAAAAA 120
85    TACTACAACC TGAAGAATGA TGGGAGGCAA GTTGAAAGC GGAGAAATAG TGGCCAGTG 180
      GTTGAAAAAT TGAAGCAATC GCAGGAATTC TTTGGGCTGA AAGTGACTGG GAAACCATG 240
      GCTGAAACCC TGAAGGTGAT GAAGCAGCCC AGATGTGGAG TGCTGATGT GGCTCAGTTT 300

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GTCCTCACTG AGGGGAACCC TCGCTGGGAG CAAACACATC TGACCTACAG GATTGAAAAT 360
 TACACGCCAG ATTTGCCAAG AGCAGATGTG GACCATGCCA TTGAGAAAGC CTTCCAACCTC 420
 TGGAGTAATG TCACACCTCT GACATTACCC AAGGTCTCTG AGGGTCAAGC AGACATCATG 480
 ATATCTTTTG TCAGGGGAGA TCATCGGGAC AACTCTCCTT TTGATGGACC TGGAGGAAAT 540
 CTTGCTCATG CTTTTCACCC AGGCCAGGT ATTGGAGGGG ATGCTCATTT TGATGAAGAT 600
 GAAAGGTGGA CCAACAATTT CAGAGAGTAC AACTTACATC GTGTTGCGGC TCATGAACTC 660
 GGCCATTCTC TTGGACTCTC CCATTCTACT GATATCGGGG CTTTGATGTA CCCTAGCTAC 720
 ACCTTCAGTG GTGATGTTCA GCTAGCTCAG GATGACATTG ATGGCATCCA AGCCATATAT 780
 GGACGTTCCC AAAATCCTGT CCAGCCCATC GGCCCAAAA CCCCAAAAGC ATGTGACAGT 840
 AAGCTAACCT TTGATGCTAT AACTACGATT CGGGGAGAAG TGATGTTCTT TAAAGACAGA 900
 TTCTACATGC GCACAAATCC CTTCTACCCG GAAGTTGAGC TCAATTTTCAT TTCTGTTTTT 960
 TGGCCACAAC TGCCAAATGG GCTTGAAGCT GCTTACGAAT TTGCCGACAG AGATGAAAGT 1020
 CGGTTTTTCA AAGGGAATAA GTACTGGGCT GTTCAGGGAC AGAATGTGCT ACACGGATAC 1080
 CCCAAGGACA TCTACAGCTC CTTTGGCTTC CCTAGAACTG TGAAGCATAT CGATGCTGCT 1140
 CTTTCTGAGG AAAACACTGG AAAAACCTAC TTCTTTGTTG CTAACAAATA CTGAGGATAT 1200
 GATGAATATA AACGATCTAT GGATCCAGGT TATCCCAAAA TGATAGCACA TGACTTTCCT 1260
 GGAATTGGCC ACAAGTTTGA TGCAGTTTTC ATGAAAGATG GATTTTTCTA TTCTTTTCAT 1320
 GGAACAAGAC AATACAAATT TGATCCTAAA ACGAAGAGAA TTTTGACTCT CCAGAAAGCT 1380
 AATAGCTGGT TCAACTGCAG GAAAAATTAG

Seq ID NO: 391 Protein sequence
 Protein Accession #: NP_002412.1

1 11 21 31 41 51
 MHSFPPLLLL LFWGVVSHSF PATLETQEQD VDLVQKYLEK YYNLKNDGRQ VEKRRNSGPV 60
 VEKLKQMGEF FGLKVTGKPD AETLKVMKQP RCGVPDVAQF VLTEGNPRWE QTHLTYYRIEN 120
 YTPDLPRADV DHAIEKAFQL WSNVTPLTFT KVSEGOADIM ISFVRGDHRD NSPFDGPGGN 180
 LAHAFQPGPG IGGDAHFDEP ERWTNNFREY NLHRVAAHEL GHSLLGLSHST DIGALMYPSTY 240
 TFSGDVQLAQ DDIDIGIAIY GRSQNPVQPI GPQTPKACDS KLTFDAITTI RGEVMEFFKDR 300
 FYMRTNPFYP EVELNFIISVF WPQLPNGLEA AYEFAADRDEV RFFKGNKYWA VQGNVNLHGY 360
 PKDIYSSFGF PRTVKHIDAA LSEENTGKTY FFWANKYWRV DEYKRSMDPG YPKMIAHDFP 420
 GIGHKVDVAV MKDGGFFYPFH GTRQYKFDPK TKRILTLQKA NSWFNCRKN

Seq ID NO: 392 DNA sequence
 Nucleic Acid Accession #: NM_002421.2
 Coding sequence: 1..1409

1 11 21 31 41 51
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 TACTACAACC TGAAGAATGA TGGGAGGCAA GTTGAAAAGC GGAGAAATAG TGGCCCACTG 180
 GTTGAAAAAT TGAAGCAATC GCAGGAATTC TTTGGGCTGA AAGTGACTGG GAAACCAGAT 240
 GCTGAAACCC TGAAGGTGAT GAAGCAGCCC AGATGTGGAG TGCTGATGT GGCTCAGTTT 300
 GTCCTCACTG AGGGGAACCC TCGCTGGGAG CAAACACATC TGACCTACAG GATTGAAAAT 360
 TACACGCCAG ATTTGCCAAG AGCAGATGTG GACCATGCCA TTGAGAAAGC CTTCCAACCTC 420
 TGGAGTAATG TCACACCTCT GACATTACCC AAGGTCTCTG AGGGTCAAGC AGACATCATG 480
 ATATCTTTTG TCAGGGGAGA TCATCGGGAC AACTCTCCTT TTGATGGACC TGGAGGAAAT 540
 CTTGCTCATG CTTTTCACCC AGGCCAGGT ATTGGAGGGG ATGCTCATTT TGATGAAGAT 600
 GAAAGGTGGA CCAACAATTT CAGAGAGTAC AACTTACATC GTGTTGCGGC TCATGCCCTC 660
 GGCCATTCTC TTGGACTCTC CCATTCTACT GATATCGGGG CTTTGATGTA CCCTAGCTAC 720
 ACCTTCAGTG GTGATGTTCA GCTAGCTCAG GATGACATTG ATGGCATCCA AGCCATATAT 780
 GGACGTTCCC AAAATCCTGT CCAGCCCATC GGCCCAAAA CCCCAAAAGC ATGTGACAGT 840
 AAGCTAACCT TTGATGCTAT AACTACGATT CGGGGAGAAG TGATGTTCTT TAAAGACAGA 900
 TTCTACATGC GCACAAATCC CTTCTACCCG GAAGTTGAGC TCAATTTTCAT TTCTGTTTTT 960
 TGGCCACAAC TGCCAAATGG GCTTGAAGCT GCTTACGAAT TTGCCGACAG AGATGAAAGT 1020
 CGGTTTTTCA AAGGGAATAA GTACTGGGCT GTTCAGGGAC AGAATGTGCT ACACGGATAC 1080
 CCCAAGGACA TCTACAGCTC CTTTGGCTTC CCTAGAACTG TGAAGCATAT CGATGCTGCT 1140
 CTTTCTGAGG AAAACACTGG AAAAACCTAC TTCTTTGTTG CTAACAAATA CTGAGGATAT 1200
 GATGAATATA AACGATCTAT GGATCCAGGT TATCCCAAAA TGATAGCACA TGACTTTCCT 1260
 GGAATTGGCC ACAAGTTTGA TGCAGTTTTC ATGAAAGATG GATTTTTCTA TTCTTTTCAT 1320
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 AATAGCTGGT TCAACTGCAG GAAAAATTAG

Seq ID NO: 393 Protein sequence
 Protein Accession #: NP_002412.1

1 11 21 31 41 51
 MHSFPPLLLL LFWGVVSHSF PATLETQEQD VDLVQKYLEK YYNLKNDGRQ VEKRRNSGPV 60
 VEKLKQMGEF FGLKVTGKPD AETLKVMKQP RCGVPDVAQF VLTEGNPRWE QTHLTYYRIEN 120
 YTPDLPRADV DHAIEKAFQL WSNVTPLTFT KVSEGOADIM ISFVRGDHRD NSPFDGPGGN 180
 LAHAFQPGPG IGGDAHFDEP ERWTNNFREY NLHRVAAHAL GHSLLGLSHST DIGALMYPSTY 240
 TFSGDVQLAQ DDIDIGIAIY GRSQNPVQPI GPQTPKACDS KLTFDAITTI RGEVMEFFKDR 300
 FYMRTNPFYP EVELNFIISVF WPQLPNGLEA AYEFAADRDEV RFFKGNKYWA VQGNVNLHGY 360
 PKDIYSSFGF PRTVKHIDAA LSEENTGKTY FFWANKYWRV DEYKRSMDPG YPKMIAHDFP 420
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Seq ID NO: 394 DNA sequence
 Nucleic Acid Accession #: NM_014331.2
 Coding sequence: 1..1506

1 11 21 31 41 51
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	AAGAGGAAAG	TCACCTTACT	GAGGGGAGTC	TCCATTATCA	TTGGCACCAT	CATGGAGCA	180
5	GGAAATCTTCA	TCTCTCTTAA	GGGCGTGTCT	CAGAACACGG	GCAGCGTGGG	CATGTCTCTG	240
	ACCATCTGGA	CGGTGTGTGG	GGTCTCTGCA	CTATTGGAG	CTTTGTCTTA	TGCTGAATTG	300
	GGAAACAATA	TAAAGAAATC	TGGAGGTGAT	TACACATATA	TTTTGGAAAT	CTTTGGTCCA	360
	TTACCAGCTT	TTGTACAGAT	CTGGGTGGAA	CTCCTCATAA	TACGCCCTGC	AGCTACTGCT	420
	GTGATATCCC	TGGCATTGGG	ACGCTACATT	CTGGAAACAT	TTTTTATTTA	ATGTGAAATC	480
10	CCTGAACCTG	CGATCAAGCT	CATTACAGCT	GTGGGCATAA	CTGTAGTGAT	GGTCTTAAAT	540
	AGCATGAGTG	TCAGCTGGAG	CGCCCGGATC	CAGATTTTCT	TAACCTTTTG	CAAGCTCACA	600
	GCAATTCTGA	TAAATATAGT	CCCTGGAGTT	ATGCAGCTAA	TTAAAGGTCA	AACGCAGAAC	660
	TTTAAAGACG	CGTTTTTCAGG	AAGAGATTCA	AGTATTACGC	GGTTGCCACT	GGCTTTTAT	720
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15	AACCTGAAA	AAACCAITTC	CTTGTCAATA	TGTATATCCA	TGGCCATTGT	CACCATGGCC	840
	TATGTGCTGA	CAATGTGGC	CTACTTTACG	ACCATTATATG	CTGAGGAGCT	GCTGCTTTCA	900
	AATGCAGTGG	CAGTGACCTT	TTCTGAGCGG	CTACTGGGAA	ATTTCTCATT	AGCAGTTCCG	960
	ATCTTTGTTG	CCCTCTCTCG	CTTTGGCTCC	ATGAACGGTG	GTGTGTTTGC	TGTCTCCAGG	1020
	TTATTTCTATG	TTGCGTCTCG	AGAGGGTCAC	CTTCCAGAAA	TCCTCTCCAT	GATTCTATGC	1080
20	CGCAAGCACA	CTCCTCTACC	AGCTGTATT	GTTTTGACCC	CTTTGACAAT	GATAATGCTC	1140
	TTCTCTGGAG	ACCTCGACAT	TCTTTGAAT	TTCTCTAGTT	TTGCCAGGTG	GCTTTTATT	1200
	GGGCTGGCAG	TTGCTGGGCT	GATTTATCTT	CGATACAAAT	GCCAGATAT	GCATCGTCTC	1260
	TTCAAGGTGC	CAGTGTTCAT	CCCAGCTTTG	TTTTCTCTCA	CATGCCTCTT	CATGGTTGCC	1320
	CTTTCCCTCT	ATTCGGACCC	ATTTAGTACA	GGGATTGGCT	TGCTCATCAC	TCGACTGGA	1380
25	GTCCCTGCGT	ATTATCTCTT	TATTATATGG	GACAAGAAAC	CCAGGTGGTT	TAGAATAATG	1440
	TCAGAGAAAA	TAAACAGAAAC	ATTACAAATA	ATACTGGAAG	TTGTACCAGA	AGAAAGATAAG	1500
	TTATGAACATA	ATGAGCTTGA	GATCTTGGCA	ATCTGCCCAA	GGGGAGACAC	AAAAATAGGA	1560
	TTTTTACTTC	ATTTTCTGAA	AGTCTAGAGA	ATTACAACCT	TGGTGATAAA	CAAAAGGAGT	1620
	CAGTTATTTT	TATTCATATA	TTTTAGCATA	TTGCAACTAA	TTTCTAAGAA	ATTTAGTTAT	1680
30	AACCTATGTG	AGTTATAGAA	AGTGAATATG	CAGTTATTTCT	ATGAGTCGCA	CAATTCCTGA	1740
	GTCTCTGATA	CCTACCTATT	GGGGTTAGGA	GAAAAGACTA	GACAATTACT	ATGTGGTCAT	1800
	TCTCTACAAC	ATATGTTAGC	ACGGCAAGA	ACCTTCAAAT	TGAAGACTGA	GATTTTTCTG	1860
	TATATATGGG	TTTTGTAAAG	ATGGTTTAC	ACACTACAGA	TGCTTACT	GTGAAAAGTG	1920
	TTTTCAATTC	TGAAAAAAG	CATACATCAT	GATTATGGCA	AAGAGGAGAG	AAAGAAATTT	1980
35	ATTTTACATT	GACATTGCAT	TGCTTCCCT	TAGATACCAA	TTTAGATAAC	AAACACTCAT	2040
	GCTTTAATGG	ATTATACCCA	GAGCACTTG	AACAAAGGTC	AGTGGGGATT	GTTGAATACA	2100
	TTAAAGAAGA	GTTTCTAGGG	GCTACTGTTT	ATGAGACACA	TCCAGGAGTT	ATGTTTAAGT	2160
	AAAAATCCTT	GAGAATTTAT	TATGTCAGAT	GTTTTTCAT	TCATTATCAG	GAAGTTTATG	2220
40	TTATCTGTCA	TTTTTTTCTT	TCACATCAGT	TTGATCAGGA	AAGTGATATA	CACATCTTAG	2280
	AGCAAGAGTT	AGTTTGTGAT	TAAATCTCA	TTAGAACAAC	CACCTGTTTC	ACTAATAACT	2340
	TACCCTGAT	GAGTCTATCT	AAACATATGC	ATTTTAAGCC	TTCAAATTAC	ATTATCAACA	2400
	TGAGAGAAAT	AACCAACAATA	GAAGATGTTT	AAAATAATAG	TCCCATATCT	GTAATCATAT	2460
	CTACATGCAA	TGTTAGTAAT	TCTGAAGTTT	TTTAAATTTA	TGGCTATTTT	TACACGATGA	2520
	TGAATTTTGA	CAGTTTGTGC	ATTTTCTTTA	TACATTTTAT	ATTTCTCTGT	TAAAATATCT	2580
45	CTTCAGATGA	AAGTGTCCAG	ATTAATTAGG	AAAAGGCATA	TATTAACATA	AAAATTGCAA	2640
	AAGAAATGTC	GCTGTAATA	AGATTTACAA	CTGATGTTTC	TAGAAAATTT	CCACTTCTAT	2700
	ATCTAGGCTT	TGTAGTAAT	TTCCACACCT	TAATTATCAT	TCAACTTGCA	AAAGAGACAA	2760
	CTGATAAGAA	GAAATTTGAA	ATGAGAATCT	TGGGATAAGT	GTTTGTGTTT	AGAAAGATGT	2820
	GTTTTTGCCAG	TATTAGAAAA	TACTGTGAGC	CGGGCATGGT	GGCTTACATC	TGTAATCCCA	2880
50	GCACCTTGGG	AGGCTGAGGG	GGTGGATCAC	CTGAGGTCGG	GAGTCTTAGA	CCAGCCTGAC	2940
	CAACATGGAG	AAACCCATC	TCTACTAAAA	ATACAAATTT	AGCTGGGCAT	GGTGGCACAT	3000
	GCTGGTAATC	TCAGCTATTG	AGGAGGCTGA	GGCAGGAGAA	TTGCTTGAAC	CCGGGAGGCG	3060
	GAGGTTGCAG	TGAGCCAAAG	TTGCACCACT	GTACTCCAGC	CTGGGTGACA	AAGTCAGACT	3120
	CCATCTCCAA	AAAAAAAAAA	AAAA				

Seq ID NO: 395 Protein sequence
Protein Accession #: NP_055146.1

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	GIFISPKVL	QNTGSVMSL	TIWTVCGVLS	LFGALSYAEL	GTTIKSSGGH	YTYILEVFGP	120
	LPAPVRVWVE	LLIIRPATA	VISLAFGRYI	LEPFFIQCEI	PELAIKLITA	VGITVVMVLN	180
	SMSVSWSARI	QIFLTFCKLT	AIIIIIVPGV	MQLIKGQTQN	FKDAFSGRDS	SITRLPLAFY	240
65	YGMAYAYGWF	YLNFTVEEVE	NPEKTIPLAI	CISMAITIGV	YVLTNVAYFT	TINAEELLS	300
	NAVAVTFSEF	LLGNFSLAVP	IFVALSCFGS	MNGGVFAVSR	LPYVASREGH	LPEILSMIHV	360
	RKHTPLPAVI	VLHPLTMIML	FSGDLDSLNL	FLSFARWLFI	GLAVAGLIYL	RYKCPDMHRP	420
	FKVPLFIPAL	FSFTCLFMVA	LSLYSDPFST	GIGFVITLTG	VPAYYLFIIW	DKKPRWFRIM	480
	SEKITRTLQI	ILEVVPBEDK	L				

Seq ID NO: 396 DNA sequence
Nucleic Acid Accession #: NM_006528
Coding sequence: 57..764

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80	GCGATGTGTC	TCAGGAGCCA	ACAGGAAATA	ACGCGGAGAT	CTGTCTCCTG	CCCCTAGACT	180
	ACGGACCTCG	CCGGCCCTGA	CTTCTCGGTT	ACTACTACGA	CAGGTACACG	CAGAGCTGCC	240
	GCCAGTTCCT	GTAAGGGGGC	TGCGAGGGCA	ACGCCAACAA	TTTCTACACC	TGGGAGGCTT	300
	GCGACGATGC	TTGCTGGAGG	ATAGAAAAAG	TTCCCAAAGT	TTGCCGGCTG	CAAGTGAGTG	360
	TGGACGACCA	GTGTGAGGGG	TCCACAGAAA	AGTATTTCTT	TAACTAAGT	TCCATGACAT	420
85	GTGAAAAATT	CTTTTCCGGT	GGGTGTCAAC	GGAAACCGGAT	TGAGAACAGG	TTTCCAGATG	480
	AAGCTACTTG	TATGGGCTTC	TGCGCACCAA	AGAAAAATTC	ATCATTTTGC	TACAGTCCAA	540
	AAGATGAGGG	ACTGTGCTCT	GCCAAATGTA	CTCGCTATTA	TTTAAATCCA	AGATACAGAA	600
	CCTGTGATGC	TTTCACTTAT	ACTGGCTGTG	GAGGGAATGA	CAATAACTTT	GTTAGCAGGG	660

AGGATTGCAA ACGTGCATGT GCAAAAGCTT TGA AAAAGAA AAAGAAGATG CCAAAGCTTC 720
 GCTTTGCCAG TAGAATCCGG AAAATTCGGA AGAAGCAATT TTAACATTC TTAATATGTC 780
 ATCTTGTTTG TCTTTATGGC TTATTTGCCT TTATGGTTGT ATCTGAAGAA TAATATGACA 840
 GCATGAGGAA ACAATCATTT GGTGATTTAT TCACCAGTTT TTATTAATAC AAGTCACTTT 900
 5 TTCAAAAATT TGGATTTTTT TATATATAAC TAGCTGCTAT TCAATGTGA GTCTACCATT 960
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 AAATATGACT CACTCATTTT TGGGGTCTG ATTCTGATT TCAGAAGAGG ATCATAACTG 1080
 AAACAACATA AGACAATATA ATCATGTGCT TTTAACATAT TTGAGAATAA AAAGGACTAG 1140
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Seq ID NO: 397 Protein sequence
 Protein Accession #: NP_006519

1 11 21 31 41 51
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 CRQFLYGGCE GNANFNPTWE ACDDACWRIE KVPKVCRLQV SVDDQCEGST EKYFFNLSSM 120
 TCEKFFSGGC HRNRIENRFP DEATCMGFCA PKKIPSPFCYS PKDEGLCSAN VTRYFNPFRY 180
 20 RTCDAPTYTG CGNDNNFVS REDCKRACAK ALKKKKKMPK LRFASRIRKI RKKQF

Seq ID NO: 398 DNA sequence
 Nucleic Acid Accession #: NM_001508.1
 Coding sequence: 1..1361

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 30 TTCTGTATGG GCTTCCTGGG GAACAGCGTC ACCATTCCGG TCACCCAGGT GCTGCAGAAG 180
 AAAGGATACT TGCAGAAGGA GGTGACAGAC CACATGGTGA GTTTGGCTTG CTCGGACATC 240
 TTGGTGTTC TCATCGGCAT GCCATGGAG TTCTACAGCA TCATCTGGAA TCCCTGACC 300
 ACGTCCAGCT ACACCTCTGC CTGCAAGCTG CACACTTTCC TCTTCGAGGC CTGCAGCTAC 360
 GCTACGCTGC TGCAGGTGCT GACGCTCAGC TTTGAGCGCT ACATCGCCAT CTGTCACCCC 420
 35 TTCAGGTACA AGGCTGTGTC GGGACCTTGC CAGGTGAAGC TGCTGATTGG CTTGCTCTGG 480
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 GTGAACGTGC CCAGCCACCG GGGTCTCACT TGCAACCGCT CCAGCACCGG CCACCCAGAG 600
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 CAGTCCAGCA TCTTCGGCGC CTTCTGGTGC TACCTCGTGG TCCTGCTCTC CGTAGCCTTC 720
 40 ATGTGCTGGA ACATGATGCA GGTGCTCATG AAAAGCCAGA AGGGCTCGCT GGGCGGGGGC 780
 ACGCGGCTCT CGCAGCTGAG GAAGTCCGAG AGCGAAGAGA GCAGGACCGC CAGGAGGCAG 840
 ACCATCATCT TCTGAGGCT GATTGTTGTG ACATTGGCCG TATGCTGGAT GCCCAACCAG 900
 ATTGCGAGGA TCATGCTGTC GGCCAAACCC AAGCACGACT GGACGAGGTC CTACTTCCGG 960
 GCGTACATGA TCCTCTCTCC CTTCTCGGAG ACGTTTTTCT ACCTCAGTTC GGTCACTAAC 1020
 45 CCGCTCTCTG ACACGGGTGC CTCGCAGCAG TTTCCGGCGG TGTTCTGTGA GGTGCTGTGC 1080
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 ACCACCGACA GCGCCGCTT TGTGCAGCGC CCGTTGCTCT TCGCTCTCCG GCGCCAGTCC 1200
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 50 AATTCTGCTG CAGAGAATGG TTTTCAGGAG CATGAAGTTT GA

Seq ID NO: 399 Protein sequence
 Protein Accession #: NP_001499.1

55 1 11 21 31 41 51
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 ATLLHLVTLF FERYIAICHP FRYKAVSGPC QVKLLIGFVW VTSALVALPL LFAMGTEYPL 180
 60 VNPSPHRLT CNRSSTRHHE QPETSNSMIC TNLSSRWTFV QSSIFGAFVV YLVVLLSVAF 240
 MCWNNMQVLM KSKQGLSAGG TRPPQLRKSE SEESRTARRQ TIIPLRLIVV TLAVCWMPNQ 300
 IRRIMAAKPK KHDWTRSYFR AYMLLPFSE TFFYLSSVIN PLLYTSSSQ FRRVFVQVLC 360
 CRLSLQHANH EKRLRVHAHS TTDSARFVQR PLLFASRRQS SARRTEKIFL STPQSEAPQ 420
 SKSQSLSLES LEPNSGAKPA NSAAENGQFE HEV

Seq ID NO: 400 DNA sequence
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 75 AAAAAAAGA AATACTTCAG CACTTGTAAG AACTGGTATA AAAAGTCCAT CTGTGGACAG 240
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 TGCCCGACAG TTTTGCCCAT TGACCATGTT TATGGCACTC TGGGCATCGT GGGAGCCACC 360
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 80 GGTTTGGAGA GCAACGTGAA TGTGGAATTA CTGAATGCTT TACATAGTCA CATGATTAAT 540
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TCAAAAGGCT TTGCACATTT CTATATGAGT GGGTTTACTG GTAAATATATG TTATTTTATA 3060
CAACTAATTT TGTACTCTCA GAATGTTTGT CATATGCTTC TTGCAATGCA TATTTTATA 3120
TCTCAACGCT TTCAATAAAA CCATTTTTC AATATAAAGA GAATTACTTC AAATTGAGTA 3180
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Seq ID NO: 401 Protein sequence
Protein Accession #: NP_006466.1

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KLREELEGKG SFTTFAPSNE AWDNLDSDIR RGLSNVNVE LNLALHSHMI NKRLMTKDLK 180
NGMIIPSMYN NLGFIINHYF NGVVTNVCAR I IHGNQIATN GVHVVIDRVL TQIGTSIQDF 240
IEAEDDLSSF RAAAITSDIL EALGRDGHFT LPAPTNEAFE KLPRGVLERF MGDKVASEAL 300
MKYHILNTLQ CSESIMGAV FETLEGNITIE IGCDGDSITV NGIKMVNKKD IVTNNGVIHL 360
IDQVLIPDSA QDFTDLVAQ QTTFTDLVAQ LGLASALRPD GEYTLAPVN NAFSDDTLSM 420
VQRLLKLILQ NHILKVKVGL NELVNGQILE TIGGKQLRVF VYRTAVCIEN SCMEKGSKQG 480
RNGAIIHRE I IKPAEKSLH EKLKQDKRFS TFLSLLEAAD LKELLTQPGD WTLFVPTNDA 540
FKGMTSEEKE ILIRDKNLTPG NIIYLHLTPG VFIGKGFEPG VTNIILKTQG SKIFLKEVND 600
TLLVNELKSK ESDIMTTNGV IHVVDKLLYP ADTPVGNLQ LLEILNKLIKY IQIKFVRGST 660
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TEVINGEPII KKYTKIIDGV PVEITEKETR EERIITGPEI KYTRISTGGG ETEETLKKLL 780
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Seq ID NO: 402 DNA sequence
Nucleic Acid Accession #: NM_002416
Coding sequence: 40..417

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GACCTTAAAC AATTGKCCCC AAGCCCTTCC TGCGAGAAAA TTGAAATCAT TGCTACACTG 240
AAGAAATGGAG TTCAACATG TCTAAACCCA GATTGAGCAG ATGTGAAGGA ACTGATTAAA 300
AAGTGGGAGA AACAGGTGAG CCAAAAGAAA AAGCAAAAGA ATGGGAAAAA ACATCAAAAA 360
AAGAAAGTTC TGAAGTTTGC AAAATCTCAA CGTCTCTGTC AAAAGAAGAC TACATAAGAG 420
ACCACTTCAC CAATAAGTAT TCTGTGTAA AAATGTTCTA TTTTAATTAT ACCGCTATCA 480
TTCCAAAGGA GGATGGCATA TAATACAAAG GCTTATTAAT TTGACTAGAA AATTTAAAC 540
ATTACTCTGA AATTGTAAC AAAGTTAGAA AGTTGATTTT AAGAATCCAA ACGTTAAGAA 600
TTGTTAAAGG CTATGATTGT CTTTGTCTT CTACCACCCA CCAGTTGAAT TTCATCATGC 660
TTAAGGCCAT GATTTAGCA ATACCCATGT CTACACAGAT GTTCACCCAA CCACATCCCA 720
CTCACAACAG CTGCCTGGAA GAGCAGCCCT AGGCTTCCAC GTACTGCAGC CTCCAGAGAG 780
TATCTGAGGC ACATGTCAGC AAGTCTTAAG CCTGTTAGCA TGCTGGTGAG CCAAGCAGTT 840
TGAAATTGAG CTGACCTCA CCAAGCTGCT GTGGCCATCA ACCTCTGTAT TTGAATCAGC 900
CTACAGGCT CACACACAT GTGCTGAGA GATTCATGCT GATTGTTATT GGGTATCACC 960
ACTGGAGATC ACCAGTGTGT GGCCTTCAGA GCCCTCTTC TGGCTTTGGA AGCCATGTGA 1020
TTCCATCTTG CCCGCTCAGG CTGACCACTT TATTTCTTTT TGTTCCTCTT TGCTTCATTC 1080
AAGTCAGCT TCTCTCACT TACCAATG CAGTGCCCTT CTCTCTCCA GTGCACCTGT 1140
CATATGCTCT GATTTATCTG AGTCAACTCC TTTCTCATCT TGTCCCCAAC ACCCCACAGA 1200
AGTGCTTTCT TCTCCCAATT CATCTCACT CAGTCCAGCT TAGTTCAAGT CCTGCCTCTT 1260
AAATAAACCT TTTGGACAC ACAATTATC TTAATACTCC TGTTCACTT GGTTCAGTAC 1320
CACATGGGTG AACACTCAAT GGTTAACATA TTCTTGGGTG TTTATCTTAT CTCTCCAACC 1380

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AGATTGTCTAG CTCCTTGAGG GCAAGAGCCA CAGTATATTT CCCTGTTTCT TCCACAGTGC 1440
CTAATAATATC TGTGGAACTA GGTTTTAAATA ATTTTAAAT TGATGTTGTT ATGGGCAGGA 1500
TGGCAACCCAG ACCATTGTCT CAGAGCAGGT GCTGGCTCTT TCCTGGCTAC TCCATGTTGG 1560
CTAGCCTCTG GTAACCTCTT ACTTATTATC TTCAGGACAC TCACTACAGG GACCAGGGAT 1620
GATGCAACAT CTTGTCTCTT TTATGACAGG ATGTTTGCTC AGCTTCTCCA ACAAATAAGAA 1680
GCACTGTGTA AAACACTTGC GGATATTCTG GACTGTTTTT AAAAAATATA CAGTTTACCG 1740
AAAATCATAT AATCTTACAA TGAAGAGGAC TTTATAGATC AGCCAGTGAC CAACCTTTTC 1800
CAACCCATAC AAAAATTCCT TTTCCGAAAG GAAAAGGGCT TTCTCAATAA GCCTCAGCTT 1860
TCTAAGATCT AACAGATAG CCACCGAGAT CCTTATCGAA ACTCATTTTA GGCAATATG 1920
AGTTTTATTG TCCGTTTACT TGTTCAGAG TTTGATTGTT GATTATCAAT TACCACACCA 1980
TCTCCCATGA AGAAGGGGAA CGGTGAAGTA CTAAGCGCTA GAGGAAGCAG CCAAGTCGGT 2040
TAGTGAAGGC ATGATTGTGT CCCAGTTAGC CTCTGCAGGA TGTGGAAGCC TCCTTCCAGG 2100
GGAGGTTCTG TGAATTGTGT AGGAGAGGTT GTCTGTGGCC AGAATTTAAA CCTATACTCA 2160
CTTCCCAAAT TTGAATTCCT GCTCACACTG CTGATGATTT AGAGTGCTGT CCGGTGGAGA 2220
TCCCACCCGA AGCTCTTATC TAATCATGAA ACTCCCTAGT TCCTTCATGT AACTTCCCTG 2280
AAAAATCTAA GTGTTTCATA AATTTGAGAG TCTGTGACCC ACTTACCTTG CATCTCACAG 2340
GTAGACAGTA TATACTAAC AACCAAGAC TACATATTGT CACTGACACA CAGCTTATAA 2400
TCATTATCA TATATATACA TACATGCATA CACTCTCAA GCAAAATAAT TTTCATCTCA 2460
AAACAGTATT GACTTGTATA CCTTGTAAAT TGAATATTTT TCTTTGTTAA AATAGAATGG 2520
TATCAATAAA TAGACCATTA ATCAG

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Seq ID NO: 403 Protein sequence
Protein Accession #: NP_002407

25
30

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1 11 21 31 41 51
MKKSGVLPLL GIILLVLIGV QGTPVVRKGR CSCISTNQGT IHLQSLKDLK QFAPSPSCEK 60
IBIIATLKNG VQTCNLNPSA DVKELIKWE KQVSQKKQK NGKKHQKKKV LKVRKSQRSR 120
QKKT

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Seq ID NO: 404 DNA sequence
Nucleic Acid Accession #: NM_006670
Coding sequence: 85..1347

35
40
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50
55
60
65
70

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1 11 21 31 41 51
CCGGCTCGCG CCCTCCGGGC CCAGCCTCCC GAGCCTTCGG AGCGGGCGCC GTCCCAGCCC 60
AGCTCCGGGG AAACGCGAGC CGCGATGCCT GGGGGGTGCT CCGGGGCGCC CGCCGCGGG 120
GACGGGCGTC TCGGCTGGC GCGACTAGCG CTGCTACTCC TGGGCTGGGT CTCCTCGTCT 180
TCTCCCACTT CCTCGGCTCT CTCTTCTTCC TCCTCGGCGC CGTTCCTGGC TTCCGCGGTG 240
TCCGCCACGC CCCGCTGCC GGACCACTGC CCCGCGCTGT GCGAGTGCTC CGAGGCAGCG 300
CGCACAGTCA AGTGCGTTAA CCGCAATCTG ACCGAGGTGC CCACGGACCT GCCCGCCTAC 360
GTGCGCAACC TCTTCTTAC CGGCAACAG CTGGCCGTGC TCCTTCCCGG CGCCTTCGCC 420
CGCCGCGCGC GCGTGGCGGA GCTGGCGCG CTCAACCTCA CGCGCAGCG CCTGGACGAG 480
GTGCGCGCGG GCGCCTTCGA GCATCTGCCC AGCCTGCGCC AGCTCGACCT CAGCCACAAC 540
CCACTGGCGC ACCTCAGTCC CTTCGCTTTC TCGGGCAGCA ATGCCAGCGT CTCGGCCCCC 600
AGTCCCTTGG TGGAACTGAT CCTGAACAC ATCGTGCCCC CTGAAGATGA GCGGCAGAAC 660
CGGAGCTTCG AGGGCATGGT GGTGGCGGCC CTGCTGGCGG GCGGTGCACT GCAGGGGCTC 720
CGCCGCTTGG AGCTGGCCAG CAACCACTTC CTTTACCTGC CGCGGGATGT GCTGGCCCAA 780
CTGCCAGACC TCAGGCACTG GGACTTAAAT AATAATTGCG TGGTGAGCCT GACCTACGTG 840
TCCTTCCGCA ACCTGACACA TCTAGAAAGC CTCCACCTGG AGGACAATGC CCTCAAGGTC 900
CTTCACAATG GCACCTGGC TGAGTTGCAA GGTCTACCCC ACATTAGGGT TTTCTTGGAC 960
AACAACTCCCT GGGTCTGCGA CTGCCACATG GCAGACATGG TGACCTGGCT CAAGGAAACA 1020
GAGGTAGTGC AGGGCAAAGA CCGGCTCACC TGTGCATATC CGGAAAAAAT GAGGAATCGG 1080
GTCTCTTGGT AACTCAACAG TGCTGACCTG GACTGTGACC CGATTCTTCC CCCATCCCTG 1140
CAAACTCTTT ATGTTCTTCT GGTATTGTT TTAGCCCTGA TAGGCGCTAT TTTCTCTCTG 1200
GTTTTGTATT TGAACCGCAA GGGGATAAAA AAGTGGATGC ATAACATCAG AGATGCCTGC 1260
AGGGATCACA TGAAGGGTA TCATTACAGA TATGAAATCA ATGCGGACCC CAGATTAAAC 1320
AACTCAGTT CTAACCTCGA TGTCTGAGAA ATATTAGAGG ACAGACCAAG GACAACCTG 1380
CATGAGATGT AGACTTAAGC TTTATCCCTA CTAGGCTTGC TCCACTTTCA TCCTCCACTA 1440
TAGATACAAC GGACTTTGAT TAAAGCAGT GAAGGGGATT TGCTTCTTGG TTATGTAAG 1500
TTCTCGGTG GTTCTGTGTA ATGTAAGAC ATGAACAGTT GTGTATAGT TTTTACCCTC 1560
TTCTTTTCTT TGAACCTCCT CAACACGTAT GGAGGGATTT TTCAGGTTTC AGCATGAACA 1620
TGGGCTTCTT GCTGTCTGTC TCTCTCTCAG TACAGTTCAA GGTGTAGCAA GTGTACCCAC 1680
ACAGATAGCA TTCACAAAAA GCTGCCTCAA CTTTTTCGAG AAAAAACTT TATTCATAAA 1740
TATCAGTTTT ATCTCATGT ACCTAAGTTG TGGAGAAAAT AATGTCATCC TATAAACTGC 1800
CTGCAGAGCT TAGCAGGCTC TTCAAAATAA CTCCATGGTG CACAGGAGCA CCTGCATCCA 1860
AGAGCATGCT TACATTTTAC TGTCTGCAT ATTACAAAAA ATAACCTGCA ACTTCATAAC 1920
TTCTTTGACA AAGTAAATTA CTTTTTTGAT TGCAGTTTAT ATGAAAATGT ACTGATTTTT 1980
TTTTAATAAA CTGCATCGAG ATCCAACCGA CTGAATTGTT AAAAAAATAA AAAAAATAAG 2040
ATTCTTAAAA GAA

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Seq ID NO: 405 Protein sequence
Protein Accession #: NP_006661

75
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85

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1 11 21 31 41 51
MPGGCSRGP AAGDRLRLAR LALVLLGWVS SSSPTSSASS FSSAPFLAS AVSAQPPLPD 60
QCPALCECSE AARTVKCNVR NLTEVPTDLP AYVRNLFLTG NQLAVLPAGA FARRPPLAEL 120
AALNLSGSLR DEVRAFAEF LPSLRQLDLS HNPLADLSPF AFGSNASVS APSPLVELIL 180
NHIVPPEDER QNRSFEGMVV AALLAGRALQ GLRRLELASN HFLYLPRLDV AQLPSLRHLD 240
LSNNLSVSLT YVSFNLTHL ESHLEDNAL KVLHNGTLAE LQGLPHIRVP LDNNFWVDC 300
HMDMVTWLK ETEVVQGDOR LTCAYPEKMR NRVLLELNSA DLDCDPIPLP SLQTSYVFLG 360
IVLALIGAIF LLVLYLNRKG IKKWMHNIRD ACRDHMEGYH YRYEINADPR LTNLSSNSDV

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Seq ID NO: 406 DNA sequence
Nucleic Acid Accession #: Eos sequence

Coding sequence: 1..927

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1      11      21      31      41      51
|      |      |      |      |      |
5  ATGCCTGGGG GGTGCTCCCG GGGCCCCGCC GCCGGGGACG GGGGTCTGCG GCTGGGCGCA 60
   CTAGCGCTGG TACTCCTGGG CTGGGTCTCC TCGTCTTCTC CCACCTCCTC GGCATCCTCC 120
   TTCTCCTCCT CGGCGCCGTT CCTGGCTTCC GCCGTGTCCG CCCAGCCCCC GCTGCCGGAC 180
   CAGTGCCCCG CGCTGTGCGA GTGCTCCGAG GCAGCGCGCA CAGTCAAGTG CGTTAACCGC 240
   AATCTGACCG AGGTGCCACG GGACCTGCCC GCCTACGTGC GCAACCTCTT CCTTACCGGC 300
10  AACCAGCTGG CCAGCAACCA CTTCCTTTAC CTGCCGCGGG ATGTGCTGGC CCAACTGCCC 360
   AGCCTCAGGC CTCTGGACTT AAGTAATAAT TCGTGGTGA GCCTGACCTA CGTGTCTTTC 420
   CGCAACCTGA CACATCTAGA AAGCTCCAC CTGGAGGACA ATGCCCTCAA GGTCCTTCAC 480
   AATGGCACCC TGGCTGAGTT GCAAGGTCTA CCCACATTA GGGTTTTCCT GGACAACAAT 540
   CCCTGGGTCT GCGACTGCCA CATGGCAGAC ATGTGACCTT GGCTCAAGGA AACAGAGGTA 600
15  GTGCAAGGCA AAGACCGGCT CACCTGTGCA TATCCGGAAT AAATGAGGAA TCGGGTCTCT 660
   TTGGAAGTCA ACAGTGCTGA CCTGGACTGT GACCCGATTC TTCCCCATC CCTGCAAAAC 720
   TCTTATGTCT TCCTGGGTAT TGTTTATGCC CTGATAGGCG CTATTTTCTT CTGTGGTTTG 780
   TATTTGAACC GCAAGGGGAT AAAAAAGTGG ATGCATAACA TCAGAGATGC CTGCAGGGAT 840
20  CACATGGAAG GGTATCATT CAGATATGAA ATCAATGCGG ACCCCAGATT AACAAACCTC 900
   AGTTCTAACT CGGATGTCTT CGAGTGA

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Seq ID NO: 407 Protein sequence
Protein Accession #: Eos sequence

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25  1      11      21      31      41      51
   |      |      |      |      |      |
   MPGGCSRGA AGDRLRLAR LALVLLGWVS SSSPTSSASS FSSSAPFLAS AVSAQPPPLPD 60
   QCPALCECSE AARTVKCVNR NLTEVPTDLP AYVRNLFPLT NQLASNHFLL LPRDVLQALP 120
   SLRHLDSLNN SLVSLTYVSF RNLTHLESLH LEDNALKVLH NGTLAEQLGL PHIRVFLDNN 180
30  PWVCDCHMAD MVTWLKETE VQKDRLTCA YPEKMRNRVL LELNSADLDC DPILPPLSLQ 240
   SYVFLGIVLA LIGAIPLVLV YLNRKGIKKW MHNIRDACRD HMEGYHYRYE INADPRLTNL 300
   SSNSDVLE

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Seq ID NO: 408 DNA sequence
Nucleic Acid Accession #: NM_000095.1
Coding sequence: 26..2299

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40  1      11      21      31      41      51
   |      |      |      |      |      |
   CAGCACCCAG CTCCCAGCCA CCGCCATGGT CCCCGACACC GCCTGCGTTC TTCTGCTCAC 60
   CTGCGCTGCC CTCGGCGCGT CCGGACAGGG CCAGAGCCCG TTGGGCTCAG ACCTGGGCCC 120
   GCAGATGCTT CGGGAAGTGC AGGAAACCAA CGCGGCGCTG CAGGACGTGC GGGACTGGCT 180
   GCGGCAGCAG GTCAGGGAGA TCACGTTTCTT GAAAAACACG GTGATGGAGT GTGACGCGTG 240
   CGGGATGCGA CAGTCAGTAC GCACCGGCTT ACCCAGCGTG CGGCCCTGCG TCCACTGCGC 300
45  GCGCGGCTTC TGCTTCCCGG GCGTGGCCTG CATCCAGACG GAGAGCGGCG GCCGCTGCGG 360
   CCCCTGCCCC GCGGGCTTCA CGGGCAACGG CTCGCACTGC ACCGACGTCA ACGAGTGCAA 420
   CGCCACCCCT TGCTTCCCGG GAGTCCGCTG TATCAACACC AGCCCGGGGT TCCGCTGCGA 480
   GGCTTGCCCG CCGGGGTACA GCGGCCCCAC CCACCAGGGC GTGGGGCTGG CTTCGCCCAA 540
   GGCCAAACAG CAGGTTTGCA CGGACATCAA CGAGTGTGAG ACCGGGCAAC ATAAGTGGCT 600
50  CCCCAACTCC GTGTGCATCA ACACCCGGGG CTCCTTCCAG TGGGGCCCGT GCCAGCCCGG 660
   CTTCTGTTGG GACCAGGCGT CCGGCTGCCA GCGCGGCGCA CAGCGCTTCT GCCCGGACGG 720
   CTCGCCACAG GAGTGCCACG AGCATGCAGA CTGGCTCCTA GAGCGCGATG GCTCGGGTCT 780
   GTGCGTGTGT CGCGTTGGCT GGGCCGGCAA CGGGATCCTC TGTGGTGGCG ACACTGACCT 840
   AGACGGCTTC CCGGACGAGA AGCTGCGCTG CCCGGAGCCG CAGTGCCGTA AGGACAATCT 900
55  CGTGAATGTC CCAACTCAG GGCAGGAGGA TGTGGACCGC GATGGCATCG GAGACGCTCG 960
   CGATCCGGAT GCCGACGGGG ACGGGGTCCC CAATGAAAAG GACAACTGCC CGCTGGTGGC 1020
   GAACCCAGAC CAGCGCAACA CCGACGAGGA CAAGTGGGGC GATGCGTGGC ACAACTGCCG 1080
   GTCCCAAGAG AACGACGACC AAAAGGACAC AGACCAGGAC GGCAGGGGCG ATGCGTGCGA 1140
   CGACGACATC GACGCGGACC GGATCCGCAA CCAGGCCGAG AACTGCCCTA GGGTACCCAA 1200
60  CTCAGACCAG AAGGACAGTG ATGGCGATGG TATAGGGGAT GCCTGTGACA ACTGTCCCA 1260
   GAAGAGCAAC CCGGATCAGG CGGATGTGGA CCACGACTTT GTGGGAGATG CTTGTGACAG 1320
   CGATCAAGAC CAGGATGGAG ACGGACATCA GGACTCTCGG GACAACTGTC CCACGGTGCC 1380
   TAACAGTGCC CAGGAGGACT CAGACCACGA TGGCCAGGGT GATGCTGCGG ACGACGACGA 1440
   CGACATGACG GGAGTCCCTG ACAGTCCGGA CAACTGCCGC CTGGTGCTTA ACCCCGGCCA 1500
65  GGAGGACGCG GACAGGGGAC GCGTGGGCGA CGTGTGCCAG GACGACTTTG ATGCAGACAA 1560
   GGTGGTAGAC AAGATCGACG TGTGTCCGGA GAACGCTGAA GTCACGCTCA CCGACTTCAG 1620
   GGCTTCCAG ACAGTCTGTC TGGACCCGGA GGGTGACGCG CAGATTGACC CCAACTGGGT 1680
   GGTGCTCAAC CAGGGAAGGG AGATCGTGCA GACAATGAAC AGCGACCCAG GCCTGGCTGT 1740
   GGGTTACACT GCCTTCAATG GCGTGGACTT CGAGGGCACG TTCCATGTGA ACACGGTCAC 1800
70  GGATGACGAC TATGCGGGCT TCATCTTTGG CTACCAGGAC AGCTCCAGCT TCTACGTGGT 1860
   CATGTGGAAG CAGATGGAGC AAACGTATTG GCAGGCCAAG CCCTTCCGTG CTGTGGCCGA 1920
   GCCTGGCATC CAACTCAAGG CTGTGAAGTC TTCCACAGGC CCGGGGAAC AGCTGCGGAA 1980
   CGCTCTGTGG CATAAGGAG ACACAGAGTC CCAGGTGCGG CTGCTGTGGA AGGACCCGCG 2040
75  AAACGTGGGT TGGAAAGGCA AGAAGTCTTA TCGTTGGTTC CTGCAGCACC GGCCCCAAGT 2100
   GGGCTACATC AGGGTGCAT TCTATGAGG CCCTGAGCTG GTGCCGACA GCAACGTGGT 2160
   CTTGGACACA ACCATGCGGG GTGGCCGCTT GGGGGTCTTC TGCTTCTCCC AGGAGAACAT 2220
   CATCTGGGCC AACCTGCGTT ACCCTGCAA TGACACCATC CCAGAGGACT ATGAGACCTA 2280
   TCAGCTGCGG CAAGCTAGG GACCAGGGTG AGGACCCGCC GGATGACAGC CACCTCACCC 2340
80  GCGGCTGGAT GGGGGCTCTG CACCCAGCCC AAGGGGTGGC CGTCTGAGG GGAAGTGAG 2400
   AAGGGCTCAG AGAGGACAAA ATAAAGTGTG TGTGCAGGG

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Seq ID NO: 409 Protein sequence
Protein Accession #: NP_000086.1

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85  1      11      21      31      41      51
   |      |      |      |      |      |
   MVPDTACVLL LTLAALGASG QQSPLGSDL GPQMLRELQE TNAALQDVDR WLRQQVREIT 60

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FLKNTVMEDC ACGMQQSVRT GLPSVRPLH CAPGFCPPGV ACIQTESGGR CGPCPAGPTG 120
 NGSHCTDVNE CNAHPCFPRV RCINTSPGFR CEACPPGYSG PTHQGVGLAF AKANKQVCTD 180
 INECETGQHN CVPNVSVICNT RGSFQCGPCQ PGFVGDAQSG CQRGAQRFCP DGSPSECHEH 240
 ADCVLERDGS RSCVCRVGWA GNGILCGRDT DLGFPDEKL RCPEPQCRKD NCVTVPNSSQ 300
 EDVDRDGIQD ACDPDADGDG VPNEKDNCPL VRNPDQRNTD EDKWDACDN CRSQKNDQDK 360
 DTDQDGRGDA CDDDDIDGRI RNQADNCPRV PMSDQKSDSG DGIGDADNC POKSNPDQAD 420
 VDHDVVGDAC DSDQDQDGDG HQDSRDNCPT VPNSAQEDSD HDGQGDACDD DDDNDGVPS 480
 RDNCRLVPNP QGEDADRQDV GDVQDDFDA DKVVDKIDVC PENAETVLT D FRAFTVVL 540
 PEGDAQIDFN WVVLNQGREI VQTMSNDPGL AVGYTAFNGV DFEGTFHVNT VTDDDYAGFI 600
 FGQDSSSFY VVMWQMEQT YWQANPFRV AEPGIQLKAV KSSTGPGEQL RNALWHTGDT 660
 ESQVRLWKD PRNVGWKDKK SYRWFLQHRP QVGYIRVRFY EGPELVADSN VVLDITMRGG 720
 RLGVPCFSQE NIIWANLRYR CNDTIPEDYE THQLRQA

Seq ID NO: 410 DNA sequence

Nucleic Acid Accession #: NM_001565.1

Coding sequence: 67..363

1 11 21 31 41 51
 | | | | | |
 20 GAGACATTCC TCAATTGCTT AGACATATTC TGAGCCTACA GCAGAGGAAC CTCCAGTCTC 60
 AGCACCATTGA ATCAAACTGC GATTCTGATT TGCTGCCTTA TCTTTCTGAC TCTAAGTGGC 120
 ATTCAGGAGG TACCTCTCTC TAGAACCGTA CGCTGTACCT GCATCAGCAT TAGTAATCAA 180
 CCTGTTAATC CAAGGTCTTT AGAAAAACTT GAAATTATTC CTGCAAGCCA ATTTTGTCCA 240
 CGTGTGAGA TCATTGTCTAC AATGAAAAAG AAGGGTGAGA AGAGATGTCT GAATCCAGAA 300
 25 TCGAAGGCCA TCAAGAAATT ACTGAAAGCA GTTAGCAAGG AAATGTCTAA AAGATCTCCT 360
 TAAAACCGA GGGGAGCAAA ATCGATGCAG TGCTTCCAAG GATGGACCAC ACAGAGGCTG 420
 CCTCTCCCAT CACTTCCCTA CTGGAGTAT ATGTCAAGCC ATAATTGTTT TTAGTTTGCA 480
 GTTACACTAA AAGGTGACCA ATGATGCTCA CCAATCAGC TGCTACTACT CCTGTAGGAA 540
 GGTTAATGTT CATCATCTCA AGCTATTGAG TAATAACTCT ACCCTGGCAC TATAATGTAA 600
 30 GCTCTACTGA GGTGCTATGT TCTTAGTGGA TGTCTGACC CTGCTTCAA TATTTCCTCT 660
 ACCTTTCCCA TCTTCCAAGG GTACTAAGGA ATCTTTCTGC TTTGGGGTTT ATCAGAATTC 720
 TCAGAACTCT AAATAACTAA AAGGTATGCA ATCAAACTG CTTTAAAG AATGCTCTTT 780
 ACTTCATGGA CTTCCACTGC CATCTCCCA AGGGGCCCAA ATTCTTTCAG TGGCTACCTA 840
 35 CATAAATTC CAAACACATA CAGGAAGGTA GAAATATCTG AAAATGTATG TGTAAGTATT 900
 CTTATTTAAT GAAAGACTGT ACAGAGTATA AGTCTTAGAT GTATATATTT CCTATATTGT 960
 TTTCACTGTA CATGGAATTA CATGTAATTA AGTACTATGT ATCAATGAGT AACAGGAAAA 1020
 TTTTAAAAAT ACAGATAGAT ATATGCTCTG CATGTTACAT AAGATAAATG TGCTGAATGS 1080
 TTTTCAATA AAAATGAGGT ACTCTCTGG AATATTAAG

Seq ID NO: 411 Protein sequence

Protein Accession #: NP_001556.1

1 11 21 31 41 51
 | | | | | |
 45 MNQTALICC LIFLTLSGIQ GVPLSRTVRC TCISISNQPV NPRSLEKLEI IPASQFCPRV 60
 EIIATMKKKG EKRCNLPESK AIKNLLKAVS KEMSKRSP

Seq ID NO: 412 DNA sequence

Nucleic Acid Accession #: XM_057014

Coding sequence: 143..874

1 11 21 31 41 51
 | | | | | |
 55 GGGAGGGAGA GAGGCGCGCG GGTGAAAGGC GCATTGATGC AGCCTGCGGC GGCCTCGGAG 60
 CGCGGCGGAG CCAGACGCTG ACCACGTTCC TCTCCTCGGT CTCCTCCGCC TCCAGCTCCG 120
 CGCTGCCCGG CAGCGCGGAG CCATGCGACC CCAAGGGCCCC GCGGCTCCCG CGCAGCGGCT 180
 CCGCGGCGCT CTGCTGCTCC TGCTGCTGCA GCTGCCCGCG CCGTCGAGCG CCTCTGAGAT 240
 CCCCAGGGG AAGCAAAAGG CGCAGCTCCG GCAGAGGGAG GTGGTGGACC TGTATAATGG 300
 60 AATGTGCTTA CAAGGGCCAG CAGGAGTGCC TGGTCGAGAC GGGAGCCCTG GGGCCAATGG 360
 CATTCCGGGT ACACCTGGGA TCCAGGTCG GGTATGATTC AAAGGAGAAA AGGGGGAATG 420
 TCTGAGGGA AGCTTTGAGG AGTCTGGAC ACCCACTAC AAGCAGTGT CATGGAGTTC 480
 ATTGAATTAT GGCATAGATC TTGGGAAAAA TGCGGAGTGT ACATTTACAA AGATGCGTTC 540
 AAATAGTGCT CTAAGAGTTT TGTTCAGTGG CTCACCTCGG CTAATAATGCA GAAATGCATG 600
 CTGTCAGCGT TGGTATTTC CATTCAATGG AGCTGAATGT TCAGGACCTC TTCCCATTTA 660
 65 AGCTATAATT TATTTGGACC AAGGAAGCCC TGAAATGAAT TCAACAATTA ATATTCATCG 720
 CACTTCTTCT GTGGAAGGAC TTTGTGAAGG AATTGGTGCT GGATTAGTGG ATGTGCTAT 780
 CTGGGTGGC ACTTGTTCAG ATTACCCAAA AGGAGATGCT TCTACTGGAT GGAATTCAGT 840
 TTCTCGCATC ATTATTGAAG AACTACCAAA ATAAATGCTT TAATTTTCAT TTGCTACCTC 900
 TTTTITATT ATGCCTTGA ATGTTCACT TAAATGACAT TTTAAATAAG TTTATGTATA 960
 70 CATCTGAATG AAAAGCAAAG CTAATATGT TTACAGACCA AAGTGTGATT TCACACTGTT 1020
 TTTAAATCTA GCATTATCA TTTTGCTTCA ATCAAAAGTG GTTTCAATAT TTTTITAGT 1080
 TGGTTAGAA ACTTCTTCTA TAGTCACATT CTCTCAACCT ATAATTGGA ATATTGTTGT 1140
 GGTCTTTTGT TTTTCTCTT AGTATAGCAT TTTTAAAAA ATATAAAAGC TACCAATCTT 1200
 75 TGTACAATTT GTAAATGTTT AGAATTTTTT TTATATCTGT TAAATAAAAA TTATTTCCAA 1260
 CAACCTTAAA AAAAAAAAAA AAAA

Seq ID NO: 413 Protein sequence

Protein Accession #: XP_057014

1 11 21 31 41 51
 | | | | | |
 80 MRPGPAASP QRLRGLLLLL LLQLPAPSSA SEIPKGKQKA QLRQREVVDL YNGMCLQGPA 60
 GVPGRDGSF ANGIPGTGPI PGRDGFKEK GECLRESFEE SWTPNYKQCS WSSLNYGIDL 120
 GKIAECTFTK MRSNSALRVL FSGSLRLKCR NACQWRWYFT FNGAECGSL PIAIYILDQ 180
 85 GSPENNSTIN IHRSSVEGL CEGIGAGLVD VAIWVGTCSD YPKGDASTGW NSVSRIIEE 240
 LPK

Seq ID NO: 414 DNA sequence
Nucleic Acid Accession #: XM_084007
Coding sequence: 138..2405

5 1 11 21 31 41 51
CTCGTGCCGA ATTCGGCAGC AGACCGCGTG TTCGCGCCTG GTAGAGATTI CTCGAAGACA 60
CCAGTGGGCC CGTGTGGAAC CAAACCTGCG CGCGTGGCCG GCGCGTGGGA CAACGAGGCC 120
10 GCGGAGACGA AGGCGCAATG GCGAGGAAGT TATCTGTAAT CTTGATCCTG ACCTTTTGCCC 180
TCTCTGTAC AAATCCCCTT CATGAACATA AAGCAGCTGC TTTCCCCCAG ACCACTGAGA 240
AAATTAGTCC GAATTTGGGAA TCTGGCATT A TGTTGACTT GGCAATTTCC ACACGGCAAT 300
ATCATCTACA ACAGCTTTTC TACCGCTATG GAGAAAATAA TTCTTTGTCA GTTGAAGGGT 360
TCAGAAAATT ACTTCAAAAT ATAGGCATAG ATAAGATTAA AAGAATCCAT ATACACCATG 420
15 ACCACGACCA TCACCTCAGAC CACGAGCATC ACTCAGACCA TGAGCGTCAC TCAGACCATG 480
AGCATCACTC AGACCCAGAG CATCACTCTG ACCATGATCA TCACTCCCAC CATAATCATG 540
CTGCTTCTGG TAAAAATAG CGAAAGGCTC TTTGCCCAGA CCATGACTCA GATAGTTTCA 600
GTAAAGATCC TAGAACAGC CAGGGGAAAG GAGCTCACCG ACCAGAACAT GCCAGTGGTA 660
GAAGGAATGT CAAGGACAGT GTTAGTGCTA GTGAAGTGAC CTCAACTGTG TACAACACTG 720
20 TCTCTGAAGG AACTCACTT CTAGAGACAA TAGAGACTCC AAGACCTGGA AAACCTCTCC 780
CCAAAGATGT AAGCAGCTCC ACTCCACCCA GTGTCAATC AAGAGCCCG GTGAGCCGGC 840
TGGCTGGTAG GAAACAAAT GAATCTGTGA GTGAGCCCGG AAAAGGCTTT ATGTATTCCA 900
GAAACACAAA TAAATCACTT CAGGAGTGT TCAATGCATC AAGACTACTG ACATCTCATG 960
GCATGGGCAT CCAGGTTCCG CTGAATGCAA CAGAGTTCAA CTATCTCTGT CCAGCCATCA 1020
25 TCAACCAATG TGATGCTAGA TCTGTCTGA TTCATACAAG TGAAAAGAAG GCTGAAATCC 1080
CTCCAAAGAC GTATTCTATA CAAATAGCCT GGGTTGGTGG TTTTATAGCC ATTTCCATCA 1140
TCAGTTTCTT GTCTCTGCTG GGGTTTATCT TAGTGCCTCT CATGAATCGG GTGTTTTTCA 1200
AATTCTCTCT GAGTTTCTCT GTGGCACTGG CCGTTGGGAC TTTGAGTGGT GATGCTTTT 1260
TACACCTTCT TCCACATTCT CATGCAAGTC ACCACCATAG TCATAGCCAT GAAGAACCAG 1320
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Protein Accession #: XP_084007

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Seq ID NO: 417 Protein sequence
Protein Accession #: NP_056234.1

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	ALAIPEAHL	WILPNRRRI	DLANTSHVYM	LPNGTSLIPK	VOVSDSGYR	CAVANQQGAD	660
	HFTVGITVTK	KSGGLPSKRG	RRPGAKALSR	VREDIVEDEG	GSGMGDEENT	SRRLHHPKIDQ	720
10	EVFLTKDDA	INGDKAKKGG	RRKLKLWKHS	EKEPETNVAE	GRRVFESESR	INMANKQINP	780
	ERWADILAKV	RGKNLPKGT	VPPLIKTTSP	PSLSLEVTPP	FPAVSPPSAS	FVQTVTSABE	840
	SSADVPLIGE	EEHVGLTSS	ASMGLEHNHN	GVILVEPEVT	STPLEEVVDD	LSEKTEEITS	900
	TEGDLKGTA	PTLISEPYEP	SPTLHTLDTV	YEKPTHEETA	TEGWSAADVG	SSPEPTSSEY	960
	EPPLDAVSLA	ESEPMQYFDP	DLETQSPDE	DKMKEDTFAH	LTPPTIWN	DSSTSOLFED	1020
	STIGEPGVPG	QSHLQGLTDN	IHLVKSSLST	QDTLLIKKGM	KEMSQLQGG	NMLEGDPHS	1080
15	RSSESEGGES	KSITLPDSTL	GIMSSMSPVK	KPAETTVGTL	LKDDTTTITV	TPRQKVAPSS	1140
	TMSTHPSRRR	PNGRRRLRP	KFRHRHKQTP	PTTFAPSETP	STQPTQAPDI	KISSQVESSL	1200
	VPTAWVDNTV	QSHLQGLTDN	NAEPTSKGTP	RRKHGKRPNK	HRVTPSTVSS	RASGSKPSPS	1260
	PENKHNRIVT	PSSETILPR	TVSLKTEGYP	DSLDMYMTTR	KIYSSYPKVQ	ETLPVITYKPT	1320
	SDGKEIKDDV	ATNVDKHKS	ILVTGESITN	AIPTSRSLVS	TMGEFKESS	PVGFPPTPTW	1380
20	NPSRTAQPR	LQTDIPVTS	GENLTDPL	KELEDVDFTS	EFLSSLTVST	PFHQEAGSS	1440
	TTLSSIKVEV	ASSQAETTL	DQDHELTIVA	ILLSETRPQN	HTPTAARMKE	PASSPSTIL	1500
	MSLGQTTTFL	PALPSPRISQ	ASRDSKENVF	LNIVGNPETE	ATPVNNEGTO	HMSGPNELST	1560
	PSSDRDAFNL	STKLELDRMV	FGSRSLPRGP	DSQRQDGRVH	ASHQLTRVPA	KPILPATATV	1620
	LPEMSTQSAS	RYFVTSQSPR	HWTNKPEITT	YPSGALPENK	QFTTPLRSST	TIPLPLHMSK	1680
25	PSIPSKFTDR	RTDQFNGYSK	VFGNNNIPEA	RNPVGKPPSP	RIPHYSNGRL	PFFTNTKLSF	1740
	PQLGVTRRPQ	IPTSFAPVMR	ERKVIPOGYN	RIHSHSTFHL	DFGPPAPPLL	HTPQTGSPS	1800
	TNLQNIPIVMS	STQSSISFIT	SSVQSSGSFH	QSSSKFPAGG	PPASKFWSLG	EKPQILTKSP	1860
	QTVSVTAETD	TVFPCEATGV	KPKPVTWTKV	STGALMTPT	RIQRFEVLKN	GTLVIRKVVQ	1920
30	QDRGQYMCFA	SNLHGLDRMV	VLLSVTVQOP	QILASHYQDV	TVYLGDTIAM	ECLAKGTPAP	1980
	QISWIFPDRR	VWQTVSPVES	RITLHENRTL	SIKEASPSDR	GVYKCVASNA	AGADSLAIRL	2040
	HVAALPPVTH	QEKLENIISL	PGLSIHICT	AKAAPLPSVR	WVLGDGTQIR	PSQFLHGNLF	2100
	VFPNGTLYIR	NLAPKDSGRY	ECVAANLVGS	ARRTVQLNVQ	RAANARITG	TSFRRTDVRY	2160
	GGTLKLDCA	SGDPWPRILW	RLPSKRMIDA	LFSFDSRIKV	FANGTLVVK	VTDKDAGDYL	2220
35	CVARNKVQDD	VVVLKVDVVM	KPAKIEHKEE	NDHKVYFGGD	LKVDVCATGL	PNPEISWSLP	2280
	DGSLVNSFMQ	SDDSGGRTRK	YVVFNNGLTY	FNEVGMREEG	DYTCFAENQV	GKDEMVRVRK	2340
	VVTAPATIRN	KTYLAVQVPY	GDVVTVACEA	KGEPMKVTW	LSPTNKVIPT	SSEKYQIYQD	2400
	GTLILQKAGR	SDSNGYTCLV	RNSAGEDRKT	VWILHVNQPP	KINGNPNPIT	TVREIAAGGS	2460
	RKLIDCKAEG	IPTRVLVAPY	PEGVVLVAPY	YGNRITVHGN	GSLDIRSLRK	SBSVQLVCM	2520
40	RNEGGEARLI	VQLTVLEPME	KPIFHDPISE	KITAMAGHTI	SLNCSAAGTP	TPSLVWVLPN	2580
	GTDLQSGQQL	QRFYHKADGM	LHISGLSSVD	AGAYRCVARN	AAGHTERLVS	LKVGLKPEAN	2640
	KQYHNLVSI	NETLKLPCPT	PPGAGQGRFS	WTLFNGMHLE	GPQTLGRVSL	LDNGILTvre	2700
	ASVFDRTGYV	CRMETEYGPS	VTSIPVIVIA	YPPRITSEPT	PVIYTRPGNT	VKLNCMAMGI	2760
	PKADITWELP	DKSHLKAGVQ	ARLYGNRFLH	PQGSLLTIQHA	TQRDAGFYKC	MAKNILGSDS	2820
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Seq ID NO: 418 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 1..5001

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	CAGTCTGTGC	TTGTGTCCTG	GGTGGATCCT	GTTCTGGAAA	AACAGAAGAA	AGTTGTGTGCA	180
55	TCAAGACAGT	ACACCGTGGC	CTATCGAGAG	AAGGGGGAAT	TGGCCAGGTG	GGATTATAAG	240
	CAGATCGCTA	ACAGCGGTG	GCTGATTGAG	AACCTGATTC	CAGACACTGT	GTATGAATT	300
	GCAGTCCGTA	TTTCACAGGG	TGAAAGAGAT	GGCAAATGGA	GTACGTCAGT	CTTCCAAAGA	360
	ACACCAAGAT	CTGCCCCCTC	CACAGCTCCT	GAAAACTTGA	ACGCTGCGCC	AGTCAATGGC	420
60	AAACCTACAG	TGTGCTGTC	ATCTTGGGAT	GCGCTACCGA	AGACTGAGGG	GAAAGTGAAA	480
	GTCTGTCTGC	TGGACACAGG	ACTGTTTTC	GTTTCTCCT	TCCAACATC	TGCCAAATCA	540
	TTTCAGAAAT	CATTCTTTCA	TACGCCCCGG	CTCTCAAACC	ATTGAGGCA	AAGTCCCTCA	600
	CCTATCCTGG	AGACACTACT	TCTGCCCTGG	TGGATGGTCT	GCAGCCTGGG	GAACGCTATC	660
	TTTTCAAAT	CCGGGCCACA	AACAGGAGAG	GCCTGGGACC	TCACTCCAAA	GCCTTCATTG	720
	TCGCTATGCC	AACAAGATG	CAGCTGTACC	CAGAAGGATT	TCAGTTGTCT	AGCTTACCTG	780
65	ATCGATATCC	AAACCAACA	AGTTAATAAA	GATCCACAAC	TGGAAGGGAG	TGTTTTTGGA	840
	CCATGTTTTC	TTTTCTACTT	CCTCACATTT	ATGCTGGATA	TTGGCGGCTT	TTCTTTCATT	900
	ATGTGCTATG	AAGACCCANN	TGTTTCTTCT	TTGACAGGCA	ATTCTTTAAA	ATCTGTTGCA	960
	GCCAGTAAGG	CGGATGTTCA	GCAGAACACG	GAGGACAATG	GGAAACCCGA	AAAACCTGAG	1020
70	CCTTCTCTAC	CTTCTCCAG	AGCTCCAGCT	TCTTCCCAAC	ACCCCTCTGT	GCCTGCTTCT	1080
	CCCCAAGGGA	GAAATGCCAA	GGACCTTCTT	CTTGACTTGA	AGAACAAAAT	ATTGGCTAAT	1140
	GGTGGGGCGC	CCCGAAATTC	CCAGCTTCGC	GCCAAGAAGG	CAGAGGAGCT	GGATCTTCAG	1200
	TCGACAGAAA	TCACTGGGGA	GGAGGAGCTG	GGTTCGGGG	AGGACTCGCC	CATGTCACCC	1260
	TCAGACACCC	AAGACCAAG	ACGGAACCTG	AGGCGGCCAA	GTAGACACGG	CAACTCGGTG	1320
	GTGTCTCCCG	GCAGGACTGC	AGTAGGGGCC	CGGATGCCAG	CGCTGCCCCG	AAGGGAAGGC	1380
75	GTAGATAAGC	CTGGCTTTTC	CCTGGCCACG	CAGCCCCGCC	CAGGGGCGCC	CCCCTCGGCT	1440
	TCGGCTCTCT	CTGCCACCA	CGCTCCACCC	CAGGGCACCT	CTCATCGTCC	TTCCCTGCCT	1500
	GCCAGCTTGA	ATGACACA	CTTGGTGGAC	TCAGACGAAG	ATGAGCGCGC	TGTGGGCTCC	1560
	CTCCACCCCA	AGGGCGCCTT	CGCCACGCCC	CGGCCAGCCC	TGTCCCCCAG	CGCCAGTCC	1620
	CGCTCCAGCG	TTCTCCGCGA	CAGAAGCTCT	GTGCACCCCG	CGCCAAAGCC	AGCCTCGCCG	1680
80	GCGCGGAGGA	CCCCCAATTC	GAGGCGCGCA	GAGGAAGATT	CCAGTGCCTC	AGCCCCACCC	1740
	TCAAGACTTT	CTCCACCCCA	TGGGGGATCA	TCTCGGCTGC	TGCCCCACCA	GCCACACCTG	1800
	AGCTCTCCAC	TTTCAAGGG	CGGGAAGGAT	GGTGAGGACG	CCCCAGCCAC	CAACTCCAAT	1860
	GCGCATCAC	GGTCCACCAT	GTCTCTCTC	ATCTCTCGTC	CAGGACGCG	CAGGACGCG	1920
	GTCTCTGAGG	GAGCGGAGGC	TTCTGATGGT	GAAAGCCACG	GTGACGCGCA	TAGGGAAGAC	1980
85	GGCGGAAGGC	AGGCGGAGGC	CACGGCCACG	ACGCTGCGGG	CCCGGCTGCG	CTCTGGACAC	2040
	TTCAATTGCT	TACAGACAAA	ACCTTTTGCT	GCCAACGGGA	GGTCTCCAAG	CAGGTTGACG	2100
	ATTGGGCGGG	GACCTCGGCT	GCAGCCCTCC	AGCTCCCCAC	AGTCGACTGT	GCCTTCCCGA	2160

	GCCACCCCA	GGGTTCCCTC	TCACTCTGAT	TCCCACCCCTA	AGCTTAGCTC	AGGTATCCAT	2220
	GGAGACGAGG	AGGATGAGAA	GCCGCTTCCT	GCCACCGTTG	TCAATGACCA	CGTGCCTTCC	2280
	TCCTCCAGGC	AGCCCATCTC	CCGGGGCTGG	GAGGACTTAA	GGAGAAGCCC	GCAGAGAGGG	2340
5	GCCAGCCTGC	ATCGGAAGGA	ACCCATCCCA	GAGAACCCCA	AATCCACAGG	GGCAGATACA	2400
	CATCCTCAGG	GCAAGTACTC	CTCCCTGGCC	TCCAAGGCTC	AGGATGTTCA	ACAGAGCACA	2460
	GACGCGGACA	CGGAGGGTCA	TTCTCCCAAA	GCACAGCCAG	GGTCCACAGA	CGCCACCGCG	2520
	TCCCTCTGCTC	AGCTCTCCGC	AGCAGCGTCA	CAGCAGCATC	CCAGTGTTC	CAGAAGGATG	2580
	ACACCCGGCC	GGGCCCCAGA	ACAGCAGCCC	CCTCCTCCCG	TCGCCACGTC	CCAGCACCAC	2640
10	CCGGGACCCC	AGAGCAGAGA	CGCGGGTGG	TCACCTTCCC	AGCCCAGGCT	CTCACTGACC	2700
	CAGGCGGGC	GGCCCGGCC	CACGTGCGAG	GGCCGCTCCC	ACTCCTCCTC	GGACCCTTAC	2760
	ACGGCGAGCT	CCAGAGGGAT	GCTCCCCACG	GCCCTCCAGA	ACCAGGACGA	GGATGCCCAG	2820
	GGCAGCTACG	ACGACGACAG	CACAGAAGTC	GAGGCCCAGG	ATGTGCGGGC	CCCCCGGCAC	2880
	CCGCGCGCG	CCAAGGAGGC	AGCTGCGTCC	CTTCCCAAGC	ACCAGCAGGT	GGAGTCTCCC	2940
15	ACAGGCGCAG	GGGCGAGTGG	CGACCACAGG	TCCAGGCGCG	GACATGCGGC	CTCCCCCGCC	3000
	AGGCCCGAGC	GACCCGCGCG	CCCCCAGTCC	CGCGCCCGGG	TCCCCAGCAG	GGCAGCGCCG	3060
	GGGAAGTCGG	AGCCTCTTTC	CAGCGCGCCC	CTGTCTCTCA	AGTCCAGCA	GTCCGTCTCA	3120
	GCCGAGGACG	AGGAGGAGGA	GGACGCGGGG	TTTTTTAAAG	GCGGGAAGA	AGACCTTCTG	3180
	TCCTCTCTG	TGCCAAAGTG	GCCCTCTTCC	TCCACTCCCA	GGGGCGGCAA	AGACGCCGAT	3240
20	GGGAGCCTCG	CCAAGGAAGA	GAGGAGCCT	GCCATCGCGC	TTGCCCTCG	CGGAGGGAGC	3300
	CTGGCTCTG	TGAAGCGACC	TCTCCCCCA	CCTCCAGGCA	GCTCCCCCAG	GGCCTCCAC	3360
	GTCCCTTCCC	GACCGCGCCG	TCCGAGCGCT	GCCACCGTGA	GCCCGTCCG	GGGACCCAC	3420
	CCCTGGCGCG	GGTACACCAC	GCGCGCCCV	CTGGCCACT	TCTCCACCAC	CCCGATGCTG	3480
	TCCTTGGGCC	AGAGGATGAT	GCATGCCAGA	TTCCGTAACC	CTCTCTCCCG	ACAGCCTGCC	3540
	AGACCTCTT	ACAGACAAGG	TTATAATGGC	AGACCAATG	TAGAAGGGAA	AGTCTCTCCT	3600
25	GGTAGTAATG	GAAAACCGAA	TGGACAGAGA	ATTATCAATG	GCCCTCAAGG	AACAAAGTGG	3660
	GTTGTGGACC	TTGATCGTGG	GTTAGTATTG	AATGCAGAAG	GAAGGTACCT	CCAAGATTCA	3720
	CATGGAATTC	CTCTTCGATG	TAAACTAGGA	GGAGATGGTC	GAACCATTTG	AGATCTGGAA	3780
	GGGACCCCG	TGTTAGATTC	TCCGCGCTC	CCACTCTTG	GGCAGGGCGG	ACATGGCACA	3840
30	CCTCTGGCCA	ATGCCCAAGA	TAAGCCAATT	TTGAGTCTTG	GAGGAAAGCC	GCTGGTGGGC	3900
	TTGGAGGTGA	TCAAAAAGAA	CACCCATCCC	CCTACCACTA	CCATGCAGCC	CACCACTACT	3960
	ACGACGCCCC	TGCCTACCAC	TACAACCCCG	AGGCCACCA	CTGCCACCAC	CATGCAGCCC	4020
	ACCCTACTTA	GACGCGCCCT	GCCTACCACT	ACACCGAGGC	CCACCACTGC	CACCACCCGC	4080
	CGCAGGACCA	CCAGCGCTCC	AACAACACCA	GTCCGAACCA	CTACGCGGAC	AACCACCAAC	4140
35	ACCACCCCA	AACCACACAC	TCCCATCCCC	ACCTGTCCCC	CTGGGACCTT	GGAACGGCAC	4200
	GACGATGATG	GCAACCTGAT	AATGAGCTCC	AATGGGATCC	CAGAGTGCTA	CGCTGAAGAA	4260
	GATGAGTTCT	CAGGCTTGGG	GACTGACACT	GCAGTACCTA	CGGAAGAGGC	CTACGTTATA	4320
	TATGATGAAG	ATTATGAATT	TGAGACGTCA	AGGCCACCA	CCACCACTGA	GCCTTCGACC	4380
	ACTGCTACCA	CACCGAGGGT	GATCCAGAG	GAAGGCGCCA	TCAGTTCTCT	TCCTGAAGAA	4440
40	GAATTTGATC	TGGCTGGAAG	GAAACGATTT	GTTGCTCCTT	ACGTGACGTA	CCTAAATAAA	4500
	GACCCATCAG	CCCCGTGCTC	TCTGACTGAT	GCATGGATC	ACTTCCAAGT	GGACAGCCTG	4560
	GATGAAATCA	TCCCAATAGA	CCTGAAGAAG	AGTGATCTGC	CTCCCCAGCA	TGCTCCCGGC	4620
	AACATCACCG	TGGTGGCGGT	GGAAGGTTGC	CACATCATTT	TCATTGTGGA	TTGGGACAAA	4680
	GCCACCCAG	GAGATTTGGT	CACAGGTTAT	TTGGTTTACA	GTGCATCCTA	TGAAGATTTC	4740
45	ATCAGGAACA	AGTTTTCAC	TCAAGCTTCA	TCAGTAACTC	ACTTGCCCAT	TGAGAACCTA	4800
	AAGCCCAACA	CGAGGTATTA	TTTTAAAGTG	CAAGCACAAA	ATCCTCATGG	CTACGGACCT	4860
	ATCAGCCCTT	CGGTCTCATT	TGTCAACGAA	TCAGATAATC	CTCTGCTTGT	TGTGAGGCC	4920
	CCAGGCGGTG	AGCTATCTGG	ATCCCATTCG	CTTTCAAACA	TGATCCGAGC	TACACGGACT	4980
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50	GTAATTAATC	GAGGTATAAA	ATCTACCTCA	GTGACAACTT	GAAAGATACA	TCTACAGCA	5100
	TTGGAGACAG	CTGGGGAAGA	GGTGAAGACC	ATTGCCAATT	TGTGGATTCA	CACCTTGATG	5160
	GAAGAACAGG	GCCTCAGTCC	TATGTAGAAG	CCCTCCCTAC	TATTCAAGGC	TACTATCGCC	5220
	AGTATCGTCA	GGAGCCTGTC	AGGTTTGGGA	ACATCGGCTT	CGGAACCCCC	TACTACTATG	5280
	TGGCTGGTA	CGAGTGTGGG	GTCTCCATCC	CTGGAAGTG	GTAATCACAG	GACCGTCATG	5340
55	CTGCAAGCTT	GCCCTGCCCA	GCCCCACCAA	CTAAGTCGCA	CTAGGGGCTG	TGAGCAAAGA	5400
	CAGCCAGCAT	GCTCAGCCCC	GCTGCCCTAG	GTGCCAGGAA	GGTCACAGAT	GGACACTGGC	5460
	CATTCTGGTC	ATCTCAGTAT	GGAACCTAGT	CCCACTTCTT	GGCCTGGACA	ATGAACAGGA	5520
	TTCACTTTTG	CTGTTAACTT	TGCTTCTCTA	CTTTTCTTTG	TTGTTTGTGA	ATAGCACATC	5580
	CCAGAGACAT	CAGAAACGAG	CAACTGATTC	AGTGTGATTT	CCGAGACTTT	TTAGGCATGA	5640
60	AATTTCGACA	CTTCAGTATT	TCCAGGAATA	GCATATGCAC	GCTGTCTTGT	CTTCATGGAA	5700
	TGCTACATGC	TTTCTGTTTT	TCTCATTTTG	GATTTCTCCA	AAACTAACTG	AATTAAAGCT	5760
	TCAGGTCCCT	TGTATGACAG	TAGAAAGGAA	TTATTAATAA	CACCACCAA	GAAAATAAAT	5820
	ATATCTACT	TGAAATTTAC	TCTATGGACT	TACCCACTGC	TAGAATAAAT	GTATCAAATC	5880
	TTATTTGTA	ATTCTCAATT	TTGATATATA	TATGTATATA	TGCATATACA	TATCCACACT	5940
65	TGCTGCAAG	AATATTGATT	AAAATTGCTA	AATTTGTA	TGTTCAACCA	AAAAAAAAA	6000

Seq ID NO: 419 Protein sequence
Protein Accession #: Eos sequence

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75	TPESAPTTAP	ENLNVWPVNG	KPTVVAASWD	ALPETEGKVK	VCLLDITGLFS	VSSFPQSAKS	180
	FQNTFFHTFR	LSNHLQSPS	PILETLLELPW	WMVCSLGNAI	FSKSGPQTGE	AWDLTPKPSL	240
	SLCQEQCSCT	QKDFSCLAYL	IDIQTKQVKN	DPQLEGSVFG	PCFLPYPLTF	MLDIGGSPFI	300
	MCYEDPVSSL	TGNSLKSVA	SKADVQNTTE	DNGKPEKPEP	SSPSPRAPAS	SQHPSPVSP	360
	QGRNAKDL	DLKNKILANG	GAPRKPQLRA	KKAEELDLQS	TEITGEEELG	SREDSPPMS	420
80	DTQDQKRTL	PPSRHGHVSV	APGRTAVRAR	MPALPRREGV	DKPGPSLATQ	PRPGAPPSA	480
	ASPAHHASTQ	GTSHRPSLP	SLNDNDLVDS	DEDERAVGSL	HPKGAFAPQR	PALSPSRQSP	540
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	SPLSKGKGQD	EDAPATNSNA	PSRSTMSSSV	SSHLSSRTQV	SEGAEASDGE	SHGDGDREDG	660
	GRQAEATAQT	LRARPAAGHF	HLRHKPFPA	NGRSPSRFSI	GRGPRLQPS	SPQSTVPSRA	720
85	HPRVPSHSDS	HPKLSGSIHG	DEDEKPLPA	TVVNDHVPSS	SRQPISRGWE	DLRRSPQRGA	780
	SLHRKEPIPE	NPKSTGADTH	PQGYSSLAS	KAQDVQQSTD	ADTEGHSPKA	QPGSTDRHAS	840
	PARPPAARSQ	QHPSPVRPMT	PGRAPQPP	PPVATSQHHP	GPQSPRDAGS	PSQPRLSLTQ	900
	AGRPRPTSQG	RSHSSDPYPT	ASSRGMPLTA	LQNQDEDAQG	SYDDSDTEVE	AQDVRAPAHA	960

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 SLAKEEREPA IALAPRGSL APVKRPLPPP PGSSPRASHV PSRPPPSAA TVSPVAGTHP 1140
 WPRYTTRAPP GHFSTTMLS LRQRMHARF RNPLSRQPAR PSYRQGYNGR PNVEGKVLPG 1200
 5 SNGKPNQRI INGPQGTWV VDLDRGLVLN AEGRYLQDSH GNPLRIKLG DGRTIVDLEG 1260
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 TPGDLVTGVL VYSASYEDFI RNKFPSTQASS VTHLPIENLK PNTRYFYKVQ AQNPFGYGP 1620
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 45 ATTTGGTTGA GGATGCCAAA AAAAAAAAAA AAAAAA

Seq ID NO: 421 Protein sequence
 Protein Accession #: NP_073580

1 11 21 31 41 51
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 SEKLYSPYDL ESNINKLTED KKEGLRQLVM TFQHFMBEEI QDASQLPPAF DLFEAPAKVI 120
 CNSFTICNAE MQEVGVGLYP SISLNNHSCD PNCISIVFNGP HLLLRVRDI EVGEELTICY 180
 55 LDMLMTSEER RKQLRDQYCF EDCDFRCQTQ DKDADMLTGD EQVWKEVQES LKKIEELKAH 240
 WKWEQVLAMC QALISSNSER LPDINIYQLK VLDCAMDACI NLGLLEALF YGRTTMEPYR 300
 IFPPGSHPRV GVQVMKVGL QLHQGMFPQA MNLRRLAFDI MRVTHGREHS LIEDLILLE 360
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Seq ID NO: 422 DNA sequence
 Nucleic Acid Accession #: NM_003014.2
 Coding sequence: 238..648

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 70 TTCTCTTCCA TCTAGTGGC GCTGTGCTGT TGGCTGCACC TGGCGCTGGG CGTGCGCGGC 300
 GCGCCCTGCG AGGCGGTGCG CATCCCTATG TGCCGGCACA TGCCCTGGAA CATCAGCGG 360
 ATGCCCAACC ACCTGCACCA CAGCACGCAG GAGAACGCCA TCCTGGCCAT CGAGCAGTAC 420
 GAGGAGCTGG TGGAGCTGAA CTGCAGCGCC GTGCTGCGCT TCTTCTTCTG TGGCATGTAC 480
 GCGCCCATTT GCACCTGGA GTTCTGCAAC GACCTATCA AGCCGTGCAA GTCGGTGTGC 540
 CAACGCGCGC GCGAGCACTG CGAGCCCTTC ATGAAGATGT ACAACACAG CTGGCCGGA 600
 75 AGCCTGGCCT GCGACGAGCT GCCTGTCTAT GACCGTGGCG TGTGCATTTC GCCTGAAGCC 660
 ATCGTCAAGG ACCTCCCGGA GGATGTTAAG TGGATAGACA TCACACCAGA CATGATGGTA 720
 CAGGAAAGGC CTCTTGATGT TGACTGTAAA GCCTAAGCC CCGATCGGTG CAAGTGTAAA 780
 AAGGTGAAGC CAACCTTGGC AACGTATCTC AGCAAAACT ACAGCTATGT TATTCATGCC 840
 AAAATAAAAG CTGTGAGAG GAGTGGCTGC AATGAGGTCA CAACGGTGGT GGATGTAAAA 900
 80 GAGATCTTCA AGTCTCATC ACCATCCCT CCGCTCCAT CAAGATGTTT TCATCATGTG TTACGAGTGG 1020
 TCTTGGCAGT GTCCACACAT CTTGCCCAT CAAGATGTTT TCATCATGTG TTACGAGTGG 1080
 CGTTCAAGGA TGATGCTTCT TGAATAATGC TTAGTTGAAA AATGGAGAGA TCAGCTTAGT 1140
 AAAAGATCCA TACAGTGGGA AGAGAGGCTG CAGGAACAGC GGAGAACAGT TCAGGACAAG 1200
 85 AAGAAAAACG CCGGGCGCAC CAGTCGTAGT AATCCCCCA AACCAAAGGG AAAGCCTCCT 1260
 GCTCCCAAAC CAGCCAGTCC CAAGAAGAAC ATTAATACTA GGAGTGCCCA GAAGAGAAAC 1320
 AATCCGAAAA GAGTGTGAGC TAACTAGTTT CCAAGCGGA GACTTCGAC TCTCTACAG 1380
 GATGAGGCTG GGCATTGCCCT GGGACAGCCT ATGTAAGGCC ATGTGCCCTT TGCCCTAAC 1440

	ACTCACTGCA	GTGCTCTTCA	TAGACACATC	TTGCAGCATT	TTTCTTAAGG	CTATGCTTCA	1440
	GTTTTTCTTT	GTAAGCCATC	ACAAGCCATA	GTGGTAGGTT	TGCCCTTTGG	TACAGAAGGT	1500
	GAGTTAAAGC	TGGTGGAAAA	GGCTTATTGC	ATTGCATTCA	GAGTAACCTG	TGTGCATACT	1560
5	CTAGAAGAGT	AGGGAATAA	ATGCTTGTTA	CAATTGACC	TAATATGTGC	ATTGTAAAT	1620
	AAATGCCATA	TTTCAACAA	AACACGTAAT	TTTTTTACAG	TATGTTTTAT	TACCTTTTGA	1680
	TATCTGTGTG	TGCAATGTGA	GTGATGTTTT	AAAATGTGAT	GAAAAATATA	TGTTTTTAAG	1740
	AAGGAACAGT	AGTGAATGA	ATGTTAAAA	ATCTTTATGT	GTTTATGGTC	TGCAGAAGGA	1800
	TTTTTGTGAT	GAAAGGGGAT	TTTTTGAATA	ATTAGAGAAG	TAGCATATGG	AAAATTATAA	1860
10	TGTGTTTTTT	TACCAATGAC	TTCAGTTTCT	GTTTTTAGCT	AGAAACTTAA	AAACAAAAAT	1920
	AATAATAAAG	AAAAATAAAT	AAAAAGGAGA	GGCAGACAAT	GTCGTGATTC	CTGTTTTTGG	1980
	GTTACCTGAT	TCCCATGATC	ATGATGCTTC	TTGTCAACAC	CCTCTTAAGC	AGCACCAGAA	2040
	ACAGTGAGTT	TGTCTGTACC	ATTAGGAGTT	AGGTAATAAT	TAGTTGGCTA	ATGCTCAAGT	2100
	ATTTTATACC	CACAAGAGAG	GTATGTCACT	CATCTTACTT	CCCAGGACAT	CCACCCTGAG	2160
	AATAATTTGA	CAAGCTTAAA	AATGCGCTTC	ATGTGAGTGC	CAAATTTTGT	TTTTCTTCAT	2220
15	TTAAATATTT	TCTTTCCTTA	AATACATGTG	AGAGGAGTTA	AATATAAATG	TACAGAGAGG	2280
	AAAGTTGAGT	TCCACCTCTG	AAATGAGAAT	TACTTGACAG	TTGGGATACT	TTAATCAGAA	2340
	AAAAAGAACT	TATTTGACAG	ATTTTATCAA	CAAATTTTAT	AATTTGGGAC	AATTTGGAGG	2400
	ATTTATTTTA	AAAAACAATT	TTATTGGCCT	TTTGCTAACA	CAGTAAGCAT	GTATTTTATA	2460
	AGGCATTCAA	TAAATGCACA	ACGCCCAAG	GAAATAAAAT	CCTATCTAAT	CCTACTCTCC	2520
20	ACTACACAGA	GCTAATCACT	ATTAGTATTT	TGGCATATTA	TTCTCCAGGT	GTTTGTCTAT	2580
	GCACTTATAA	AATGATTTGA	ACAAATAAAA	CTAGGAACCT	GTATACATGT	GTTTCATAAC	2640
	TCGCCTCCTT	TGCTTGGCCC	TTTATTGAGA	TAAGTTTTC	TGTCAAGAAA	GCAGAAACCA	2700
	TCTCATTTCT	AACACCTGTG	TTATATTCCA	TAGTATGCAT	TACTCAACAA	ACTGTTGTGC	2760
25	TATTGGATAC	TTAGTGTGTT	TCTTCACTGA	CAATACTGAA	TAAACATCTC	ACCGGAATTC	

Seq ID NO: 423 Protein sequence
Protein Accession #: NP_003005.1.

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	YEELVDVNC	AVLRFFFCAM	YAPICTLEFL	HDPIKPCKSV	QQRARDDECP	LMKMYNHSWP	120
	ESLACDELVP	YDRGVCSIFE	AIVTDLPELV	KWIDITPDMM	VQERPLDVDC	KRLSPDRCKC	180
	KKVKPTLATY	LSKNYSYVIH	AKIKAVQRSG	CNEVTTVDV	KEIFKSSSPI	PRQVPLITN	240
35	SSQCCHILP	HQDVLIMCYE	WRSRMMLLEN	CLVEKWRDQL	SKRSIQWEER	LQEQRRVTQD	300
	KKKTAGRTSR	SNPPKPKGKP	PAPKPASPKK	NIKTRSAQKR	TNPKRV		

Seq ID NO: 424 DNA sequence
Nucleic Acid Accession #: BC010423
Coding sequence: 248..1780

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45	AGCTACGGCT	GGGTGTGTAG	AACGGGGCCG	GGGCTGGGGC	TGGGTCCCCT	AGTGGAGACC	120
	CAAGTCGGAG	AGGCAAGAAC	TCTGCAGCTT	CCTGCCTTCT	GGGTCACTTC	CTTATTCAAG	180
	TCTGCAGCGG	GCTCCAGGAG	AGATCTCGGT	GGAACTTCAG	AAACGCTGGG	CAGTCTGCCT	240
	TTCAACCATG	CCCCTGTCCC	TGGGAGCCGA	GATGTGGGGG	CCTGAGGCCT	GGCTGTGCTG	300
	GCTGTACTAG	CTGGCATCAT	TTACAGGCCG	GTGCCCGCCG	GGTGAGCTGG	AGACCTCAGA	360
50	CGTGGTAAC	GTGGTCTGCG	GCCAGGACGC	AAAACCTGCC	TGCTTCTACC	GAGGGGACTC	420
	CGGCGAGCAA	GTGGGGCAAG	TGGCATGGGC	TCGGTGGGAC	GCGGGCGAAG	GCGCCCAAGG	480
	ACTAGCGCTA	CTGCACTCCA	AATACGGGCT	TCATGTGAGC	CCGGCTTACG	AGGGCCCGCT	540
	GGAGCAGCGG	CGGCCCCAC	GCAACCCCTC	GGACGGCTCA	GTGCTCCTGC	GCAACGCAGT	600
	GCAGGCGGAT	GAGGGCGAGT	ACGAGTGCCG	GGTCAGCACC	TTCCCGCCCG	GCAGCTTCCA	660
55	GGCGCGGCTG	CGGCTCCGAG	TGCTGGTGCC	TCCCTGCCCC	TCAGTGAATC	CTGGTCCAGC	720
	ACTAGAAGAG	GGCCAGGGCT	TGACCTGGC	AGCCTCCTGC	ACAGCTGAGG	GCAGCCAGC	780
	CCCCAGCGTG	ACCTGGGACA	CGGAGGTCAA	AGGCACAACG	TCCAGCCGTT	CCTTCAAGCA	840
	CTCCCGCTCT	GCTGCGGTCA	CCTCAGAGTT	CCACTTGGTG	CCTAGCCGCA	GCATGAATGG	900
60	GCAGCCACTG	ACTTGTGTGG	TGTCCCATCC	TGGCCTGCTC	CAGGACCAAA	GGATCAACCA	960
	CATCCTCCAC	GTGTCTTCCC	TTGCTGAGGC	CTCTGTGAGG	GGCCTTGAAG	ACCAAAATCT	1020
	TGTGGCATT	GGCAGAGAAG	GAGCTATGCT	CAAGTGCCCTG	AGTGAAGGGC	AGCCCCCTCC	1080
	CTCATACAAC	TGGACACGGC	TCTGCGGGCC	TCTGCGCAGT	GGGGTACGAG	TGGATGGGGA	1140
	CACTTTGGGC	TTTCCCCCAC	TGACCACTGA	GCACAGCGGC	ATCTACGTCT	GCCATGTCTG	1200
	CAATGAGTTC	TCTCAAGGG	ATTCTCAGGT	CACTGTGGAT	GTCTTGTACC	CCAGGAAGA	1260
65	CTCTGGGAAG	CAGGTGGACC	TAGTGTGAGC	CTCGGTGGTG	GTGGTGGGTG	TGATCGCCCG	1320
	ACTCTTGTTC	TGCTTCTGCG	TGGTGGTGGT	GGTGTCTCAT	TCCCGATACC	ATCGGCGCAA	1380
	GGCCAGCAG	ATGACCCAGA	AATATGAGGA	GGAGCTGACC	CTGACCAAGG	AGAACTCCAT	1440
	CCGGAGGCTG	CATTCCCATC	ACACGGACCC	CAGGAGCCAG	CCGGAGGAGA	GTGTAGGGCT	1500
	GAGAGCCGAG	GGCCACCCTG	ATAGTCTCAA	GGACAACAGT	AGCTGCTCTG	TGATGAGTGA	1560
70	AGAGCCCGAG	GGCCGCGAGT	ACTCCACGCT	GACCAACGGT	AGGGAGATAG	AAACACAGAC	1620
	TGAATGCTG	TCTCCAGGCT	CTGGCGGGGC	CGAGGAGGAG	GAAGATCAGG	ATGAAGGCAT	1680
	CAACAGGCC	ATGAACCAAT	TTGTTACAGG	GAATGGGACC	CTACGGGCCA	AGCCCAAGGG	1740
	CAATGGCATT	TACATCAATG	GGCGGGGACA	CCTGGTCTGA	CCCAGGCTTG	CCTCCCTTCC	1800
	CTAGGCTGCG	CTCCTTCTGT	TGACATGGGA	GATTTTAGCT	CATCTTGGGG	GCCTCCTTAA	1860
75	ACACCCCAT	TTCTTGCGGA	AGATGCTCCC	CATCCCACTG	ACTGCTTGAC	CTTTACCTCC	1920
	AACCTTCTG	TTTATCGGGA	GGGCTCCACC	AATGAGTCT	CTCCCAACAT	GCATGCAGGT	1980
	CAGTGTGTGT	TGCAATGTGT	GGCTGTGTGA	GTGTGTGACT	ACTGTGTGTG	TGTGGAGGGG	2040
	TGACTGTCCG	TGGAGGGGTG	ACTGTGTCCG	TGGTGTGTAT	TATGCTGTCA	TATCAGAGTC	2100
	AAAGTGAAGT	TGGTGTATGT	GCCACGGGAT	TTGAGTGTGT	GCGTGGGCAA	CACTGTGAGG	2160
80	GTTTGGCGTG	TGTGTCATGT	GGCTGTGTGT	GACCTCTGCC	TGAAAAAGCA	GGTATTTTCT	2220
	CAGACCCAG	AGCAGTATTA	ATGATGCAGA	GGTTGGAGGA	GAGAGGTGGA	GACTGTGGCT	2280
	CAGACCCAGG	TGTGCGGGCA	TAGCTGGAGC	TGGAATCTGC	CTCCGGTGTG	AGGGAACCTG	2340
	TCTCTTACCA	CTTCGGAGCC	ATGGGGGCAA	GTGTGAAGCA	GCCAGTCCCT	GGGTGAGCCA	2400
	GAGGCTTGAA	CTGTTACAGA	AGCCCTCTGC	CCTCTGGTGG	CCTCTGGGCC	TGCTGCATGT	2460
85	ACATATTTTC	TGTAAATATA	CATGCGCCGG	GAGCTTCTTG	CAGGAATACT	GCTCCGAATC	2520
	ACTTTTAATT	TTTTTCTTTT	TTTTTCTTTT	CCCTTTCCAT	TAGTTGTATT	TTTTTATTAT	2580
	TTTTATTTTT	ATTTTTTTTT	AGAGTTTGAG	TCCAGCCTGG	ACGATATAGC	CAGACCTGTG	2640

CTGTAAAAA ACCAAACCC AAAAAAAAAA AAAAAAAAAA

Seq ID NO: 425 Protein sequence

Protein Accession #: AAH10423

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QVQGVAVARV	DAGEGAQELA	LLHSKYGLHV	SPAYEGRVEQ	PPPPRNPLDG	SVLLRNAVQA	120
DEGEYECRV	TFPAGSPQAR	LRLRVLPPL	PSLNPFGPALE	EGQGLTLAAS	CTAEGSPAPS	180
VTWDTVEKGT	TSSRSFKHSR	SAAVTSEFHL	VPSRSMNGQP	LTCVVSHPL	LQDQRITHIL	240
HVSFLAEASV	RGLEDQNLWH	IGREGAMLKC	LSEQGPSPSY	NWTRLDGFLP	SGVRVDGDTL	300
GFPLLTTEHS	GIYVCHVSNE	FSSRDSQVTV	DVLDPQEDSG	KQVDLVASV	VVVGVIALL	360
FCLLVVVVVL	MSRYHRRKQA	QMTQKYEEL	TLTRENSIRR	LHSHHTDPRS	QPEESVGLRA	420
EGHPDSLKDN	SSCSVMSSEF	BGRSYSTLTT	VREIETQTEL	LSPGSGRAEE	EEDQDEGIQ	480
AMNHFVQENG	TLRAKPTGNG	IYINGRGHLV				

Seq ID NO: 426 DNA sequence

Nucleic Acid Accession #: NM_003474.2

Coding sequence: 37..3036

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CTTTTITAAA	AATGAAAGGC	TAGAAGAGCT	CAGCGGCGGC	GCGGGCCGTG	CGCGAGGGCT	180
CCGGAGCTGA	CTCGCCGAGG	CAGGAAATCC	CTCGGTCGCG	GACGCCCGGC	CCCGCTCGGC	240
GCCCCGCTGG	GATGGTGCAG	CGCTCGCCGC	CGGGCCCGAG	AGCTGCTGCA	CTGAAGGCCG	300
GCGACGATGG	CAGCGCGCCC	GCTGCCCGTG	TCCCCCGCCC	GCGCCCTCCT	GCTCGCCCTG	360
GCCGCTGCTC	TGCTCGCGCC	CTGCGAGGCC	CGAGGGGTGA	GCTTATGGAA	CGAAGGAAGA	420
GCTGATGAAG	TTGTCACTGC	CTCTGTTGCG	AGTGGGGACC	TCTGGATCCC	AGTGAAGAGC	480
TTGCACTCCA	AGAATCACTC	AGAAGTGCTG	AATATTCGAC	TACAACGGGA	AAGCAAAGAA	540
CTGATCATAA	ATCTGGAAG	AAATGAAGGT	CTCATTGCCA	GCAGTTTCAC	GGAAACCCAC	600
TATCTGCAAG	ACGGTACTGA	TGCTCTCCCTC	GCTCGAAATT	ACACGGTAAT	TCTGGGTCAC	660
TGTTACTACC	ATGGACATGT	ACGGGGATAT	TCTGATTGAG	CAGTCAGTCT	CAGCAGCTGT	720
TCTGTGCTCA	GGGGAATCTAT	TGTGTTTGAA	AATGAAAGCT	ATGCTCTAGA	ACCAATGAAA	780
AGTGCAACCA	ACAGATACAA	ACTCTTCCCA	GCGAAGAAGC	TGAAAAGCGT	CCGGGGATCA	840
TGTGGATCAC	ATCAACAACAC	ACCAAACTTC	GCTGCAAGAA	ATGTGTTTCC	ACCACTCTCT	900
CAGACATGGG	CAAGAAGGCA	TAAAAGAGAG	ACCTCAAGG	CAACTAAGTA	TGTGAGCTG	960
GTGATCGTGG	CAGACAACCG	AGAGTTTCAG	AGGCAAGGAA	AAGATCTGGA	AAAAGTTAAG	1020
CAGCGATTAA	TAGAGATTGC	TAATCAAGTT	GACAAGTTTT	ACAGACCACT	GAACATTTCG	1080
ATCGTGTGG	TAGGCGTGGA	AGTGTGGAAT	GACATGGACA	AATGCTCTGT	AAGTCAGGAC	1140
CCATTACCA	GCCTCCATGA	ATTTCTGGAC	TGGAGGAAGA	TGAAGCTTCT	ACCTCGCAA	1200
TCCCATGACA	ATGGCGACAG	TGTCACTGGG	GTTTATTTCC	AAGGGACCAC	CATCGGCATG	1260
GCCCCAATCA	TGAGCATGTG	CACGCGAGAC	CAGTCTGGGG	GAATTGTCT	GGACCATTC	1320
GACAAATCCCC	TTGGTGCAGC	CGTGACCTTG	GCACATGAGC	TGGGCCACAA	TTTCGGGATG	1380
AATCATGACA	CAGTGCAGTC	GGGCTGTAGC	TGTCAAATGG	CGGTTGAGAA	AGGAGGCTCG	1440
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GGAACAGCGT	GCAGGAGCTC	CAGCAACTCC	TGTGACCTCC	CAGAGTTCTG	CACAGGGGCC	1800
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CCAGGTGCTA	AACCTGCCCC	TGGGATCTGC	TTTGAGAGAG	TCAATTCTGC	AGGTGATCCT	1980
TATGGCAACT	GTGGCAAGT	CTCGAAGAGT	TCCTTTGCCA	AATGCGAGAT	GAGAGATGCT	2040
AAATGTGGAA	AAATCCAGTG	TCAAGGAGGT	GCCAGCCGGC	CAGTCATTGG	TACCAATGCC	2100
GTTTCCATAG	AAACAAACAT	CCCCCTGCAG	CAAGGAGGCC	GGATTCTGTG	CCGGGGGACC	2160
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GGCCCATCTC	GGCAAGCAGA	TAACCAAGGT	TTAACCATAG	GAATTCGGT	GACCATCTCT	2460
TGTCTTCTTG	CTGCCGGATT	TGTGTTTAT	CTCAAAAGGA	AGACCTTGAT	ACGACTGCTG	2520
TTTACAAATA	AGAAGACCAC	CATTGAAAAA	CTAAGGTGTG	TGCGCCCTTC	CCGGCCACCC	2580
CGTGGCTTCC	AACCTGTCCA	GGCTCACCTC	GGCCACCTTG	GAAAAGGCCT	GATGAGGAAG	2640
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CTTCTCCCC	TCCACCGGGC	CCCACGTGCA	CCTAGCGTCC	CTGCCAGACC	CCTGCCAGCC	2820
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5	TGAACCATTA	ACCAGATCTA	GTCAATCAAG	TCTGTTTACT	GCAAGGTTCA	ACTTATTAAC	4080
	AATTAGGCAG	ACTCTTTATG	CTTGCAAAAA	CTACAACCAA	TGGAATGTGA	TGTTTCATGGG	4140
	TATAGTTCAT	GTCTGCTATC	ATTATTCGTA	GATATTGGAC	AAAGAACCTT	CTCTATGGGG	4200
	CATCCTCTTT	TTCCAACCTG	GCTGCAGGAA	TCTTTAAAG	ATGCTTTTAA	CAGAGTCTGA	4260
	ACCTATTTCT	TAAACACTTG	CAACCTACCT	GTTGAGCATC	ACAGAAATGTG	ATAAGGAAAT	4320
10	CAACTTGCTT	ATCAACTTCC	TAAATATTAT	GAGATGTGGC	TTGGGCAGCA	TCCCTTGAA	4380
	CTCTTCACTC	TTCAAATGCC	TGACTAGGGA	GCCATGTTTC	ACAAGGTCTT	TAAAGTGAAT	4440
	AATGGCATGA	GAATACAAA	AATACTCAGA	TAAGGTAAAA	TGCCATGATG	CCTCTGTCTT	4500
	CTGGACTGGT	TTTCACATTA	GAAGACAATT	GACAACAGTT	ACATAATTCA	CTCTGAGTGT	4560
	TTTATGAGAA	AGCCTTCTTT	TGGGGTCAAC	AGTTTTCTTA	TGCTTTGAAA	CAGAAAAATA	4620
	TGTACCAAGA	FYCTTGNRTT	GCCTTCCAGA	AAACAAAAC	GCATTTCACT	TTCCCGGTGT	4680
15	TCCCACTGT	ATCTAGGCAG	CATAGTATTC	ATGACTATGG	ATAAACTAAA	CACGTGACAC	4740
	AAACACACAC	AAAAGGGGAC	CCAGCTCTAA	TACATTCCAA	CTCGTATAGC	ATGCATCTGT	4800
	TTATTCTATA	GTTTATAAGT	TCTTTAAAT	GTAAGGCAT	GCTGGAAAA	AATACTGCTG	4860
	AGATACATAC	AGAATTACTG	TAAGTGATTA	CACCTGGTAA	TTGTACTAAA	GCCAAACATA	4920
	TATATACTAT	TAAAAAGGTT	TACAGAAATT	TATGGTGCAT	TACGTGGGCA	TTGTCTTTTT	4980
20	AGATGCCAA	ATCCTTAGAT	CTGGCATGTT	AGCCCTTCTC	CCAATTATAA	GAGGATATGA	5040
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Seq ID NO: 427 Protein sequence
Protein Accession #: NP_003465

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30	YHGHVRGYS	SAVSLSTCSG	LRGLIVFENE	SYVLEPMKSA	TNRYKLFPK	KLKSVRGSCG	180
	SHINTPNLAA	KNVFPSPST	WARRHKRETL	KATKYVELVI	VADNREFQRQ	GKDLKVKQR	240
	LIBIANHVDK	FYRPLNIRIV	LVGVEVWDM	DKCSVSQDPF	TSLEHEFLWR	KMKLLPRKSH	300
	DNAQLVSGVY	FQGTITIGMAP	IMSMCTADQS	GGIVMDHSDN	PLGAAVTLAH	ELGHNFGMNH	360
	DTLDRGCSQ	MAVEGGGCM	NASTGYPPFM	VFSSCSRKDL	ETSLEKMGV	CLFNLPEVRE	420
35	SFGGQKGNR	FVEEGECCD	GEPEECMNR	CNATTCTLKP	DAVCAHGLCC	EDCQLKPAGT	480
	ACRDSNSCD	LPEFCTGASP	HCPANVYLHD	GHSCQDVG	CYNGICQTHE	QQCVTLWPG	540
	AKPAPGICFE	RVNSAGDPYG	NCGVKSSSF	AKCEMRDAK	GKIQCGGAS	RPVIGTNAV	600
	IETNIPLQQG	GRILRCRTHV	YLGDDMPDPG	LVLAGTKCAD	GKICLNRCQ	NISVFGVHEC	660
40	AMQCHGRGVC	NNRKNCHCEA	HWAPPFCDF	GFGGSTDSP	IROADNQLT	IGILVTILCL	720
	LAAGFVVYLK	RKTLIRLLFT	NKKTITIEKL	CVRPSRPPRG	FQPCQAHGLH	LGKGLMRKPP	780
	DSYFPKDNPR	RLQCQNVDI	SRPLNGLNVP	QPQSTQRLVP	PLHRAPRAPS	VPARPLFAKP	840
	ALRQAQGTCK	PNPPQKPLPA	DPLARTTRLT	HALARTPGQW	ETGLRLAPLR	PAPQYPHQVP	900
	RSHTTAYIK						

Seq ID NO: 428 DNA sequence
Nucleic Acid Accession #: NM_003714
Coding sequence: 135..1043

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	GAGGAGGAGG	GAAAAGGCGA	GCAAAAAGGA	AGAGTGGGAG	GAGGAGGGGA	AGCGGCGAAG	60
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	TAATACCAAG	AACCATGTGT	GCCGAGCGGC	TGGGCCAGTT	CATGACCCCTG	GCTTTGGTGT	180
55	TGGCCACCTT	TGACCCGGCG	CGGGGACCGC	ACGCCACCAA	CCCACCCGAG	GGTCCCCAAG	240
	ACAGGAGCTC	CCAGCAGAAA	GGCCGCCTGT	CCCTGCAGAA	TACAGCGGAG	ATCCAGCACT	300
	GTTTGGTCAA	CGCTGGCGAT	GTGGGGTGTG	GCGTGTTTGA	ATGTTTCGAG	AACAACCTCT	360
	GTGAGATTCT	GGGCTTACAT	GGGATTGCA	TGACTTTTCT	GCACAACGCT	GGAAAAATTG	420
	ATGCCACGGG	CAAGTCATTC	ATCAAAGACG	CCTTGAAATG	TAAGGCCAC	GCTCTGCGGC	480
60	ACAGGTTCGG	CTGCATAAGC	CGGAAGTGCC	CGGCCATCAG	GGAAATGGTG	TCCCAAGTGC	540
	AGCGGGAATG	CTACCTCAAG	CACGACCTGT	GCGCGGCTGC	CCAGGAGAAC	ACCCGGGTGA	600
	TAGTGGAGAT	GATCCATTTT	AAGGACTTGC	TGCTGCACGA	ACCTACGCTG	GACCTCGTGA	660
	ACTTGTCTGT	GACCTGTGGG	GAGGAGGTGA	AGGAGGCCAT	CACCCACAGC	GTGCAGGTTC	720
	AGTGTGAGCA	GAACTGGGGA	AGCCTGTGCT	CCATCTTGAG	CTTCTGCACC	TCGGCCATCC	780
65	AGAAGCCTCC	CACGGCGCCC	CCCGAGCGCC	AGCCCCAGGT	GGACAGAAC	AAGCTCTCCA	840
	GGGCCACACA	CGGGGAAGCA	GGACATCACC	TCCAGAGGCC	CAGCAGTAGG	GAGACTGGCC	900
	GAGGTGCCAA	GGGTGAGCGA	GGTAGCAAGA	GCCACCCAAA	CGCCCATGCC	CGAGGCAGAG	960
	TCGGGGGCTT	TGGGGCTCAG	GGACCTTCCG	GAAGCAGCGA	GTGGGAAGAC	GAACAGTCTG	1020
	AGTATTCTGA	TATCCGAGG	TGAAATGAAA	GGCCTGGCCA	CGAAATCTTT	CCTCCACGCC	1080
70	GTCCATTCTT	TTATCTATGG	ACATTCCAAA	ACATTTACCA	TTAGAGAGGG	GGGATGTAC	1140
	ACGCAGGATT	CTGTGGGGAC	TGTGAGCTTC	ATCGAGGTGT	GTGTTCCGGG	AACGGACAGG	1200
	TGAGATGGAG	ACCCCTGGGG	CCGTGGGGTC	TCAGGGGTGC	CTGGTGAATT	CTGCACTTAC	1260
	ACGTACTCAA	GGGAGCGCGC	CCGCGTTATC	CTCGTACCTT	TGTCTTCTTT	CCATCTGTGG	1320
	AGTCAGTGGG	TGTGCGCGCC	TCTGTGTGGG	GGGAGGTGAA	CCAGGGAGGG	GCAGGGCAAG	1380
75	GCAGGGCCCC	CAGAAGCTGG	CACACAGTGC	GGTGTCTGGC	CTCGCCCGCA	AGCTTCTGGT	1440
	GCAGCAGCTT	CTGGTCTGTG	CTCCGCGGAA	GTCAGGGCGG	CTGGATTCCA	GGACAGGAGT	1500
	GAATGTAAAA	ATAAATATCG	CTTAGAATGC	AGGAGAAGGG	TGGAGAGGAG	GCAGGGGCGG	1560
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	CTCTTGGCGA	GGGTGGAGGG	AGGAGTGTCA	TTTCTATGTG	TAATTTCTGA	GCCATTGTAC	1680
80	TGTCTGGGCT	GGGGGGGACA	CTGTCCAAGG	GAGTGGCCCC	TATGAGTTTA	TATTTTAAAC	1740
	ACTGCTTCAA	ATCTCGATT	CACCTTTTTT	ATTTATCCAG	TTATATCTAC	ATATCTGTCA	1800
	TCTAAATAAA	TGGCTTTCAA	ACAAAGCAAC	TGGGTCATTA	AAACCAGCTC	AAAGGGGGTT	1860
	TAAAAAATAA	AAACACAGCC	CATCCTTTGA	GGCTGATTTT	TCTTTTTTTT	AAGTTCTATT	1920
	TAAAAAGCTA	TCAAACAGCG	ACATAGCCAT	ACATCTGACT	GCCTGACATG	GACTCCTGCC	1980
85	CACCTGGGGG	AAACCTTATA	CCCAGAGGAA	AATACACACC	TGGGGAGTAC	ATTTGACAAA	2040
	TTTCCCTTAG	GATTTCGTTA	TCTCACCTTG	ACCCTCAGCC	AAGATTGGTA	AAGCTGCGTC	2100
	CTGGCGATTG	CAGGAGACCC	AGCTGGAAAC	CTGGCTTCTC	CATGTGAGGG	GATGGGAAAG	2160
	GAAAGAAGAG	AATGAAGACT	ACTTAGTAAT	TCCCATCAGG	AAATGCTGAC	CTTTTACATA	2220

AAATCAAGGA GACTGCTGAA AATCTCTAAG GGACAGGATT TTCCAGATCC TAATTGGAAG 2280
 TTTAGCAATA AGGAGAGGAG TCCAAGGGGA CAAATAAAGG CAGAGAGAGA GAGAGAGAGA 2340
 GGGAGAGGAA GAAAAGAGAG AGAGAAAAGA GCCTCGTGCC

5 Seq ID NO: 429 Protein sequence
 Protein Accession #: NP_003705

10 1 11 21 31 41 51
 MCAERLQQFM TLALVLATFD PARGTDATNP PEGPQDRSSQ QKGRLSLQNT AEIQHCLVNA 60
 GDVGGCVFEC FENNSCIEIRG LHGICMTFLH NAGKFDAQGK SPFKDALKCK AHALRHRFGC 120
 ISRKCPAIRE MVSQIQRECY LKHDLCAAQ ENTRVIVEMI HFQDLLLHEP YVDLVNLLLT 180
 CGEEVKRAIT HSVQVQCQN WSLCSILSF CTSAIQKPPT APPERQPOVD RTKLSRAHHG 240
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 RR

Seq ID NO: 430 DNA sequence
 Nucleic Acid Accession #: NM_005940
 Coding sequence: 23..1489

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 25 TCTGCCGCGG GACGTCCACC ACCTCCATGC CGAGAGGAGG GGGCCACAGC CCTGGCATGC 180
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 CAGCCTCAGG CCTCCCCGCT GTGGCGTGCC CGACCCATCT GATGGGCTGA GTGCCCGCAA 300
 CCGACAGAAG AGGTTCTGTC TTTCTGGCGG GCGCTGGGAG AAGACGGACC TCACCTACAG 360
 GATCCTTCGG TCCCATGGG AGTTGGTGCA GGAGCAGGTG CGGCAGACGA TGGCAGAGGC 420
 30 CCTAAAGGTA TGGAGCGATG TGACGCCACT CACCTTTACT GAGGTGCACG AGGGCCGTGC 480
 TGACATCATG ATCGACTTCG CCAGGTACTG GCATGGGGAC GACCTGCCGT TTGATGGGCC 540
 TGGGGGCATC CTGGCCCATG CCTCTTCCC CAAGACTCAC CGAGAAGGGG ATGTCCACTT 600
 CGACTATGAT GAGACCTGGA CTATCGGGGA TGACCAGGGC ACAGACCTGC TGCAGGTGGC 660
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 35 GTCCGCTTTC TACACCTTTC GCTACCCACT GAGTCTCAGC CCAGATGACT GCAGGGCGT 780
 TCACACCTTA TATGGCCAGC CCTGGCCAC TGTCACTTCC AGGACCCAG CCCTGGGCCC 840
 CCAGGCTGGG ATAGACACCA ATGAGATTGC ACCGCTGGAG CCAGACGCCC CGCCAGATGC 900
 CTGTAGGGCC TCCTTTGAGC CGGCTCTCAC CATCCGAGGC GAGCTCTTTT TCTTCAAAGC 960
 GGGCTTTGTG TGGGCGCTCC GTGGGGGCCA GCTGCAGCCC GGCTACCCAG CATTTGGCCTC 1020
 40 TCGCCACTGG CAGGGACTGC CCAGCCCTGT GGACGCTGCC TTCGAGGATG CCCAGGGCCA 1080
 CATTTGGTTC TTCCAAGGTG CTCAGTACTG GGTGTACGAC GGTGAAAAGC CAGTCTCTGG 1140
 CCCCACACCC CTCACCGAGC TGGGCTGGT GAGGTTCCCG GTCCATGCTG CCTTGGTCTG 1200
 GGGTCCCGAG AAGAACAAGA TCTACTTCTT CCGAGGCAGG GACTACTGGC GTTTCACCC 1260
 CAGCACCCGG COTGTAGACA GTCCCGTGCC CCGCAGGGCC ACTGACTGGA GAGGGGTGCC 1320
 45 CTCTGAGATC GACGTGCTT TCCAGGATGC TGATGGCTAT GCCTACTTCC TGGCGGCGCG 1380
 CCTTACTTGG AAGTTTGACC CTGTGAAGGT GAAGGCTCTG GAAGGCTTCC CCGTCTCTGT 1440
 GGGTCTGTAC TTCTTTGAGC GTGCCGAGCC TGCCCAACT TTCTCTGAGC CATGGCTTGG 1500
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 50 GGTGGGGTAC AACCAAGGTG ACAACTGCCG GGAGGGCCAC GCAGGTCTGT GTACACTGCC 1680
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 GGGACCCGCT ATGCAAGTCC TGGCAAACCT GGCTGCCCTG TCTCATCCCT GTCCCTCAGG 1800
 GTAGACCAT GGCAGGACTG GGGGAACCTG AGTGTCTTGT CTGTATCCCT GTTGTGAGGT 1860
 TCCTTCCAGG GGCTGGCACT GAAGCAAGGG TGCTGGGGCC CCATGGCCTT CAGCCCTGGC 1920
 55 TGAGCAACTG GGCTGTAGGG CAGGGCCACT TCCTGAGGTC AGGTCTTGGT AGGTGCCTGC 1980
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 GTTCACAGTC AAATGGGAG GGGTATTCTT CATGCAGGAG ACCCCAGGCC CTGGAGGCTG 2100
 CAACATACCT CAATCTGTGC CCAGGCCGGA TCCTCCTGAA GCCCTTTTCG CAGCACTGCT 2160
 60 ATCCTCCAAA GCCATTGTAA ATGTGTGTAC AGTGTGTATA AACCTTCTTC TTCTTTTTTT 2220
 TTTTAAACT GAGGATTGTC ATTAACACA GTTGTTTTCT

Seq ID NO: 431 Protein sequence
 Protein Accession #: NP_005931

65 1 11 21 31 41 51
 MAPAAWLRS AARALLPPLM LLLLQPPPLL ARALPPDVH LHAERRGPQP WHAALPSSPA 60
 PAPATQEAPR PASSLRPPRC GVPDPDGLS ARNRQKRFVL SGGRWKTDL TYRILRFPWQ 120
 70 LVQEQVQRTM AEALKVWSDV TPLTFTEVHE GRADIMIDFA RYWHGDDLFP DPGGILAHA 180
 FFPKTHREGD VHFYDETWT IGDDQGTDL QVAHEFGHV LGLQHTTAAK ALMSAFYTFR 240
 YPLSLSPDDC RGVQHLYGQP WPTVTSRTPA LGPQAGIDTN EIAPLEPDAP PDACEASFDA 300
 VSTIRGELFF FKAGFVWRLR GGQLQPGYFA LASRHWGLP SPVDAAFEDA QGHIWFFQGA 360
 QYVWYDGEKP VLGPAPLTEL GLVRFPVHAA LVWGPEKNKI YFPRGRDYWR FHPSTRRVDS 420
 75 PVPRATDWR GVPSEIDAP QDADGYAYFL RGRLYWKFDP VKVKALEGGP RLVGPDFFGC 480
 AEPANTFL

Seq ID NO: 432 DNA sequence
 Nucleic Acid Accession #: NM_024022
 Coding sequence: 202..1563

80 1 11 21 31 41 51
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 GGAAGGGGCT GTGTTATAGG GAAGCCAGTA ACACGTGGCC CTACTATCTC TTCCGTGGTG 120
 85 CATCTACAT TTTTGGGACT CGGGAATTAT GAGGTAGAGG TGGAGGCGGA GCCGGATGTC 180
 AGAGGTCCTG AATAGTCAAC CATGGGGGAA AATGATCCGC CTGTGTTGA AGCCCCCTTC 240
 TCATTCCGAT CGCTTTTTGG CCTTGATGAT TTGAAAATAA GTCCTGTGTC ACCAGATGCA 300

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TCAGGGAAGT ACAGATGTGC CTCATCTTTT AAGTGTATCG AGCTGATAGC TCGATGTGAC 480
GGAGTCTCGG ATTGCAAGA CGGGGAGGAC GAGTACCGCT GTGTCCGGGT GGGTGGTCAG 540
AATGCGGTGC TCCAGGTGTT CACAGCTGCT TCGTGGAGA CCAATGTGCTC CGATGACTGG 600
AAGGGTCACT AGCAAAATGT TGCCTGTGCC CAACTGGGTT TCCCAAGCTA TGTGAGTTCA 660
GATAACCTCA GAGTGAAGTC GCTGGAGGGG CAGTTCCGGG AGGAGTTTGT GTCCATCGAT 720
CACCTCTTGC CAGATGACAA GGTGACTGCA TTACACCACT CAGTATATGT GAGGGAGGGA 780
TGTGCCTCTG GCCAGTGGT TACCTTGCAG TGCACAGCCT GTGGTCATAG AAGGGGCTAC 840
AGCTCACGCA TCGTGGGTGG AAACATGTCC TTGCTCTGCG AGTGGCCCTG GCAGGCCAGC 900
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GACAGCTGCC AGGGGGACAG CGGGGGGCC CTGGTGTGTC AAGAGAGGAG GCTGTGGAAG 1440
TTAGTGGGAG CGACAGCTT TGGCATCGGC TGCGCAGAGG TGAACAAGCC TGGGGTGTAC 1500
ACCCGTGTCA CCTCTTCTCT GGACTGGATC CACGAGCAGA TGGAGAGAGA CCTAAAAACC 1560
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TCCCCGTGAC TCCCTGTAG GAACCTGCAC ACGAGCAGAC ACCCTTGAG CTCTGAGTTC 1680
CGGCACCACT AGCAGGCCCG AAAGAGGCAC CCTTCCATCT GATTCCAGCA CAACCTTCAA 1740
GCTGCTTTT TTTTGTGTT TTTTGTAGG GTAGTCTGCG TCTGTTGCC AGGCTGGAGT 1800
GCAGTGGCGA AATCCCTGCT CACTGCAGCC TCCGCTTCCC TGGTTCAGC GATTCTCTTG 1860
CCTCAGCTTC CCCAGTAGCT GGGACCAAG GTGCCGCCA CCACACCAA CTAATTTTGT 1920
TATTTTGTAG AGAGACAGG TTTACCATG TTGCCAGGC TGCTCTCAA CCCCTGACCT 1980
CAAATGATGT GCCTGCTTCA GCCTCCACA GTGCTGGGAT TACAGGCATG GGCACCACG 2040
CCTAGCTTCA CGCTCCTTTC TGATCTTAC TAAGAACAAA AGAAGCAGCA ACTTGCAAG 2100
GCGGCTTTT CCACTGTGCC ATCTGGTTT CTCTCCAGG GTCTTGCAA ATTCCTGAGC 2160
AGATAAGCAG TTATGTGACC TCACGTGCAA AGCCACCAAC AGCCACTCAG AAAAGACGCA 2220
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AACCACCCCT TTCTACTTCC AAGACTTATT TTCACATGT GGGAGGTTAA TCTAGGAATG 2340
ACTCGTTTAA GGCCTATTTT CATGATTCTT TTGTAGCATT TGGTGCTTGA CGTATTATTG 2400
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Seq ID NO: 433 Protein sequence
Protein Accession #: NP_076927

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MGENDPPAVE APFSFRSLFG LDDLKISPVA PDADAVAAQI LSLPLKFFP IIVIGIILI 60
LALAIGLGH FDCSKYRCR SSFKCIELIA RCDGVSDCKD GEDEYRCVRV GGQNAVILQVF 120
TAASWKMTCS DWWKGYANV ACAQLGFPSY VSSDNLRVSS LEGOFREEFV SIDHLLPDDK 180
VTALHHSVYV REGCAGSHVU TLQCTACGHR RGYSSRIVGG NMSLLSQWPW QASLQFQGYH 240
LCGGSVITPL WIITAHCYV DLYLPSKWTI QVGLVSLLDN PAPSHLVEKI VYHSKYKPKR 300
LGNDIALMKL AGPLTFNEMI QPVCLEPNEE NFPDGKVCWT SGWGATEDGG DASPLVNHA 360
VPLISNKICN HRDVYGGIIS PSMCLAGYLT GGVSDSCQGS GGLVLCQERR LWKLVGATSF 420
GIGCAEVNKP GYVTRVTSFL DWIHEQMERD LKT
  
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Seq ID NO: 434 DNA sequence
Nucleic Acid Accession #: NM_000493.2
Coding sequence: 97..2139

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ACAGGCATAA AAGGCCCACT ACCCAACACC AAGACACAGT TCTTCATTCC CTACACCATA 240
AAGAGTAAAG GTATAGCAGT AAGAGGAGAG CAAGGTACTC CTGGTCCACC AGGCCCTGCT 300
GGACCTCGAG GGCACCCAGG TCCTTCTGGA CCACCAAGAA AACCAGGCTA CGGAAGTCTC 360
GGACTCCAAG GAGAGCCAGG GTTGCCAGGA CCACCGGAC CATCAGCTGT AGGGAACCA 420
GGTGTGCCAG GACTCCCAGG AAAACCAGGA GAGAGAGGAC CATATGGACC AAAAGGAGAT 480
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GCTGGAGCCC CAGGCCAGCC AGGGATTCCA GGAACAAAAG GTCTCCCTGG GGCTCCAGGA 960
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GAAAGAGGAC CTGCTGGCCT TCCTGGGGGT CCAGGTGCCA AAGGGGAACA AGGGCCAGCA 1080
GGTCTTCTGT GGAAGCCAGG TCTGACTGGA CCCCTGGGA ATATGGGACC CCAAGGACCA 1140
AAAGGCATCC CGGGTAGCCA TGGTCTCCCA GGGCCTAAAG GTGAGACAGG GCCAGCTGGG 1200
CCTGACAGAT ACCCTGGGCC TAAGGGTGAA AGGGGTTCCT CTGGGTGAGA TGGAAAAACA 1260
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CCAGGAAGTC CGGTCTCTCC TGGCCAGCT GGCATAGCAA CTAAGGGCCT CAATGGACCC 1560
ACCGGCCAC CAGGCCCTCC AGTCCAAAGA GGCCACTCTG GAGAGCCTGG TCTTCCAGG 1620
CCCCCTGGGC CTCCAGGCC ACCAGGTCAA GCAGTCATGC CTGAGGGTTT TATAAGGCA 1680
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CATGTTTGGG TAGGCTGTGA TAAGAATGGC ACCCTGTAA TGTACACCTA TGATGAATAC 1980
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TGCTCACTT ATTAAGCAC AAAATGTTT ACCTACTCCT TATTACGAC ACAATAAAAT 3180
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Seq ID NO: 435 Protein sequence
Protein Accession #: NP_000484.2

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TPGPPGPAGP RGHPPGSPGP GKPGYGSPL QGEPGLPGPP GPSAVGKPGV PGLPGKPER 120
GPYGPKGDVG PAGLPGRGP PGPPGIPGPA GISVPGKPGQ QGPTGAPGPR GPPGEGKAGP 180
VPGMNGQKGE MGVGAPGRGP ERGLPGPQGP TGPSGPPGVG XRGENGVPQG PGIKGDRGFP 240
GEMGPPIPPG PQGPPGERGP EGIGKPGAAG APGQPGIPGT KGLPGAPGIA GPPGPPFGK 300
PGLPGLKGER GPAGLPGGPG AKGEQGPAGL PGKPLGTGPP GNMGPQGPKG IPGSHGLPGP 360
KGETGPAGPA GYPGAKGERG SPGSDGKPGY PGKPLGDGPK GNPGLPGPKG DPGVGGPPGL 420
PGPVGPAGAK GMPGHNGEAG PRGAPGIPGT RGPPIPPGIP GFPGSKGDPG SPGPPGPAGI 480
ATKGLNGPTG PPGPPGPRGH SGEPGLPGPP GPPGPPGQAV MPEGFIKAGQ RPSLSGTPLV 540
SANGVVTGMP VSAFTVILSK AYPAGTPIPI FDKILYNRQO HYDPRTGIFT CQIPGIYFYS 600
YHVHVKGTHV WVGLYKNGTP VMYTYDEYTK GYLDQAGSSA IIDLTENDQV WLQLPNAESN 660
GLYSSEYVHS SFGGFLVAPM
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Seq ID NO: 436 DNA sequence
Nucleic Acid Accession #: XM_062811
Coding sequence: 1..888

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GCGCGCCTGG ACCAGGGCGG CTGCGACAAT GACCGCCAGC AGGGCGCTGG CGAGCCTGGC 300
CGGGCGGACA AAGACGGCCC CGACGGCTCG GCAGTGCCCA TCTACGTGCC GTTCCTCATT 360
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CAGTATCTGC ATCCCCCATA CGTGGGGTAC ACGGTGCAGC ACGACTCTGT GCCCATGACA 780
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Seq ID NO: 437 Protein sequence
Protein Accession #: XP_062811

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| | | | |
MWGARRSSVS SSWNAASLLQ LLLAALLAAG ARASGEYCHG WLDAQGVWRI GFQCPERFDG 60
GDATICCGSC ALRYCCSSAE ARLDQGGCDN DRQQAGGEPG RADKDGPDGS AVPIYVPLFI 120
VGSVVFVPII LGSIVAACCC RCLRPKQDPQ QSRAPGGNRL METIPMIPSA STSRGSSSRQ 180
SSTAASSSSS ANSGARAPPT RSQTNCLPE GTMNVVIVNM PTNFSVLNQC QATQIVPHQG 240
QYLHPYVGY TVQHDSVPMT AVPPFMDGLQ PGYRQIQSPF PHTNSEQKMY PAVTV
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Seq ID NO: 438 DNA sequence
Nucleic Acid Accession #: NM_004004.1
Coding sequence: 1..681

80
85

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1 11 21 31 41 51
| | | | |
ATGGATTGGG GCACGCTGCA GACGATCCTG GGGGGTGTGA ACAAACTC CACCAGCATT 60
GGAAAGATCT GGCTCACCGT CCTCTTCATT TTTGCGATTA TGATCCTCGT TGTGGCTGCA 120
AAGGAGGTGT GGGGAGATGA GCAGGCCGAC TTTGTCTGCA ACACCTGCA GCCAGGCTGC 180
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AAGAACGTGT GCTACGATCA CTACTTCCCC ATCTCCACCA TCCGGCTATG GGCCCTGCAG 240
 CTGATCTTCG TGTCCAGCCC AGCGCTCCTA GTGGCCATGC ACCTGGCCTA CCGGAGACAT 300
 GAGAAGAAGA GGAAGTTCAT CAAGGGGGAG ATAAAGAGTG AATTAAAGGA CATCGAGGAG 360
 ATCAAAACCC AGAAGGTCCG CATCGAAGGC TCCCTGTGGT GGACCTACAC AAGCAGCATC 420
 TTCTTCCGGG TCATCTTCGA AGCCGCTTC ATGTACGTCT TCTATGTCAT GTACGACGGC 480
 TTCTCCATGC AGCGGCTGGT GAAGTGCAAC GCCTGGCCTT GTCCCAACAC TGTGGACTGC 540
 TTTGTGTCCC GGCCACGGGA GAAGACTGTC TTCACAGTGT TCATGATGTC AGTGTCTGGA 600
 ATTTGCATCC TGCTGAATGT CACTGAATTG TGTATTTCG TAATTAGATA TTGTTCTGGG 660
 AAGTCAAAAA AGCCAGTTTA A

Seq ID NO: 439 Protein sequence
 Protein Accession #: NP_003995.1

1 11 21 31 41 51
 MDWGTLTQTL GGVNKHSTSI GKIWLTVLFI PRIMILVVAA KEVWGDEQAD FVCNTLQPGC 60
 KNVCYDHYFP ISHIRLWALQ LIFVSSPALL VAMHVAYRRH EKRRKFIKGE IKSEPKDIEE 120
 IKTKQVRIEG SLWWTYTSSI PFRVIFEAAP MYVFVVMYDG FSMQRLVKCN AWPCCPNTVDC 180
 FVSRPTEKTV FTFVMIASVG ICILLNVTEL CYLLIRYCSG KSKKPV

Seq ID NO: 440 DNA sequence
 Nucleic Acid Accession #: XM_061091.1
 Coding sequence: 1..2481

1 11 21 31 41 51
 ATGCCAAATA CTTCAGGAAC AACCAGGATT GAAATTGGGC TTCTCCAAGA GCCGCCCGGG 60
 CACCGAGCGC TGGTGCCTCG TCTCTTCCG GTGAGTCCCA GCCCCGAGTT GGCTCTGGCG 120
 CCCGGGTACC CGCCAGTGCC GGCTGCCGAT GACCGATTCA CGCTCCCGAT GATTGGAGGT 180
 CAGATGCATG GTGAGAAGGT AGATCTCTGG AGCCTTGGTG TTCTTTGCTA TGAATTTTAA 240
 GTTGGGAAGC CTCCTTTTGA GGCAACGAA GTCCATGTAA GCAAGAAAC CATCGGGAAG 300
 ATTTTCAGCTG CCAGCAAAAT GATGTGGTGC TCGGCTGCAG TGGACATCAT GTTCTGTGTA 360
 GATGGGTCTA ACAGCGTCCG GAAAGGGAGC TTTGAAAGGT CCAAGCACTT TGCCATCACA 420
 GTCTGTGACG GTCTGGACAT CAGCCCCGAG AGGGTCAGAG TGGGAGCATT CCAGTTCAGT 480
 TCCACTCCTC ATCTGGAATT CCCCTTGGAT TCATTTTCAA CCCAACAGGA AGTGAAGGCA 540
 AGAATCAAGA GGATGTTTTT CAAAGGAGGG CGCACGGAGA CGGAACCTGC TCTGAAATAC 600
 CTTCTGCACA GAGGGTTGCC TGGAGGCAGA AATGCTTCTG TGCCCCAGAT CCTCATCATC 660
 GTCACTGATG GGAAGTCCCA GGGGGATGTG GCACTGCCAT CCAAGCAGCT GAAGGAAAGG 720
 GGTGTCACTG TGTGTGCTGT GGGGGTCAGG TTTCAGAGGT GGGAGGAGCT GCATGCACTG 780
 GCCAGCGAGC CTAGAGGGCA CACGCTGCTG TTGGCTGAGC AGGTGGAGGA TGCCACCAAC 840
 GGCTCTTTCA GCACCTTCAG CAGCTCGGCC ATCTGCTCCA GCGCCACGCC AGCTGGGAGC 900
 CCCGAGCTTG TCTTCATGGA GCGGTTAATG GGCATCTCTC TGATAGGCCC CTGTGACTCG 960
 CAGCCCTGCG AGAATGGTGG CAGATGTGTT CCAGAAGGAC TGGACGGCTA CCAGTGCTCT 1020
 TGCCCGCTGG CCTTTGGAGG GGAGGCTAAC TGTGCCCTGA AGCTGAGCCT GGAATGCAGG 1080
 GTGACCTCCC TCTTCTGCTT GGACAGCTCT GCGGGCACCA CTCTGGACGG CTCTCTGGCG 1140
 GCCAAAGTCT TCGTGAAGCG GTTTGTGCGG GCGGTGCTGA GCGAGGACTC TCGGGCCCGA 1200
 GTGGGTGTGG CCACATACAG CAGGGAGCTG CTGGTGGCGG TGCCGTGTGG GGAGTACCAG 1260
 GATGTGCTCG ACCTGGTCTG GAGCCTCGAT GGCATTCCCT TCCGTGGTGG CCCCACCTCG 1320
 ACGGCGAGTG CCTTGCCTGA GCGGCGAGAG CGTGGCTTCG GGAGCGCCAC CAGGACAGGC 1380
 CAGGACCGGC CACGTAGAGT GGTGGTTTTG CTCACTGAGT CACACTCCGA GGATGAGGTT 1440
 GCGGGCCAGC CGCGTCAAGC AAGGGCGCGA GAGCTGCTCC TGCTGGGTGT AGGCAGTGAG 1500
 GCGGTGCGGG CAGAGTACCA GGAGATCACA GGCAGCCCAA AGCATGTGAT GGTCTACTCG 1560
 GATCCTCAGG ATCTGTTCAA CCAAATCCCT GAGCTGCAGG GGAAGCTGTG CAGCCGGCAG 1620
 CGGCCAGGGT GCGCGACACA AGCCCTGGAC CTGCTCTTCA TGTGGGACAC CTCTGCCTCA 1680
 GTAGGGCCCG AGAATTTTGC TCAGATGCAG AGCTTTGTGA GAAGCTGTGC CCTCCAGTTT 1740
 GAGGTGAACC CTGACGTGAC ACAGGTCCGC CTGGTGGTGT ATGGCAGCCA GGTGCAGACT 1800
 GCCTTCGGGC TGGACACCAA ACCCAACCGG GCTGCGATGC TGCGGGCCAT TAGCCAGGCC 1860
 CCCTACCTAG TTGGGGTGGG CCGGCTGGT GTCCCAAG CTGTGGTGGT GCTCACAGGC 1920
 ATGACCGTCC AGAGGGGTGC CCGGCTGGT GTCCCAAG CTGTGGTGGT GCTCACAGGC 1980
 GGGAGAGGCG CAGAGGATGC AGCCGTTCCT GCCCAGAAAG TGAGGAACAA TGGCATCTCT 2040
 GTCTTGGTCC TGCGCGTGGG GCCTGCTCTA AGTGAGGGTC TGCGGAGGCT TGCAGGTTCC 2100
 CCGGATTCCC TGATCCACGT GGCAGCTTAC GCGACCTGC GGTACCACCA GGAGTGTCTC 2160
 ATTGAGTGGC TGTGTGGAGA AGCCAAGCAG CCAGTCAACC TCTGCAAAAC CAGCCCGTGC 2220
 ATGAATGAGG GCAGCTGCGT CCTGCAGAAAT GGGAGCTACC GCTGCAAGTG TCGGGATGGC 2280
 TGGGAGGGCC CCCACTGCGA GAACCGTGAG TGGAGCTCTT GCTCTGTATG TGTGAGCCAG 2340
 GGATGGATTG TTGAGACGCC CCTGAGGCAC ATGGCTCCCG TGCAAGAGGG CAGCAGCGGT 2400
 ACCCTCCCA GCAACTACAG AGAAGGCTCG GGCATGAAA TGGTGCCTAC CTTCTGGAAT 2460
 GTCTGTGCCC CAGGTCTCTTA G

Seq ID NO: 441 Protein sequence
 Protein Accession #: XP_061091.1

1 11 21 31 41 51
 MPNTSGTTRI EIWLLQEPFG HRALVAALLP VSPSPALALA PGYPPVPAAD DRFTLPMIGG 60
 QMHGKVDLW SLGLVLCYEFV VGKPPFEANE VHVSKETIGK ISAASKMMWC SAAVDIMPLL 120
 DGSNSVKGKS FERSKHFAIT VCDGLDISPE RVRVGAFQFS STPHLEFPLD SFSTQOEKVA 180
 RIKRMVFHGG RTETELALKY LLHRGLPGGR NASVPQILII VTDGKSQGDV ALPSKQLKER 240
 GVTTFVAVGVR FPRWEELHAL ASEPRGQHLV LAEQVEDATN GLFSTLSSSA ICSSATPAGS 300
 PELVFMERLM GISLIGPCDS QPCQNGGTCV PEGLDGYQCL CPLAFGGEAN CALKLSLECR 360
 DVLLFLDLSS AGTTLDFGLR AKVFKRFVR AVLSEDSRAR VGVATYSREL LVAVPVGEYQ 420
 VDPDLVWSLD GIPFRGGPTL TGSALRQAAE RFGSATRTG QDRPRRVVVL LTESHSEDEV 480
 AGPARHARAR ELLLLGVGSE AVRAELEBIT GSPKHMVMS DPQDLFNQIP ELQGLKCSRQ 540
 RFGCRTQALD LVFMLDTSAS VGPFNAQMQ SFVRSALQF EVNPDVTQVG LVVYGSQVQT 600
 AFGLDTKPRI AMLRAISQA PYLGGVGSAG TALLHIYDKV MTVQRGARPG VPKAVVVLTG 660
 GRGAEDAAVP AQKLRRNGIS VLVVGVGPVL SEGLRLRAGP RDSLHVAAY ADLRVHQDVL 720

IEWLCCGEARQ PVNLCKPSPC MNEGSCVLQN GSYRCKCRDG WEGPHCENRE WSSCSVCVSQ 780
 GWILETPLRH MAPVQEGSSR TPPSNYREGL GTEMVPTFWN VCAPGP

Seq ID NO: 442 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 1..2424

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    TCTCTCCCTC TCCAGGAAGT CCATGTAAGC AAAGAAACCA TCGGAAGAT TTCAGCTGCC 120
    AGCAAAATGA TGTGTGTCTC GGCTGCAGTG GACATCATGT TTCTGTAGA TGGGTCTAAC 180
    AGCGTCGGGA AAGGGAGCTT TGAAGGTCC AAGCACTTG CCATCACAGT CTGTGACGGT 240
    CTGGACATCA GCCCGAGAGG GGTGAGAGTG GGAGCATTCC AGTTCACTTC CACTCCTCAT 300
15  CTGGAATTCC CTTTGGATTG ATTTTCAACC CAACAGGAAG TGAAGGCAAG AATCAAGAGG 360
    ATGTTTTCCT AAGGAGGGCG CACGGAGACG GAACCTGCTC TGAATACCT TCTGCACAGA 420
    GGGTTGCCTG GAGGCAGAAA TGCTTCTGTG CCCAGATCC TCAATCATCGT CACTGATGGG 480
    AAGTCCCAGG GGGATGTGGC ACTGCCATCC AAGCAGCTGA AGGAAAGGGG TGTCATGTG 540
    TTTGCTGTGG GGGTCAGGTT TCCAGGTGG GAGGAGCTGC ATGCACTGGC CAGCGAGCCT 600
20  AGAGGGCAGC ACGTCTGTTT GGCTGAGCAG GTGGAGGATG CCACCAACGG CCTCTTCAGC 660
    ACCCTCAGCA GCTCGGCCAT CTGCTCCAGC GCCACGCCAG ACTGCAGGGT CGAGGCTCAC 720
    CCTGTGAGC ACAGGACGCT GGAGATGGTC CGGGAGTTGG CTGGCAATGC CCCATGCTGG 780
    AGAGGATCCG GCGGACGCTT TGCGGTGCTG GCTGCACACT GTCCCTTCTA CAGCTGGAAG 840
    AGAGTGTTC TAACCCACCC TGCCACCTGC TACAGGACCA CCTGCCCAGG CCCTGTGAC 900
25  TCGCAGCCCT GCCAGAATGG AGGCACATGT GTTCCAGAAG GACTGGACGG CTACCACTGC 960
    CTCTGCCCGC TGGCCTTTGG AGGGGAGGCT AACTGTGCCG TGAAGCTGAG CCTGGAATGC 1020
    AGGGTCGACC TCCTCTTCTT GCTGGACAGC TCTGCGGGCA CCACTCTGGA CGGCTTCTCTG 1080
    CGGGCCAAAG TCTTCTGTAA GCGGTTTGTG CGGGCCGTGC TGAGCGAGGA CTCTCGGGCC 1140
    CGAGTGGGTG TGGCCACATA CAGCAGGGAG CTGCTGGTGG CGGTGCCCTGT GGGGGAGTAC 1200
30  CAGGATGTGC CTGACCTGGT CTGGAGCCTC GATGGCATTC CCTTCGCTGG TGGCCCCACC 1260
    CTGACGGGCA GTGCTTGTGC GCAGGCGGCA GAGCGTGGCT TCGGGAGCGC CACCAGGACA 1320
    GGCCAGGACC GGCACAGTAT AGTGGTGGTT TTGCTCACTG AGTCACACTC CGAGGATGAG 1380
    GTTGCGGGCC CAGCGCGTCA CGCAAGGGCG CGAGAGCTGC TCCTGCTGGG TGTAGGCAGT 1440
    GAGGCGGTGC GGGCAGAGCT GGAGGAGATC ACAGGCAGCC CAAAGCATGT GATGGTCTAC 1500
35  TCGGATCCTC AGGATCTGTT CAACCAATC CTTGAGCTGC AGGGGAAGCT GTGCAGCCGG 1560
    CAGCGGCCAG GGTGCCGGAC ACAAGCCCTG GACCTCGTCT TCATGTTGGA CACCTCTGCC 1620
    TCAGTAGGGC CCGAGAATTT TGCTCAGATG CAGAGCTTTG TGAGAAGCTG TGCCCTCCAG 1680
    TTTGAGGTGA ACCCTGACGT GACACAGGTC GGCCTGGTGG TGTATGGCAG CCAGGTGCAG 1740
    ACTGCCCTTC GGCTGGACAC CAAACCCACC CGGGCTGCGA TGCTGCGGGC CATTAGCCAG 1800
40  GCGCCCTACC TAGGTGGGGT GGGCTCAGCC GGCACCGCCC TGCTGCACAT CTATGACAAA 1860
    GTGATGACCG TCCAGAGGGT TGCCCGGCCT GGTGTCCCA AAGCTGTGGT GGTGCTCACA 1920
    GCGGGGAGAG GCGCAGAGGA TGCAGCCGTT CCTGCCCAGA AGCTGAGGAA CAATGGCATC 1980
    TCTGTCTTGG TCGTGGGCGT GGGGCTGTCT CTAAGTGAGG GTCTGCGGAG GCTTGCAGGT 2040
45  CCCCAGGATT CCCTGATCCA CGTGGCAGCT TACGCGACCT TGCGGTACCA CCAGGACGTG 2100
    CTCATTGAGT GGCTGTGTGG AGAAGCCAAG CAGCCAGTCA ACCTCTGCAA ACCCAGCCCG 2160
    TGCATGAATG AGGGCAGCTG CGTCTGCAG AATGGGAGCT ACCGCTGCAA GTGTCGGGAT 2220
    GGCTGGGAGG GCCCCACTGC CGAGAACCGT GAGTGGAGCT CTTGCTCTGT ATGTGTGAGC 2280
    CAGGGATGGA TTCTTGAAGC GCCCCTGAGG CACATGGCTC CCGTGCAGGA GGCAGCAGC 2340
50  CGTACCCTCT CCAGCAACTA CAGAGAAGGC CTGGGCATG AAATGGTGCC TACCTTCTGG 2400
    AATGTCTGTG CCCCAGGTCC TTAG
  
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Seq ID NO: 443 Protein sequence

Protein Accession #: Eos sequence

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55  1      11      21      31      41      51
    MPPFLLEAV CVFLFSRVPP SLPLQEVHVS KETIGKISAA SKMMWCSAAV DIMFLLDGSN 60
    SVKGGSFERS KHFAITVCDG LDISPERVRV GAFQFSSTPH LEFPLDSFST QQEVKARIKR 120
    MVFKGGRTEI ELALKYLHR GLPGGRNASV PQILIIIVTDG KSGQDVALPS KQLKERVTV 180
60  FAVGVPRPRW EELHALASEP RGQHVLLAEQ VEDATNGLFS TLSSSAICSS ATPDCRVEAH 240
    PCEHRTLEMV REFAGNAPCW RGSRRTLAVL AAHCFFYSWK RVFLTHPATC YRTTCTPGPCD 300
    SQPCQNGGTC VPEGLDGYQC LCPLAFGGEA NCALKLSLEC RVDLLFLDLS SAGTTLDGFL 360
    RAKVFKRFPV RAVLSDSRA RVGVATYSRE LLVAVPVGEY QDVDPDVWSL DGIPFRGGPT 420
    LTGSALRQAA ERFGSATRT QQDRPRRVVV LLTESHSEDE VAGPARHARA RELLLLGVGS 480
65  EAVRAELEBI TGSPKHMVYV SDPQDLFNQI PELQKLCRSR QRPQCRTQAL DLVFMLD TSA 540
    SVGPENFAQM QSFVRSCALQ FEVNPVDVTQV GLVVYGSQVQ TAFGLDKPT RAAMLRAISQ 600
    APYLGGVGS A GTALLHIYDK VMTVQRGARP GVPKAVVVLT GGRGAEDAAV PAQKLNRNGI 660
    SVLVVGVGPV LSEGLRRLAG PRDSLHVAA YADLRYHQDV LIEWLCGEAK QPVNLCKPSP 720
70  CMNEGSCVLQ NGSYRCKCRD WEGPHCENR EWSSCSVCVS QGWILETPLR HMAPVQEGSS 780
    RTPPSNYREG LGTEMVPTFW NVCAPGP
  
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Seq ID NO: 444 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 89..2356

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75  1      11      21      31      41      51
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    GTCGCCGCTC TCTTCCGTTT ATATCAACAT GCCCCTTTTC CTGTTGTCTG AAGCCGCTCT 120
80  TGTTTTCTCT TCTTCCAGAG TGCCCCCATC TCTCCTCTC CAGGAAGTCC ATGTAAGCAA 180
    AGAAACCATC GGAAGATTTT CAGCTGCCAG CAAAATGATG TGGTGCTCGG CTGCAGTGGA 240
    CATCATGTTT CTGTTAGATG GGTCTAACAG CGTCGGGAAA GGGAGCTTTG AAAGGTCCAA 300
    GCACTTTGCC ATCAGAGTCT GTGACGGTCT GGACATCAGC CCGAGAGGGG TCAGAGTGGG 360
85  AGCATTCCAG TTCAGTTCCA CTCCTCATCT GGAATCCCC TTGGATTCAT TTTCAACCCA 420
    ACAGGAAGTG AAGGCAAGAA TCAAGAGGAT GGTTTTCAAA GGAGGGCGCA CGGAGACGGA 480
    ACTTGCTCTG AAATACCTTC TGCAAGAGG GTTGCTTGA GGCAGAAATG CTTCTGTGCC 540
    CCAGATCCTC ATCATCGTCA CTGATGGGAA GTCCAGGGG GATGTGGCAC TGCCATCCAA 600
  
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	GCAGCTGAAG	GAAAGGGGTG	TCAGTGTGTT	TGCTGTGGGG	GTCAGGTTTC	CCAGGTGGGA	660
	GGAGCTGCAT	GCACTGGCCA	GCGAGCCTAG	AGGGCAGCAC	GTGCTGTGG	CTGAGCAGGT	720
	GGAGGATGCC	ACCAACGGCC	TCTTCAGCAC	CCTCAGCAGC	TCGGCCATCT	GCTCCAGCGC	780
5	CACGCCAGAC	TGCAGGGTCG	AGGCTCACCC	CTGTGAGCAC	AGGACGCTGG	AGATGGTCCG	840
	GGAGTTGCT	GGCAATGCC	CATGCTGGAG	AGGATCGGG	CGGACCCCTG	CGGTGCTGGC	900
	TGCACACTGT	CCCTTCTACA	GCTGGAAGAG	AGTGTTCCTA	ACCCACCCCTG	CCACCTGCTA	960
	CAGGACCACC	TGCCCAGGCC	CCTGTGACTC	GCAGCCCTGC	CAGAATGGAG	GCACATGTGT	1020
	TCAGAAGGA	CTGGAAGGCT	ACCAGTGCCT	CTGCCCGCTG	GCCTTTGGAG	GGGAGGCTAA	1080
10	CTGTGCCCTG	AAGCTGAGCC	TGGAATGCAG	GGTCCGACCTC	CTCTTCCTGC	TGGACAGCTC	1140
	TGCGGGCACC	ACTCTGGACG	GCTTCCTGCG	GGCCAAAGTC	TTCTGTAAGC	GGTTTGTGCG	1200
	GGCCGTGCTG	AGCAGGAGCT	CTCGGGCCCG	AGTGGGTGTG	GCCACATACA	GCAGGGAGCT	1260
	GCTGTGGCG	GTGCCCTGTG	GGGAGTACCA	GGATGTGCCT	GACCTGGTCT	GGAGCCTCGA	1320
	TGGCATTCCC	TTCCGTGGTG	GCCCCACCTT	GACGGGCAGT	GCCTTGGCGC	AGGCGGCAGA	1380
	GCGTGGCTTC	GGGAGCGCCA	CAGGACACGG	CCAGGACCGG	CCACGTAGAG	TGGTGGTTTT	1440
15	GCTCACTGAG	TCACACTCCG	AGGATGAGGT	TGCGGGCCCA	GCGGTACACG	CAAGGGCGCG	1500
	AGAGCTGCTC	CTGCTGGGTG	TAGGCAGTGA	GGCCGTGCGG	GCAGAGCTGG	AGGAGATCAC	1560
	AGGAGGCCCA	AAGCATGTGA	TGGTCTACTC	GGATCCTCAG	GATCTGTTC	ACCAATCCC	1620
	TGAGCTGCAG	GGGAAGCTGT	GCAGCCGGCA	GCGGCCAGGG	TGCCGGACAC	AAGCCCTGGA	1680
	CCTCGTCTTC	ATGTTGGACA	CCTCTGCCTC	AGTAGGGCCC	GAGAATTTTG	CTCAGATGCA	1740
20	GAGCTTTGTG	AGAAGCTGTG	CCCTCCAGTT	TGAGGTGAAC	CCTGACGTGA	CACAGGTCCG	1800
	CCTGGTGGTG	TATGGCAGCC	AGGTGCAGAC	TGCCTTCGGG	CTGGACACCA	AACCCACCCG	1860
	GGCTGCGATG	CTGCGGGCCA	TAGCCAGGCG	CCCCTACCTA	GGTGGGGTGG	GCTCAGCCGG	1920
	CACCGCCCTG	CTGCACATCT	ATGACAAAGT	GATGACCGTC	CAGAGGGGTG	CCCGGCTCGG	1980
25	TGTCCCCAAA	GCTGTGGTGG	TGCTCACAGG	CGGGAGAGGC	GCAGAGGATG	CAGCCGTTCC	2040
	TGCCCAGAAG	CTGAGGAACA	ATGGCATCTC	TGTCTTGGTC	GTGGGCGTGG	GGCCTGTCTT	2100
	AAGTGAGGGT	CTGCGGAGTC	TCTCAGGTCC	CCGGGATTCC	CTGATCCACG	TGGCAGCTTA	2160
	CGCCGACCTG	CGGTACCACC	AGGACGTGCT	CATTGAGTGG	CTGTGTGGAG	AAGCCAAGCA	2220
	CGCAGTCAAC	CTCTGCAAA	CCAGCCCGTG	CATGAAATGAG	GGCAGCTGCG	TCCTGCAGAA	2280
30	TGGGAGCTAC	ELHALASEP	RGQHVLLAEQ	VEDATNGLFS	TLSSSAICSS	ATPDCRVEAH	2340
	CTTGAGACGC	CCCTGAGGCA	CATGGCTCCC	GTGCAGGAGG	GCAGCAGCCG	TACCCCTCCC	2400
	AGCAACTACA	GAGAAGGCGT	GGGCACTGAA	ATGGTGCCTA	CCTTCTGGAA	TGTCTGTGCC	2460
	CCAGGTCTCT	AGAATGTCTG	CTTCCGCGCG	TGGCCAGGAC	CACTATTCTC	ACTGAGGGAG	2520
	GAGGATGTCC	CAACTGCAGC	CATGCTGCTT	AGAGACAAGA	AAGCAGCTGA	TGTACCCAC	2580
35	AAACGATGTT	GTGAAAAAGT	TTTGTATGTT	AAGTAAATAC	CCACTTTCTG	TACCTGCTGT	2640
	GCCTTGTGTA	GCGTATGTCA	TTCGCCACCT	TTCCTTGGAG	GATAAACAAG	GGGTCTTGAA	2700
	GACTTAAATT	TAGCGGCGCT	ACGTTCTCTT	GCACACAATC	AATGCTCGCC	AGAATGTTGT	2760
	TGACACAGTA	ATGCCACGA	GAGGCCCTTA	CTAGAGCATC	CTTTGGACGG		

Seq ID NO: 445 Protein sequence
Protein Accession #: Eos sequence

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45	MPPFLLEAV	CVFLFSRVPP	SLPLQEVHVS	KETIGKISAA	SKMMWCSAAV	DIMFLLDGSN	60
	SVGKGSFERS	KHFAITVCDG	LDISPERVRV	GAQFSSSTPH	LEFPLDSFST	QDEVKARIKR	120
	MVFKGGRTET	ELALKYLLHR	GLPGGRNASV	PQILIIIVTDG	KSQGDVALPS	KQLKERGVTV	180
	FAVGVRFPWR	ELHALASEP	RGQHVLLAEQ	VEDATNGLFS	TLSSSAICSS	ATPDCRVEAH	240
	PCEHRTLEMV	REFAGNAPCW	RGSRRTLAVL	AAHCPFYSWK	RVFLTHPATC	YRTTCPPGCD	300
50	SQPCQNGTGC	VPEGLDGYQC	LCPLAFGGEA	NCALKLSLEC	RVDLLFLDLS	SAGTTLDGFL	360
	RAKVFVKRFV	RAVLSEDSRA	RVGVATYSRE	LLVAVPVGVE	QDVLDLVWSL	DGIPFRGGPT	420
	LTGSALRQAA	ERGFSGSATR	QDRPRRVVV	LLTESHSEDE	VAGPARHARA	RELLLLGVGS	480
	EAVRAELEEI	TGSPKHVMVY	SDPDQLFNQI	PELQKLCISR	QRPGCRTQAL	DLVFMLDTS	540
	SVGPENFAQM	QSFVRSALQ	FEVNPDTVQV	GLVVYGSQVQ	TAFLDLTKPT	RAAMLRAISQ	600
55	APYLGGVGS	GTALLHIYDK	VMTVQRGARP	GVPKAVVVLT	GGRGAEDA	PAQKLRLNNGI	660
	SVLVVGVGPV	LSEGLRRLAG	PRDSLIVHAA	YADLRYHQDV	LIEWLCGEAK	QVNLCKPSP	720
	CMNEGSCVLQ	NGSYRCKCRD	GWEGPHCENR	FLRRP			

Seq ID NO: 446 DNA sequence
Nucleic Acid Accession #: NM_031942.1
Coding sequence: 145..1260

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65	CCCGAGCCCC	GCCCCCTCCG	GCCCCGGTCG	GCGCGCCCG	CCTGCCAGCC	GCGCTGCTGC	60
	TGCTCTCTCT	GCTGTGGGAC	CGCTGACCGC	GCGGCTGCTC	CGCTCTCCCC	GCTCCAAGCG	120
	CCGATCTGGG	CACCCGCCAC	CAGCATGGAC	GCTCGCCCGG	TGCCGAGAA	AGATCTCAGA	180
	GTAAAGAAGA	ACTTAAAGAA	ATTCAGATAT	GTGAAGTTGA	TTTCCATGGA	AACCTCGTCA	240
	TCCTCTGATG	ACAGTTGTGA	CAGCTTTGCT	TCTGATAATT	TTGCAAAAC	GAGGCTGCAG	300
70	TCAGTTCCGG	AAGGCTGTAG	GACCCGCAGC	CAGTGCAGGC	ACTCTGGACC	TCTCAGGGTG	360
	GCGATGAAGT	TTCCAGCGCG	GAGTACCAGG	GGAGCAACCA	ACAAAAAGC	AGAGTCCCGC	420
	CAGCCCTCAG	AGAAATCTGT	GACTGATTCC	AACTCCGATT	CAGAAGATGA	AAGTGGAAATG	480
	AATTTTGTGG	AGAAAAGGGC	TTTAAATATA	AAGCAAAACA	AAGCAATGCT	TGCAAACTC	540
	ATGTCTGAAT	TAGAAAGCTT	CCCTGGCTCG	TTCCGTGGAA	GACATCCCTT	CCCAGGCTCC	600
75	GACTCACAA	CAAGAGAGCT	GCGAAGCGGT	ACATTCCTCG	GTGTTGCTTC	CAGGAGAAAC	660
	CCTGAACGGA	GAGCTCGTCC	TCTTACCAGG	TCAAGGTCCC	GGATCCTCGG	GTCCTTGAC	720
	GCTCTACCCA	TGGAGGAGGA	GGAGGAAGAG	GATAAGTACA	TGTTGGTGAG	AAAGAGGAAG	780
	ACCGTGGATG	GCTACATGAA	TGAAGATGAC	CTGCCAGAA	GCCGTCGCTC	CAGATCATCC	840
	GTGACCCCTT	CGCATATAAT	TCGCCAGTG	GAAGAAATTA	CAGAGGAGGA	GTTGGAGAAC	900
80	GTCTGCAGCA	ATTCTCGAGA	GAAGATATAT	AACCGTTCAC	TGGGCTCTAC	TTGTCTATCA	960
	TGCCGTCAGA	GAACTATTGA	TACCAAAACA	AACCTGCAGAA	ACCCAGACTG	CTGGGGCGTT	1020
	CGAGGCCAGT	TCTGTGGCCC	CTGCCCTTGA	AACCGTTATG	GTGAAGAGGT	CAGGGATGCT	1080
	CTGCTGGATC	CGAACTGGCA	TGCCCCGCTT	TGTCGAGGAA	TCTGCAACTG	CAGTTTCTGC	1140
	CGGACGCGAG	TGAGGAGGCT	TGCGACTGGG	GTCCTTGTGT	ATTAGCCAA	ATATCATGGC	1200
85	TTTGGGAATG	TGCATGCCTA	CTTGAAGAGC	CTGAACAGG	AATTTGAAAT	GCAAGCATAA	1260
	TATCTGGAAA	ATTTGCTGCC	TGCCTTCTAC	TTCTCAAATC	TTTCTGTGAA	AAGTTTCCAA	1320
	TTTTTTCATC	GAAACCTGAG	TAAAAATCT	TGATGATCAG	CCTGTTTCAT	AAGAACTCC	1380
	AATCAAGTTA	ATCTTAGCAG	ACATGTGTTT	CTGGAGCATC	ACAGAAGGTA	TATTGCTAGT	1440

TACACTTTGC CCTCCTGCAG TTTCTTCTCT GCTCCCAACC CCCATCTCAT AGCATCCCC 1500
 TCTATTTCCA ATGCTCCTCT CCAACCGCTT AGTTTCTGAA TTTCTTTTAA ATTACAGTTT 1560
 TATGAAAGCA TATTTTATTT ACTTGGTGTT GAAATAGCCC TCATAAAACC TAAGCACTTG 1620
 GAAACACAAT AATAGTATTA ACTAACTAGA TCTATTGAAT TTCAGAGAAG AGCCTTCTAA 1680
 CTTGTTTACA CAAAAACGAG TATGATTTAG CACTCATACT AGTTGAAATT TTTAATAGAA 1740
 TCAAGGCACA AAAGTCTTAA AACCATGTGG AAAAATTAGG TAATTATTGC AGATTGATGT 1800
 CTCTCAATCC CATGTATTGC GCTTATGTTA CAAGTTGTTG TCACAGTTGA GACTTAATTT 1860
 CTCTAATTT CTCTGCCCG AAGGGTAAGT GGTGCGTCCA GCTTACACGA TCATAATTCA 1920
 AAGGTTGGTG GGCAATGTAA TACTTAATTA AAATAATGAT GGAAGAGCTA TCTGGAGATT 1980
 ATGAGTAAGC TGATTGTAAT TTTCAGTATA AAACCTTAGT ATAATTGTAG TTTGCAAAGT 2040
 TTATTTCACT TCACATGTAA GGTATTGCAA ATAAATCTCT GGACAAATTT GTATGGAAAC 2100
 TTGATATTAA AAACAGTCT GTGGTTCTTT GCAGTTTCTT GTAAATTTAT AAACCAAGCA 2160
 CAAGGTTCAA GTTTAGATTT TAAGCACTTT TATAACAATG ATAAGTGCCT TTTTGGAGAT 2220
 GTAACTTTGA GCAGTTTGT AACCTGACAT CTCTGCCAGT CTAGTTTCTG GGCAGGTTTC 2280
 CTGTGTCACT ATTCCCTCT CTCTTGCAT TAATCAAGGT ATTTGGTAGA GGTGGAATCT 2340
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 GATGCATAAT TGGACCTTGA ATCGATAAGT GTAAATACAG CTTTGTGATCT GTAATGCTTT 2460
 TATACAAAAG TTTATTTTAA TAATAAAATG TTTGTCTTAA AAAAAAAAAA

Seq ID NO: 447 Protein sequence
 Protein Accession #: NP_114148.1

1 11 21 31 41 51
 MDARRVPQKD LRVKKNLKKP RYVKLISMET SSSSDSDSCDS FASDNFANTR LQSVREGCRT 60
 RSQCRHSGPL RVAMKFPARS TRGATNKKAE SRQPSSENSVT DSNDSSEDES GMNFLEKRAL 120
 NIKQNKAMLA KLMSELESFP GSFRGRHPLP GSDSQSRPR RRTFPGVASR RNPERRARPL 180
 TRSRRIILGS LDALPMEEEE EEDKYMLVRK RKTVDGYMNE DDLPRSRRSR SSVTLPHIIR 240
 PVEEITEEEL ENVCNSRREK IYNRLSGSTC HQCRQKTDIT KTCNRPDCW GVRGQFCGPC 300
 LRNRYGEEVR DALLDPNWHC PPCRGICNCS PCRQRDGRCA TGVLVYLAKY HGFGNVHAYL 360
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Seq ID NO: 448 DNA sequence
 Nucleic Acid Accession #: NM_019894
 Coding sequence: 1..1314

1 11 21 31 41 51
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 CTGAGCCTGG CGAGTATCAT CATTGTGGTT GTCCTCATCA AGGTGATTCT GGATAAATAC 180
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 GCAGTGGCAG TCCGCTCTTC CAAGGACCGA TCCCACTGCA AGGTGCTGGA CTCGGCCACA 360
 GGGAACTGGT TCTCTGCTGT TTTGACAAC TTCACAGAAG CTCTCGCTGA GACAGCCTGT 420
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 CTCACGGCAG CCCACTGCTT CAGGAAACAT ACCGATGTGT TCAACTGGAA GGTGCGGGCA 780
 GGCTCAGACA AACTGGGCGA CTTCCTCATC CTGGCTGTGG CCAAGATCAT CATCATTGAA 840
 TTCAACCCCA TGTACCCCAA AGACAAATGAC ATCGCCCTCA TGAAGCTGCA GTTCCCACTC 900
 ACTTTCTCAG GCACAGTCAG GCCCATCTGT CTGCCCTTCT TTGATGAGGA GCTCACTCCA 960
 GCCACCCCACT TCTGGATCAT TGGATGGGGC TTTACGAAGC AGAATGGAGG GAAGATGTCT 1020
 GACATACTGC TGACGGCGTC AGTCCAGGTC ATTGACAGCA CACGGTGCAA TGCAGACGAT 1080
 GCGTACCAGG GGGAAAGTCA CGAGAAGATG ATGTGTGCAG GCATCCCGGA AGGGGGTGTG 1140
 GACACCTGCC AGGGTGACAG TGGTGGGCCC CTGATGTACC AATCTGACCA GTGGCATGTG 1200
 GTGGGCATCG TTAGCTGGGG CTATGGCTGC GGGGGCCCCG GCACCCCAAG AGTATACACC 1260
 AAGTCTCAG CCTATCTCAA CTGGATCTAC AATGTCTGGA AGGCTGAGCT GTAA

Seq ID NO: 449 Protein sequence
 Protein Accession #: NP_063947.1

1 11 21 31 41 51
 MLQDPDSQDP LNSLDVKPLR KPRIPMETFR KVGIPIIIAL LSLASIIIV VLIKVILDKY 60
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 GNWFSACFDN FTEALAEATC RQMGYSKPT FRAVEIGPDQ DLDVVEITEN SQELMRNNS 180
 GPCLSGSLVS LHCLACGKSL KTRPVVGGEE ASVDSWPQV SIQYDKQHVC GGSILDPHWV 240
 LTAHCFERKH TDVFNWVRA GSDKLGSPFS LAVAKIIIE FNPMPKOND IALMKLQFPL 300
 TFSGTVRPIC LPFFDEELTP ATPLWIIGWG FTKQNGGKMS DILLQASVQV IDSTRCNADD 360
 AYQGEVTEKM MCAGIPEGGV DTCQDGGSGP LMYQSDQWHV VGIVSWGYGC GGPSTPGVYT 420

Seq ID NO: 450 DNA sequence
 Nucleic Acid Accession #: XM_051860.2
 Coding sequence: 52..3042

1 11 21 31 41 51
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 GACCGGGGCA GAGCCTGCCG GAGCTACCGT GTACGGTTCC TCTGTGGGAA GCCTGTGAGG 180
 CCCAACTCA CAGTCACCAT TGACACCAAT GTGAACAGCA CCATTCTGAA CTTGGAGGAT 240
 AATGTACAGT CATGGAAACC TGGAGATACC CTGGTCATTG CCAGTACTGA TTACTIONATG 300
 TACCAGGCAG AAGAGTTCCA GGTGCTTCCC TGCAGATCCT GCGCCCCCAA CCAGGTCAAA 360

	GTGGCAGGGA	AACCAATGTA	CCTGCACATC	GGGGAGGAGA	TAGACGGCGT	GGACATGCGG	420
	GCGGAGGTTG	GGCTTCTGAG	CCGGAAACATC	ATAGTGATGG	GGGAGATGGA	GGACAAATGC	480
	TACCCCTACA	GAACACCAT	CTGCAATTTT	TTTGACTTCG	ATACCTTTGG	GGGCCACATC	540
5	AAGTTTGCTC	TGGGATTAA	GGCAGCACAC	TTGGAGGGCA	CGGAGCTGAA	GCATATGGGA	600
	CAGCAGCTGG	TGGGTCACTA	CCCGATTAC	TTCCACCTGG	CCGGTGATGT	AGACGAAAGG	660
	GGAGGTTATG	ACCCACCCAC	ATACATCAGG	GACCTCTCCA	TCCATCATAC	ATTCTCTCGC	720
	TGCGTCACAG	TCCATGGCTC	CAATGGCTTG	TTGATCAAGG	ACGTTGTGGG	CTATAACTCT	780
	TTGGGCCACT	GCTTCTTCAC	GGAAGATGGG	CCGGAGGAAC	GCAACACTTT	TGACCACTGT	840
10	CTTGGCTCC	TTGTCAAGTC	TGGAACCCCT	CTCCCTCGG	ACCGTGACAG	CAAGATGTGC	900
	AAGATGATCA	CAGGAGACTC	CTACCCAGGG	TACATCCCA	AGCCCAAGCA	AGACTGCAAT	960
	GCTGTGTCCA	CCTTCTGGAT	GGCCAATCCC	AACAACAACC	TCATCAACTG	TGCCGCTGCA	1020
	GGATCTGAGG	AAACTGGATT	TTGGTTTATT	TTTACCACG	TACCAACGGG	CCCCCTCCGT	1080
	GGAAATGACT	CCCCAGTTA	TTCAGAGCAC	ATTCCACTGG	GAAATTTCTA	TAACAACCGA	1140
15	GCACATTCCA	ACTACCGGGC	TGGCATGATC	ATAGACAACG	GAGTCAAAAC	CACCGAGGCC	1200
	TCTGCCAAGG	ACAAGCGGGC	GTTCCTCTCA	ATCATCTCTG	CCAGATACAG	CCCTCACCCAG	1260
	GACGCCGACC	CGCTGAAGCC	CCGGAGGCCG	GCCATCATCA	GACACTTCAT	TGCCTACAGC	1320
	AACCAGGACC	ACGGGGCCTG	GCTGCGCGGC	GGGGATGTGT	GGCTGGACAG	CTGCCGTTT	1380
	GCTGACAATG	GCATTGGCCT	GACCTTGGCC	AGTGGTGGAA	CCTTCCCGTA	TGACGACGGC	1440
20	TCCAAGCAAG	AGATAAAGAA	CAGCTTGTIT	TTTGGCGAGA	GTGGCAACGT	GGGGACGGAA	1500
	ATGATGGACA	ATAGGATCTG	GGGCCCTGGC	GGCTTGGACC	ATAGCGGAAG	GACCTTCCCT	1560
	ATAGGCCAGA	ATTTTCCAAT	TAGAGGAAAT	CAGTTATATG	ATGGCCCCAT	CAACATCCAA	1620
	AACTGCACCT	TCCGAAAGTT	TGTGGCCCTG	GAGGGCCGGC	ACACCAGCGC	CCTGGCCTTC	1680
	CGCTCGAATA	TGCTTGGCA	GAGCTGCCCC	CATAACAACG	TGACCGGCAT	TGCCTTTGAG	1740
25	GACGTTCCGA	TTACTTCCAG	AGTGTCTTTC	GGAGAGCCTG	GGCCCTGGTT	CAACCAGCTG	1800
	GACATGGATG	GGGATAAGAC	ATCTGTGTTC	CATGACGTCG	ACGGCTCCGT	GTCGAGTAC	1860
	CCTGGCTCCT	ACCTCACGAA	GAATGACAAC	TGGCTGGTCC	GGCACCAGAA	CTGCATCAAT	1920
	GTTCGCGACT	GGAGAGGGGC	CATTTGCAGT	GGGTGCTATG	CACAGATGTA	CATTCAAGCC	1980
	TACAAGACCA	GTAACCTGCG	AATGAAGATC	ATCAAGAATG	ACTTCCCCAG	CCACCTCTTT	2040
30	TACCTGGAGG	GGGCGCTCAC	CAGGAGCACC	CATTACCAAC	AATACCAACC	TTTGTGCACC	2100
	CTGCAGAAAG	GCTACACCAT	CACTGGGAC	CAGACGGCCC	CCGCGAAGT	GGCCATCTGG	2160
	CTCATCAACT	TCAACAAGGG	CGACTGGATC	CGAGTGGGGC	TCTGTACCCC	GCGAGGCACC	2220
	ACATTTCTCCA	TCTCTCTGGA	TTTTCACAA	CGCCTGCTGA	AGCAAACTGC	CAAGACGGCC	2280
	GTCTTCTGTA	GGACCTTGCA	GATGGACAAA	GTGGAGCAGA	GCTACCTCTG	CAGGAGCCAC	2340
35	TACTACTGGG	ACGAGGACTC	AGGGCTGTGT	TTCCTGAAGC	TGAAAGCTCA	GAACGAGAGA	2400
	GAGAAGTTTG	CTTTCTGCTC	CATGAAAGGC	TGTGAGAGGA	TAAAGATTAA	AGCTCTGATT	2460
	CCAAAGAACG	CAGGCGCTAG	TGACTGCACA	GCCACAGCTT	ACCCCAAGTT	CACCGAGAGG	2520
	GCTGTGCTAG	ACGTGCCGAT	GCCCAAGAAG	CTCTTTGGTT	CTCAGCTGAA	AACAAAGGAC	2580
40	CATTCTCTTG	AGGTGAAGAT	GGAGAGTTCC	AAGCAGCACT	TCTTCCACCT	CTGGAAACGAC	2640
	TTGCTTTACA	TTGAAGTGGA	TGGGAAGAAG	TACCCAGATT	CGGAGGATGG	CATCCAGGTG	2700
	GTGGTGATTG	ACGGGAACCA	AGGGCGCGTG	GTGAGCCACA	CGAGCTTCAG	GAACCTCCATT	2760
	CTGCAAGGCA	TACCATGGCA	GCTTTTCAAC	TATGTGGCGA	CCATCCCTGA	CAATTCCATA	2820
	GTGCTTATGG	CATCAAGAGG	AAGATACGTC	TCCAGAGGCC	CATGGACCAG	AGTGCTGGAA	2880
	AAGCTTGGGG	CAGACAGGGG	TCTCAAGTTG	AAAGAGCAAA	TGGCATTGCT	TGGCTTCAAA	2940
45	GGCAGCTTCC	GGCCCTCTG	GGTGACACTG	GACACTGAGG	ATCACAAGC	CAAAATCTTC	3000
	CAAGTTGTGC	CCATCCCTGT	GGTGAAGAAG	AAGAAGTTGT	GAGGACAGCT	GCCGCCCGGT	3060
	GCCACCTCGT	GGTAGACTAT	GACGGTGACT	CTTGGCAGCA	GACCAGTGGG	GGATGGCTGG	3120
	GTCCCCAGC	CCCTGCCAGC	AGCTGCCCTG	GAAGGCCGTG	TTTCAGCCCT	GATGGGCCAA	3180
	GGGAAGGCTA	TCAGAGACCC	TGGTGCTGCC	ACCTGCCCTT	ACTCAAGTGT	CTACCTGGAG	3240
50	CCCTCGGGG	GGTGCTGGCC	AATGCTGGAA	ACATTCACTT	TCCTGCAGCC	TCTTGGGTGC	3300
	TTCTCTCCTA	TCTGTGGCTC	TTCAGTGGGG	GTTTGGGGAC	CATATCAGGA	GACCTGGGTT	3360
	GTGCTGACAG	CAAGATCCCA	CTTTGGCAGG	AGCCCTGACC	CAGCTAGGAG	GTAAGTCTGA	3420
	GGGCTGGTCA	TTACAGATGC	CCCATGGTCT	TCAGCAGACA	AGTGAGGGTG	GTAAGTGTAG	3480
	GAGAAGAGGC	CTTGGCCTTA	AGGAAATCTT	TACTCTGTGA	AGCAAGAGCC	AACCTCACAG	3540
55	GATTAGGAGC	TGGGGTAGAA	CTGGCTATCC	TTGGGGAAGA	GGCAAGCCCT	GCCTCTGGCC	3600
	GTGTCCACCT	TTCAGGAGAC	TTTGAGTGGC	AGGTTTGGAC	TTGGACTAGA	TGACTCTCAA	3660
	AGGCCCTTTT	AGTTCTGAGA	TTCCAGAAAT	CTGCTGCATT	TCACATGGTA	CCTGGAACCC	3720
	AACAGTTCAT	GGATATCCAC	TGATATCCAT	GATGCTGGGT	GCCCCAGCGC	ACACGGGATG	3780
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60	GTCCATGTGC	ACTGCAATGC	CAGGTGGAGA	AATCACAGAG	AGGTAAGATG	GAGGCGAGTG	3900
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	CTGCTGCTG	AGGCTGGTGA	CTACGGGGTC	GCCCTTTGCT	CACGTCTCTC	TGGCCCACTC	4080
	ATGATGGAGA	AGTGCTGGTA	GAGGGGAGCA	ATGGGCTTTG	CTGCTTATGA	GCACAGAGGA	4140
65	ATTGAGTCCC	CAGGAGCCCC	TGCTCTGAC	TCCAAGAGGG	TGAAGTCCAC	AGAAGTGAGC	4200
	TTCTGCTCTA	GGGCTCTGTT	TGCTCTTCAT	CCAGGGAAC	GAGCACAGGG	GGCCTCCAGG	4260
	AGACCTTAGA	TGTGCTGCTA	CTCCCTCGGC	CTGGGATTTT	AGAGCTGGAA	ATATAGAAAA	4320
	TATCTAGCCC	AAAGCCTTCA	TTTTAACAGA	TGGGGAAAGT	GAGCCCCCAA	GATGGGAAAG	4380
70	AACCAACAG	CTAAGGGAGG	GCCTGGGGAG	CCCCACCCTA	GCCCTTGCTG	CCACACCACA	4440
	TTGCCTCAAC	AACCGGCCCC	AGAGTGCCCA	GGCACTCCTG	AGGTAGCTTC	TGGAATGGG	4500
	GACAAGTCCC	CTCGAAGGAA	AGGAAATGAC	TAGAGTAGAA	TGACAGCTAG	CAGATCTCTT	4560
	CCCTCCTGCT	CCCGCGCAC	ACAAACCCGC	CCTCCCTTGT	GTGTGGCGG	TCCCTGTGGC	4620
	CTTCACTTTG	TTCACTACCT	GTCAGCCGAG	CCTGGGTGCA	CAGTAGCTGC	AACTCCCCAT	4680
	TGGTGCTACC	TGGCTCTCCT	GTCTCTGAG	CTCTACAGGT	GAGGCCAGC	AGAGGGAGTA	4740
75	GGGCTCGCCA	TCTTCTGCTG	GAGCCAAATT	GGCTGATCTT	GGGTGTCTGA	ACAGCTATTG	4800
	GGTCCACCCC	AGTCCCTTTC	AGCTGCTGCT	TAATGCCCTG	CTCTCTCCCT	GGCCCACTTT	4860
	ATAGAGAGCC	CAAGAGGCTC	CTGTAAAGAG	GAGAACTCTA	TCTGTGGTTT	ATAATCTTGC	4920
	ACGAGGCACC	AGAGTCTCCC	TGGGTCTTGT	GATGAACACT	ATTATCCCC	TTTCTGCCCC	4980
	CAACCACAAA	CTCTTTCCTT	CAAAGAGGGC	CTGCCTGGCT	CCCTCCACCC	AACTGCACCC	5040
80	ATGAGACTCG	GTCCAAGAGT	CCATTCCCA	GGTGGGAGCC	AACTGTCAAG	GAGGTCTTTC	5100
	CCACCAACCA	TCTTTTCAAG	GCTGGGAGGT	GACCATAGGG	CTCTGCTTTT	AAAGATATGG	5160
	CTGCTTCAAA	GGCCAGAGTC	ACAGGAAGGA	CTTCTTCCAG	GGAGATTAGT	GGTGATGGAG	5220
	AGGAGAGTTA	AAATGACCTC	ATGTCTTCTT	TGTCCACGGT	TTTGTGAGT	TTTCACTCTT	5280
85	CTAATGCAAG	GTCTCTCACAC	TGTGAACAC	TTAGGATGTG	ATCACTTCA	GGTGGCCAGG	5340
	AATGTTGAAT	GTCTTGGGCT	CAGTTCAATT	AAAAAGATA	TCTATTGAA	AGTTCTCAGA	5400
	GTGTGACATA	TGTTTACAGC	TACAGGATCT	GTACATAAAA	GTTTCTTTCC	TAAACCATTC	5460
	ACCAAGAGCC	AATATCTAGG	CATTTTCTTG	GTAGCACAAA	TTTTCTTATT	GCTTAGAAAA	5520
	TTGTCTCCTT	TGTTATTCTT	GTTTGTAAAG	CTTAAGTGAG	TTAGGTCTTT	AAGGAAAGCA	5580

ACGCTCCTCT GAAATGCTTG TCTTTTTTCT GTTGCCGAAA TAGCTGGTCC TTTTCGCGGA 5640
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Seq ID NO: 451 Protein sequence
 Protein Accession #: XP_051860.2

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 DMRAEVLGSL RNIIVMGEME DKCYPYRNHI CNPFDFTDFG GHIKFGALGFK AAHLEGTELK 180
 15 HMGQQLVGGY PIHPLHAGDV DERGGYDPPT YIRDLISIHHT FSRCTVTHGS NGLLIKDVVG 240
 YNSLGHCFPT EDGPEERNFT DHCLGLLVKS GTLLPSDRDS KMCKMITGDS YPGYIPKPRQ 300
 DCNAVSTFWM ANPNNNLINC AAAGSEETGF WPIFHHVPTG PSVGMYSPPGY SEHIPLGKPY 360
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 20 AYKNQDHGAW LRGGDVLWDS CRFADNGIGL TLASGGTFFY DDGSKQBIKN SLFVGESGNV 480
 GTEMMDNRIW GPGGLDHSGR TLPIGQNFPI RGIQLYDGP I NIQNTCFRKF VALEGRHTSA 540
 LAPRLNNAWQ SCPHNNVTGI APEDVPITSR VFFGEPGPWF NQLDMGDKT SVPHDVGDSV 600
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 HPLYLEGALT RSTHYQQYQP VVTLQKGYTI HWDQTAPAEI AIWLINFNKG DWIRVGLCYP 720
 RGTTFSILSD VHNRLKQTS KTGVPVRTLQ MDKVBQSPYG RSHYVWEDS GLLFLKLKAQ 780
 25 NEREKFAFCS MGKCEFIKTK ALIPKNAGVS DCTATAYPKF TERAVVDVPM PKKLFSGSLK 840
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Seq ID NO: 452 DNA sequence
 Nucleic Acid Accession #: Eos sequence
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 60 AGGTTGTCTA CAAAAGAGGC CAGGATTATA GGTTTGCTTG CTACGACCGG GCGACGACCT 1440
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 85 GGGAGCAATG GGTCTTGTCT CTTATGAGCA CAGAGGAATT CAGTCCCGAG GCAGCCCTGC 2940
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Seq ID NO: 453 Protein sequence
 Protein Accession #: Eos sequence

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 STILNLEDNV QSWKPGDTLV IASTDYSMYQ AEEFQVLPCR SCAPNQVKVA GKPMYHIGE 480
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 GTELKHMGGQ LVGQYPIHFH LAGDVDERGG YDPPTYIRDL SIHHTFSRCV TVHGSNGLLI 600
 KDVVGYNSLG HCFTEDEGPE ERNTFDHCLG LLVKSGLLP SDRDSKMKCM ITEDSYPGYI 660
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Seq ID NO: 454 DNA sequence
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Seq ID NO: 455 Protein sequence
Protein Accession #: NP_037414.2

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DVIYHVKYDD YPENGVVQMN SRDVRARART IIKWQDLEVG QVVMNLNPNP NPKERGFWD 240
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PECRNDASEV VLAGERLRES KKKAKMASAT SSSQRDWGKG MACVGRTEK TIVPSNHYG 420
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Nucleic Acid Accession #: NM_001200.1
Coding sequence: 325..1514

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Seq ID NO: 457 Protein sequence
Protein Accession #: NP_001191.1

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Seq ID NO: 458 DNA sequence
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Seq ID NO: 459 Protein sequence
Protein Accession #: NP_001990.1

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Seq ID NO: 463 Protein sequence
 Protein Accession #: Eos sequence

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	ATTTAGGAAT	TTAGGGAATT	ACAAATTAAT	AATTGCAATG	TGTACTAAAT	AATGTATACA	9420
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	AGTGATACAT	ACAGTTCAAT	GTGTACAAAA	TAATGTAATC	ATATTTTACA	TGTGTATCAT	9540
45	ACAGTTGTAT	AGATACATAT	GTACACATAT	ACATATACGT	AAAAACATGA	TTCTGTTTTT	9600
	ACATACATGT	ATATACATAT	ACACATATAA	CCCAATGTAT	TTATATATTC	AGGACTCATA	9660
	TTTTACCTAT	TAGAATAATA	ATGTCTATTA	AAGTGAACCT	TCTGTATTTC	ACATTTATTG	9720
	CCAAATAAAC	GATCTCCAC	ATAGTCAATT	CATTGTAAAG	GTGTATTAGA	GATCGACAGT	9780
	TAGTCATATC	AGTTCTTTT	TTCCATTGT	ATAGCTTGAA	GAGAACTCA	CTGCTGAGAA	9840
50	ATTGATGGAA	TGGACAAGTT	TGCAGAAAT	GAGAGAGACA	TGTGTCGATT	TACACTTACC	9900
	TCCGTTCAAA	ATGAGGAGTA	GCTATGACCT	CAAGGACACG	TTGAGAACCA	TGGGAATGGT	9960
	GAATATCTTC	AATGGGGATG	CAGACCTCTC	AGGCATGACC	TGGAGCCACG	GTCTCTCAGT	10020
	ATCTAAAGTC	CTACACAAGG	CCTTTGTGGA	GGTCACTGAG	GAGGGAGTGG	AAGCTGCAGC	10080
	TGCCACCGCT	GTAGTAGTAG	TGCAATTATC	ATCTCCTTCA	ACTAATGAAG	AGTTCTGTTG	10140
55	TAATCACCTT	TTCTATTTCT	TCATAAGGCA	AAATAAGACC	AACAGCATCC	TCTTCTATGG	10200
	CAGATTCTCA	TCCCCATAGA	TGCAATTAGT	CTGTCACTCC	ATTTAGAAAA	TGTTACCTTA	10260
	GAGGTGTTCT	GCTTAACTGA	TTGCTGGCAA	CAACAGATTG	TCTTGGCTCA	TATTTCTTTT	10320
	CTATCTCATC	TTGATGATGA	TAGTCATCAT	CAAGAATTTA	ATGATTAAAA	TAGCATGCCT	10380
	TTCTCTCTTT	CTCTTAATAA	GCCACATAT	AAATGTACTT	TTCCTTCCAG	AAAAATTTCC	10440
60	CTTGAGGAAA	AATGTCCAAG	ATAAGATGAA	TCATTTAATA	CCGTGCTTTC	TAAATTTGAA	10500
	ATATAATTCT	GTTTCTGACC	TGTTTAAAT	GAACCAAAAC	AAATCATACT	TTCTCTTCAA	10560
	ATTTAGCAAC	CTAGAAACAC	ATATTTCTTT	GAATTTAGGT	GATACCTAAA	TCCTTCTTAT	10620
	GTTTCTAAAT	TTTGTGATCT	TATAAAACAC	ATCATCAATA	AAATAATGAC	ATAAAAATCA	10680
	TTTTGCTTTA	CCTGTTTCT	CTCTGGAAAG	GGCAAGTGTC	CAGTTACACA	TAGGAAAGAT	10740
65	AATTTAGAGA	TATATTAATC	ATATATAAAG	GAAAAATAAA	AACAGAGTAG	TTCATGATGA	10800
	GCCTGGAGTA	GAAGGCAATG	CCAGAACACG	GAGGAGCCTT	GTAACCCACA	TAGGAACCTC	10860
	CTATTTTATG	CTAAAGGGAT	AAGAACTCA	TTACAGGCTT	TGATGGTTGT	TTGTCAAAGA	10920
	GGGGCATAAA	ATTATCATAT	CCACATCTAG	AAAATACATC	TCTGGCTACG	CTGATATCAA	10980
	TGGATGCGAG	GAAGAGACAG	TGTGGTTACC	ATATATAAAT	TAGGAAATCA	TTAGAGTATT	11040
70	GGGAGTGGAA	ATGGAGAGAA	AGAAAGAGCC	TGGGGGAATT	ATTTAGGAAA	TAATAGTTAC	11100
	AGAAAGACAT	CTAAGTTGCT	GACCTATCTG	ACTGGATGGA	TGGAAGATA	TCTTGTCTT	11160
	GAGAGAAAAA	AAGACTTTGG	GTTTAAATTT	GTACTTGTAT	AATTAAGGTA	CTTTAATAT	11220
	TCAAATGGAT	TTGCCTGGCA	GGCACTTGAA	GATATTAGTC	TAAATCTCAG	AAACAGAATA	11280
	TGATCTGAAG	CTCTAAATTT	GTGATATTCA	ATATAAATAG	TTTAGAGTCA	TTGGGATAAA	11340
75	TATGGTAGTT	GTAGCTGATG	GCAAAAATAA	GATACTAGGG	AGAAAGGATA	AAGTTAGAA	11400
	AAAGAAGAA	CTAGAATTGA	CCTTGAAGTA	TATCAGCATG	TGTAAGATC	AGGAATTGAT	11460
	CATTTTATT	TTCCAGAAAG	TAGCTTTTCT	TAGGGTTCCA	TATTTACTCC	CATAGATTCT	11520
	TCCC						

Seq ID NO: 465 Protein sequence
Protein Accession #: BAB21525.1

1	11	21	31	41	51	
MNSLSEANTK	FMFDLFQOFR	KSKENNIFYS	PISITSALGM	VLLGAKONTA	QQISKVLHFD	60
QVTENTTEKA	ATYHVDRSGN	VHHQFQKLLT	EFNKSTDAYE	LKIANKLFG	KTYQFLQBYL	120
DAIKKFQTS	VESTDRKINSW	EESRKINSW	VESQTNKIK	NLPDPGTIGN	DTTLVLVNAI	180
YFKGQWENK	KKENTKBEK	WPNKNTYKSV	QMMRQYNSFN	FALLEDEVQAK	VLEIPYKGRD	240

LSMIVLLPNE IDGLQKLEEK LTAELKMEWT SLQNMRETCV DLHLPRFKME BSYDLKDTLR 300
 TMGMVNI FNG DADLSGMTWS HGLSVSKVLH KAFVEVTEEG VEAAAATAVV VVELSSPSTN 360
 EEPCCNHPFL FFIRQNKNTS ILFYGRFSSP

5

Seq ID NO: 466 DNA sequence
 Nucleic Acid Accession #: NM_001910.1
 Coding sequence: 50..1240

10	1	11	21	31	41	51	
	GGAGAGAAGA	AAGGAGGGGG	CAAGGGAGAA	GCTGCTGGTC	GGACTCACAA	TGAAAACGCT	60
	CCTTCTTTTG	CTGCTGGTGC	TCCTGGAGCT	GGGAGAGGCC	CAAGGATCCC	TTACACAGGT	120
	GCCCCCTCAG	AGGCATCCGT	CCCTCAAGAA	GAAGCTGCGG	GCACGGAGCC	AGCTCTCTGA	180
15	GTTCCTGAAA	TCCCATAAAT	TGGACATGAT	CCAGTTCACC	GAGTCCTGCT	CAATGGACCA	240
	GAGTGCCAAG	GAACCCCTCA	TCAACTACTT	GGATATGGAA	TACTTCGGCA	CTATCTCCAT	300
	TGGCTCCCCA	CCACAGAACT	TCACTGTCTG	CTTCGACACT	GGCTCCTCCA	ACCTCTGGGT	360
	CCCTCTGTG	TACTGCACAT	GCCCAGCCTG	CAAGACGCAC	AGCAGGTTCC	AGCCTTCCCA	420
	GTCACGACCA	TACAGCCAGC	CAGGTCAATC	TTTCTCCATT	CAGTATGGAA	CCGGGAGCTT	480
20	GTCCGGGATC	ATTGGAGCCG	ACCAAGTCTC	TGTGGAAGGA	CTAACCCTGG	TTGGCCAGCA	540
	GTTTGGAGAA	AGTGTACAG	AGCCAGGCCA	GACCTTTGTG	GATGCAGAGT	TTGATGGAAT	600
	TCTGGGCTCG	GGATACCCCT	CCTTGGCTGT	GGGAGGAGTG	ACTCCAGTAT	TTGACAACAT	660
	GATGGCTCAG	AACCTGGTGG	ACTTGCCGAT	GTTTTCTGTC	TACATGAGCA	GTAACCCAGA	720
	AGGTGGTGGC	GGGAGCGAGC	TGATTTTGG	AGGCTACGAC	CACCTCCATT	TCTCTGGGAG	780
	CCTGAATTGG	GTCCCACTCA	CCAAGCAAGC	TTACTGGCAG	ATTGCACCTG	ATAACATCCA	840
25	GGTGGGAGGC	ACTGTTATGT	TCTGCTCCGA	GGGCTGCCAG	GCCATTGTGG	ACACAGGGAC	900
	TTCCCTCATC	ACTGGCCCTT	CCGACAAGAT	TAAGCAGCTG	CAAAACGCCA	TTGGGGCAGC	960
	CCCCGTGGAT	GGAGAATATG	CTGTGGAGTG	TGCCAACCTT	AACGTCATGC	CGGATGTCTC	1020
	CTTCACCATT	AACGGAGTCC	CCTATACCTT	CAGCCCAACT	GCCTACACCC	TACTGGACTT	1080
	CGTGGATGGA	AGTGTACAG	GCAGCAGTGG	CTTTCAAGGA	CTTGACATCC	ACCTCTCCAGC	1140
30	TGGGCCCTCT	TGGATCCTGG	GGGATGTCTT	CATTGACAG	TTTACTCAG	TCTTTGACCG	1200
	TGGGAATAAC	CGTGTGGGAC	TGGCCCCAGC	AGTCCCCTAA	GGAGGGGGCT	TGTGCTGTG	1260
	CCTGCCTGTG	TGACAGAGCT	TGAATATGTT	AGGCTGGGGC	ATTCTTTACA	CCTACAAAAA	1320
	GTTATTTTCC	AGAGAATGTA	GCTGTTTCCA	GGGTGCAAC	TTGAATTAAG	ACCAAAACAGA	1380
	ACATGAGAAT	ACACACACAC	ACACACATAT	ACACACACAC	ACACTTCACA	CATACACACC	1440
35	ACTCCACCA	CCGTGATGAT	GGAGGAATTA	CGTTATACAT	TCATATTTTG	TATGATTTT	1500
	TGATTATGAA	AATCAAAAAT	TTTCACATTT	GATTATGAAA	ATCTCCAAAC	ATATGCACAA	1560
	GCAGAGATCA	TGGTATAATA	AATCCCTTTG	CAACTCCACT	CAGCCCTGAC	AACCCATCCA	1620
	CACACGGCCA	CGCCTGTTTA	TTACACATGC	TGCCCACTCC	TCTCTCCAGC	TCCACATGCT	1680
	GTACCTGGAT	CATTCTGAAG	CAAATTCGGA	GCATTACATC	ATTTTGTCCA	TAAATATTT	1740
40	TAACATCCTT	AAATATACAA	TCGGAATTCA	AGCATCTCCC	ATTGTCCAC	AAATGTTTGG	1800
	CTGTTTTTGT	AGTTGGAGTG	TTTGTATTAG	GATTCAAGCA	AGGCCCATAT	ATTGCATTTA	1860
	TTTGAATGT	CTGTAAGTCT	CTTTCCATCT	ACAGAGTTTA	GCACATTGTA	ACGTTGTCTG	1920
	TTGAAATCCC	GAGGTGTCAT	TTGACATGGT	TCTCTGAAC	TATCTTTCCT	ATAAAATGGT	1980
	AGTTAGATCT	GGAGGTCTGA	TTTGTGGCA	AAAATATTC	CTAGGTGGTG	CTGGGTACTT	2040
45	CTTGTTCAT	CCTGTGAGGA	GGCAGATAAT	GCTGGTGCTT	CTCTATTGGT	AATGTTAAGA	2100
	CTGCTGGGTG	GGTTTGGAGT	TCTTGGCTTT	AATCATTTCAT	TACAAAGTTC	AGCATTTT	

Seq ID NO: 467 Protein sequence
 Protein Accession #: NP_001901.1

50

1	11	21	31	41	51		
	MKTLLELLLV	LLELGEAQS	LHRVPLRRHP	SLKKKLARS	QLSEFWKSHN	LDMIQFTESC	60
	SMDQSAKEPL	INYLDMVEYF	TISIGSPPQN	FTVIFDTGSS	NLWVPSVYCT	SPACKTHSRF	120
55	QPSQSSTYSQ	PGQSFSIQYQ	TGSLSGIIGA	DQVSVEGLTV	VGQQFGESVT	EPGQTFVDAE	180
	FDGILGLGYP	SLAVGAVTPV	FDNMAQNLV	DLPMFSVYMS	SNPEGGAGSE	LIFGGYDHS	240
	FSGSLNWVPV	TKQAYWQIAL	DNIQVGGTVM	FCSEGCQAIV	DTGTSITGP	SDKIKQLQNA	300
	IGAAPVDGEY	AVECANLNMV	PDVTFPTINGV	PYTLSPYAT	LLDFVDGMQP	CSSGPGQLDI	360
	HPPAGPLWIL	GDVFRQFYS	VFDRGNRRVG	LAPAVP			

60

Seq ID NO: 468 DNA sequence
 Nucleic Acid Accession #: NM_018058.1
 Coding sequence: 319..1575

65

1	11	21	31	41	51		
	TACGCGCTGC	GGGACCGGCA	GGGGAACGCC	ATCGGGGTCA	CAGCCTGCGA	CATCGACGGG	60
	GACGGCCGGG	AGGAGATCTA	CTTCCTCAAC	ACCAATAATG	CCTTCTCGGG	GGTGGCCACG	120
70	TACACCGACA	AGTTGTTCAA	GTTCCGCAAT	AACCGGTGGG	AAGACATCCT	GAGCGATGAG	180
	GTCAACGTGG	CCCGTGGTGT	GGCCAGCCTC	TTTGCCGGAC	GCTCTGTGGC	CTGTGTGGAC	240
	AGAAAGGGCT	CTGAGCGCTA	CTCTATCTAC	ATTGCCAATT	ACGCCCTACG	TAATGTGGGC	300
	CCTGATGCCC	TCATTGAAAT	GGACCCTGAG	GCCAGTGACC	TCTCCCGGGG	CATTCTGGCG	360
	CTCAGAGATG	TGGCTGCTGA	GGCTGGGGTC	AGCAAATATA	CAGGGGGCCG	AGGCGTCAGC	420
	GTGGGCCCCA	TCCCTCAGCAG	CAGTGCCTCG	GATATCTTCT	GCGACAATGA	GAATGGGCTT	480
75	AACCTTCCTT	TCCACAACCG	GGGCGATGGC	ACCTTTGTGG	ACGCTGCGGC	CAGTGTGGGT	540
	GTGGACGACC	CCCACACGAC	TGGGGGAGGT	GTCGCCCTGG	CTGACTTCAA	CCGTGATGGC	600
	AAAGTGGACA	TCGTCTATGG	CAACTGGAAT	GGCCCCCACC	GCCTCTATCT	GCAAAATGAGC	660
	ACCATGGGA	AGGTCCGCTT	CCGGGACATC	GCCTCACCCA	AGTTCTCCAT	GCCTCCCCCT	720
	GTCCGCACCG	TCATCACCGC	CGACTTTGAC	AATGACCAGG	AGCTGGAGAT	CTTCTTCAAC	780
80	AACATTGCCT	ACCAGGCTTC	CTCAGCCAAC	CGCCTCTTCC	GCGTCATCCG	TAGAGAGCAC	840
	GGAGACCCCC	TCATCGAGGA	GCTCAATCCC	GGCGACGCCT	TGGAGCCTGA	GGGCCGGGGC	900
	ACAGGGGGTG	TGGTGACCGA	CTTCGACGGA	GACGGGATGC	TGGACCTCAT	CTTGTCCCAT	960
	GGAGAGTCCA	TGGCTCAGCC	GCTTCCCTC	TTCCGGGGCA	ATCAGGGCTT	CAACAACAAC	1020
	TGGCTGCGAG	TGGTGCCACG	CACCGGGT	GGGCGCTT	CCAGGGGAGC	TAAGGTCGTG	1080
85	CTCTACACCA	AGAAGAGTGG	GGCCACCTG	AGGATCATCG	ACGGGGGCTC	AGGCTACCTG	1140
	TGTGAGATGG	AGCCCGTGGC	ACACTTGGC	CTGGGGAAGG	ATGAAGCCAG	CAGTGTGGAG	1200
	GTGACGTGGC	CAGATGGCAA	GATGTTGAGC	CGGAACGTGG	CCAGCGGGGA	GATGAACCTA	1260

GTGCTGGAGA TCCTCTACCC CCGGGATGAG GACACACTTC AGGACCCAGC CCCACTGGAG 1320
 ACACCAATGA ATGCATCCAG TTCCCATTCG TGTGCCCTCG AGACAAGCCC GTATGTGTCA 1380
 ACACCTATGG AAGCTACAGG TGCCGGACCA ACAAGAAGTG CAGTCGGGGC TACGAGCCCA 1440
 ACGAGGATGG CACAGCCTGC GTGGGGACTC TCGGCCAGTC ACCGGGGCCC CGCCCCACCA 1500
 5 CCCCCACCGC TGCTGCTGCC ACTGCCGCTG CTGCTGCCGC TGCTGGAGCT GCCACTGCTG 1560
 CACCGGTCTC COTAGATGGA GATCTCAATC TGGGGTCGGT GGTAAAGGAG AGCTCGGAGC 1620
 CCAGCTGCTG AGCAGGGGTG GGACATGAAC CAGCGGATGG AGTCCAGCAG GGGAGTGGGA 1680
 AAGTGGGCTT GTGCTGCTGC CTAGACAGTA GGGATGTAAA GGCCTGGGAG CTAGACCCCTC 1740
 CCAAAGCCCA TCCATGCACT TACTTAGCT AACCAATTAGG GAGACTCGTA AGGCCAGGCC 1800
 10 CTGTGCTGGG CACATAGCTG TGATCACAGC AGACAGGGTC GCTGCCCTGA TGGCGCTTAC 1860
 ATTCCAGTGG GTCTAATGAC CATATCTTAG GACACAGATG TGCCAGGGA GGTGGTGTCA 1920
 CTGCACAGGA AGTATGAGGA CTTTAGTGTG CTGAGTTCAA ATCCTGATTC AGGAACTCAC 1980
 AAAGCTATGT GACCTTACAC CAGTCACTTA ACTTGTATGC CATCCATTAT CGCATCTGCA 2040
 15 AAATGGGGAT TAAGAATAGA ATCTTGGGGT TAGTGTGGAG ATTAGATTAA ATGTATGTAA 2100
 GACACTTGGC ACAAACCTG GCACATAGTA AAGGCTCAAT AAAAAAAGT GCCTCTCACT 2160
 GGGCTTTGTC AACACGTG

Seq ID NO: 469 Protein sequence
Protein Accession #: NP_060528.1

1 11 21 31 41 51
 MDPEASDLR GILALRDVA EAGVSKYTG RGVSVGPILS SSASDIFCDN ENGNFLFHN 60
 RGDGTFVDA ASAGVDDPHQ HGRGVALADF NRDGKVDIVY GNWNGPHRLY LQMSTHGKVR 120
 25 FRDIASPKFS MSPVRTVIT ADFDNDQELE IFFNNIAYRS SSANRLPRVI RREHGDPLIE 180
 ELNPGDALEP EGRGTGGVVT DFDGDMMLDL ILSHGESMAQ PLSVFRGNQG FNNWLRVVP 240
 RTRVGAFARG AKVVLVYTKS GAHLRIIDGG SGYLCMEFV AHFGLKDEA SSVETWPDG 300
 KMVSRNVASG EMNSVLEILY PRDEDTLQDP APLETPMNAS SSHSCALET S PYVSTPMEAT 360
 GAGPTRSAVG ATPSPRMAQP AWGLSASHRA PAPPFPPPLL PLPLLLPLE LPLLHRSS

Seq ID NO: 470 DNA sequence
Nucleic Acid Accession #: AJ279016
Coding sequence: 1..1962

1 11 21 31 41 51
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 CAGCGGGCTG AACCATGTT CACTGCAGTC ACCAACTCAG TTCTGCTCTC TGACTATGAC 120
 40 AGTAATCCCA CCCAGCTCAA CTATGGTGTG GCAGTTACTG ATGTGGACCA TGATGGGGAC 180
 TTTGAGATCG TCGTGGCGGG GTACAATGGA CCCAACCTGG TTCTGAAGTA TGACCGGGCC 240
 CAGAAGCGCG TGGTGAACAT CGCGTTCGAT GAGCGCAGCT CACCCCTACT CGCGCTGCGG 300
 GACCGGCAGG GGAACGCCAT CGGGGTCACT GCCTGCGACA TCGACGGGGA CGGCCGGGAG 360
 GAGATCTACT TCCTCAACAC CAATAATGCC TTCTCGGGGG TGGCCACGTA CACCGACAAG 420
 45 TTGTTCAAGT CCGCAATAA CCGGTGGGAA GACATCCTGA GCGATGAGGT CAACGTGGCC 480
 CGTGGTGTGG CCAGCCTCTT TGCCGAGCGC TCTGTGGCCT GTGTGGACAG AAAGGGCTCT 540
 GGACGCTACT CTATCTACAT TGCCAATTAC GCCTACGGTA ATGTGGGGCC TGATGCCCTC 600
 ATTGAATAGG ACCCTGAGGC CAGTGACCTC TCCCGGGGCA TTCTGGCGCT CAGAGATGTG 660
 GCTGCTGAGG CTGGGGTCAG CAAATATACA GGGGGCCGAG GCGTCAGCGT GGGCCCCATC 720
 50 CTCAGCAGCA GTGCCTCGGA TATCTTCTGC GACAATGAGA ATGGGCCTAA CTTCCTTTTC 780
 CACAACCGGG CGGATGGCAC CTTTGTGGAC GCTGCGGCCA GTGCTGGTGT GGACGACCCC 840
 CACCAGCATG GCGAGGTGTG CGCCCTGGCT GACTTCAACC GTGATGGCAA AGTGGACATC 900
 GTCTATGGCA ACTGGAATGG CCCCCACCGC CTCTATCTGC AAATGAGCAC CCATGGGAAG 960
 55 GTCCGCTTCC GGGACATCGC CTCACCCAAG TTCTCCATGC CCTCCCTGTG CCGCACGGTC 1020
 ATCACCGCCG ACTTTGACAA TGACCAGGAG CTGGAGATCT TCTTCAACAA CATTGCCTAC 1080
 CGCAGCTCTC CAGCCAACCG CCTCTTCCGC GTCATCCGTA GAGAGCACGG AGACCCCTC 1140
 ATCGAGGAGC TCAATTCGGG CGAGCCTTGG GAGCCTGAGG GCCGGGGCAC AGGGGGTGTG 1200
 GTGACCGACT TCGACGAGA CGGGATGCTG GACCTCATCT TGTCCCATGG AGAGTCCATG 1260
 GCTCAGCCGC TGTCCGTCTT CCGGGGCAAT CAGGGCTTCA ACAACAACTG GCTGCGAGTG 1320
 60 GTGCCAGCA CCGGTTTGG GGCCTTTGCC AGGGGAGCTA AGGTCGTGCT CTACACCAAG 1380
 AAGAGTGGGG CCCACCTGAG GATCATCGAC GGGGGCTCAG GCTACCTGTG TGAGATGGAG 1440
 CCCGTGGCAC ACTTTGGCTT GGGGAAGGAT GAAGCCAGCA GTGTGGAGGT GACGTGGCCA 1500
 GATGGCAAGA TGGTGAGCCG GACGTGGGCC AGCGGGGAGA TGAACCTCAG GCTGGAGATC 1560
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 65 TTCTCCAGC AGGAAAATGG CCATTGCATG GACACCAATG AATGCATCCA GTTCCCATTC 1680
 GTGTGCCCTC GAGACAAGCC CGTATGTGTC AACACCTATG GAAGCTACAG GTGCCGGACC 1740
 AACAGAAGT GCAGTCGGGG CTACGAGCCC AACGAGGATG GCACAGCTG CGTGGGGACT 1800
 CTCGGCCAGT CACCGGGGCC CGGCCCCACC ACCCCACCGC CTGCTGTGTC CACTGCCGCT 1860
 70 GCTGCTGCCG CTGCTGGAGC TGCCACTGCT GCACCGGTCC TCGTAGATGG AGATCTCAAT 1920
 CTGGGTGCGG TGGTTAAGGA GAGCTGCGAG CCCAGCTGCT GAGCAGGGGT GGGACATGAA 1980
 CCAGCGGATG GAGTCCAGCA GGGGAGTGGG AAAGTGGGCT TGTGCTGCTG CCTAGACAGT 2040
 AGGGATGTAA AGGCCTGGGA GCTAGACCCT CCCAAGCCCC ATCCATGCAC ATTACTTAGC 2100
 TAACAATTAG GGAGACTCGT AAGGCCAGGC CCTGTGCTGG GCACATAGCT GTGATCACAG 2160
 CAGACAGGGT CGTGCCCTG ATGGCGCTTA CATTCAGTG GGTCTAATGA CCATATCTTA 2220
 75 GGACACAGAT GTGCCCAAGG AGTGGTGTG ACTGCACAGG AAGTATGAGG ACTTTAGTGT 2280
 CCTGAGTTCA AATCTGATT CAGGAAGTCA CAAAGCTATG TGACCTTACA CCAGTCACTT 2340
 AACTTGTTAG CCATCCATTA TCGCATCTGC AAAATGGGGA TTAAGAATAG AATCTTGGGG 2400
 TTAGTGTGGA GATTAGATTA AATGTATGTA AGACACTTGG CACAAAACCT GGCACATAGT 2460
 AAAGGCTCAA TAAAAACAAG TGCCTCTCAC TGGGCTTTGT CAACACG

Seq ID NO: 471 Protein sequence
Protein Accession #: CAC08451

1 11 21 31 41 51
 MSRMPLPFL LWFPLITEGS QRAEPMFTAV TNSVLPPDYD SNPTQLNYGV AVTDVDHGDG 60
 FEIVVAGYNG PNLVLKYDRA QKRLVNIADV ERSSPYALR DRQNAIGVT ACDIDGDGRE 120
 85 EIYFLNTNNA FSGVATYTDK LFKFRNNRWE DILSDEVNVA RGVASLFAGR SVACVDRKGS 180

GRYSIIYANY AYNGVGPDAL IEMDPEASDL SRGILALRDV AAEAGVSKYT GGRGVSVGPI 240
 LSSASDIFC DNENGNFLF HNRGDGTVD AAASAGVDDP HQHGRGVALA DFNDRGKVDI 300
 VYGNWNGPHR LYLQMSHKG VFRFDIASPK FSPMPSPVRTV ITADFDNDQE LEIPFNIAIY 360
 5 RSSANRLFR VIRREHGDPL IEELNPGDAL EPEGRTGGV VTDGFDGML DLILSHGESM 420
 AQLPSVFRGN QGFNNWLRV VPRTRFGAFA RGAKVVLTK KSGAHLRIID GSGYLCEME 480
 FVAHFLGKD EASSVEVTPW DGMVSRNVA SGEMNSVLEI LYPRDEDTLQ DPAPLECGQG 540
 FSQQENGHCN DTNECIQFPF VCPDRKPCV NTYGSYRCRT NKKCSRGEYEP NEDGTACVGT 600
 LGQSPGPRPT TPTAAATAA AAAAAGAATA APVLVDGDLN LGSVVKESCE PSC

Seq ID NO: 472 DNA sequence
 Nucleic Acid Accession #: FGENESH
 Coding sequence: 1..4794

15 1 11 21 31 41 51
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 AGCGGCTCCT CCCAGCATC CCTCCCAT TCCTCCTCCA GGTACAATGG ACCCAACTG 120
 GTTCTGAAGT ATGACCGGGC CCAGAAGCGG CTGGTGAACA TCGCGGTGGA TGAGCGCAGC 180
 20 TCACCTACT ACAGCGTCGCG GGACCGGCAG GGAACGCCA TCGGGGTAC AGCCTGCGAC 240
 ATCGACGGGG ACAGCGGGGA GGAGATCTAC TTCCTCAACA CCAATAATGC CTTCTCGGG 300
 CACAGCAGCT CAGCGCAGGT CCTTCTGGG CTCCACAGAA ACAGGCTGT GCTGAAGCCT 360
 CCACCTACAA CCTCTGCAGG CCTCTGGGT CTGCTCCAC TCAGCGGAAG GGACTTTTCC 420
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 25 GGGGTGGCCA CGTACACCGA CAAGTTGTTT AAGTTCCGCA ATAACCGGTG GGAAGACATC 600
 CTGAGCGATG AGGTCAACGT GGCCGTGGT GTGGCCAGCG TCTTTGCCG ACCTCTGTG 660
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 GGTAATGTGG GCCCTGATGC CCTCATTTGAA ATGGACCTTG AGGCCAGTGA CCTCTCCCG 780
 GGCACTCTGG CGCTCAGAGA TGTGGCTGCT GAGGCTGGGG TCAGCAATA TACAGAAGGC 840
 30 TTCTCCACA CTGCTCTCC AAGCATTGGT GAGATATCTG GCAGAACCGA GGAGCGGGAA 900
 GGAGGAGACC CAGAGGAGGC AGATGAGGAG CACAGTGGGG ATGGAAGCAC CAGCCAACCTG 960
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 TCCAAAAGAG ATTTGGTCTG CAGAAGCTTA TTTGGCCAC CATGTTACTA TTTGTCTGCT 1140
 35 GCGCTTCTC CAGCCACCCC TTTCCCTGCC CGCCAAGCCC CCCAACCTA CCTGTAGCC 1200
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 40 CTGAGAAGCT GGGAGGAAG CAGGCAGAAG GGGCAGGCCA TGTCCAGATG TGCACTCAGG 1440
 GAGCTGGGAG GTCCCTGGAG CCAAGCCACA CAGCACCTGC CTGCTAGAGA GCTGTATGAC 1500
 CTGGGAGAAC TCCCATTTT ACAGAAGAAC GACCGAGATC CAGGGAGGAG AAGGGACTCG 1560
 CCAAGGTCA CACAGGAGTG CCATCTAGTG GCCACCATGC CAGCTCTCGG GGGACTCGAG 1620
 GGCCCGGGGA GGGTGGCCAA GCGAGAGATT GGGAGAGAGA CTGGGGCAGT AGGAAGACCA 1680
 45 CTCTCCCATC CCTGTGCTCC CACTTCCCC AGCTGCTTGA GGCCTCTTGA AGCCGGGACA 1740
 GTGCCGGGAG CTGCCCTGCC TGGGAATCCT GGGAACTGGG TTCTGGACAT GGCCAAGGCC 1800
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 55 CCACATTGCC ATCATGTTT GTCTATGAGC TTTACAAGGA CCGGTCACG GTTCTATTCA 2340
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 60 GCGCTGGCTG ACTTCACTA TGTGGCAA GTGGACATCG TCTATGGCAA CTGGAATGGC 2640
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 70 GTCCAATCAC TACCAGGAAA AGGGGCTACG GGGTCCAATC ACTACCAGGA AAAGGGGCTA 3240
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5 GGAAGCTACA GGTGCCGAGC CAACAAGAAG TGCAGTCCGG GCTACGAGCC CAACGAGGAT 4560
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Seq ID NO: 473 Protein sequence
Protein Accession #: FGENESH predicted

1 11 21 31 41 51
MACPGGLPAR CSGWMGLGGP SGSSPASPPH SSSRYNGPNL VLKYDRAQKR LVNIAVDERS 60
15 SPYYALRDRQ GNAIVTACD IDGDGREIY FLNTNNAFSG HSSSAQVPSG LHRNRPVLKP 120
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GVATYTDKLF KFRNNRWEDI LSDEVNVARV VASLFAGRSV ACVDRKSGSR YSIYIANYAY 240
20 GNVGPDALIE MDPEASDLR GILALRDVAA EAGVSKYTEG FSHTASPSIG EISGRTEERE 300
GGDPPEADEE HSGDGSTSQL CRLGWDGQF KEEAAALVEE QREAGAAGVP RGRVRTALQT 360
SKSHLADKNL FGPPCYYSVC APSPAHPFPA RQAPQHYPA PLVTQLMTHG RLAGKLARSV 420
PHPRAPGMDP KCKGRHAEPG LMAEALGAWP ALSTTVVPGG LRSWEESRQK QAMSRCALR 480
ELGGPWSQAT QHLPARELYD LGEPPILQRT DGDPRRRRDS PKVTQECHLV ATMPALGGLE 540
GPRVAKREI GRETAGVGRP LSHPLVPNFP SCLRPLEAGT VPGAALPGNP GNWVLDMAKA 600
25 LAWNQMEKEE KKHGDHEPR FRLRKAREAE FPPGSSEEPL LQPPSGLRGS PVLQVGLGLA 660
SATHCGSMSF LGGRGVSVGP ILSSASDIF CDNENGNPFL FHNRGDGTFF DAAASAERRL 720
AFIVHLKYHL CRDFPHSLCH LAETGPSSSC CPWHARLLQA PHCHHGLSMS FTRTGSRFYS 780
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30 LSSERVNVGV DDPHVGGRV ALADFNDRGK VDIVYGNWNG PHRLYLQMS T HGVKVRFRDIA 900
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RGPIITTRKR GYVQSLPGKG ATGSNHYQEK GLQGPITTRK RGYGLQSLPG KGATGSNHYH 1140
35 RKGLRAPITT RKRGVGVQSL PGKATGSNH YQEKGLRGP TTRKRGYGLQ SLPGKATGS 1200
NHYQEKGLQG PITTRKRGYR VQSLPQKGAT GSNHYQEKGL RGPITTRKR YGLQSLPGKE 1260
AMGSNHYQEK GLRAPITTRK RGYGVQSLPG KGATGSNVIR REHGDPLIEE LNPGDALPE 1320
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KVVLVTKKGS AHLRIIDGGS GYLCEMEPVA HFGLGKDEAS SVEVTWPDGK MVSRRNVASGE 1440
40 MNSVLEILYP RDEDTLQDPA PLECCQGFSQ QENGHCMDTR ECIQFPFVCP RDKPVCVNTY 1500
GSYRCRTNKK CSRGYEPNED GTACVGTTELQ SRHTMTWKPR PKKELQLSQG ICTPVVWSFFL 1560
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Seq ID NO: 474 DNA sequence
Nucleic Acid Accession #: NM_003661.1
Coding sequence: 1..1152

1 11 21 31 41 51
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50 CAAAACGTTT CAAGTGGGAC AGATACTGGA GATCCTCAAA GTAAGCCCTT CGGTGACTGG 120
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AAGGAAAAAG TGAGCACACA GAATCTGCTA CTCCTGCTGA CTGATAATGA GGCCTGGAAC 240
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55 GACAACCTTG CAAGACAAAT GATCATGAAA GACAAAAACT GGCACGATAA AGGCCAGCAG 360
TACAGAAACT GGTTCCTGAA AGAGTTCTCT CGGTGAAAA GTGAGCTTGA GGATAACATA 420
AGAAGGCTCC GTGCCCTTGC AGATGGGGTT CAGAAGGTCC ACAAGGCAC CACCATCGCC 480
AATGTGGTGT CTGGCTCTCT CAGCATTTCC TCTGGCATCC TGACCCTCGT CGGCATGGGT 540
CTGGCACCCT TCACAGAGGG AGGCAGCCTT GTACTCTTGG AACCTGGGAT GGAGTTGGGA 600
60 ATCAGAGCCG CTTTGACCCG GATTACCAGC AGTACCATGG ACTACGAAA GAAGTGGTGG 660
ACACAAGCCC AAGCCACAGA CTGTGTCATC AAAAGCCTTG ACAAAATTGA GGAGGTGAGG 720
GAGTTTTTGG GTGAGAACAT ATCCAACCTT CTTTCTTAG CTGGCAATAC TTACCAACTC 780
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GTACCGCATG CCTCAGCCTC ACGCCCCCGG GTCATGAGC CAATCTCAGC TGAAGCGGT 900
65 GAACAGGTGG AGAGGGTTAA TGAACCCAGC ATCCTGGAAG TGAGCAGAGG AGTCAAGCTC 960
ACCGATGTGG CCCCTGTAAG CTTCTTTCTT GTGCTGGATG TAGTCTACCT CGGTACGAA 1020
TCAAAGCACT TACATGAGGG GGCAAGTCA GAGACAGCTG AGGAGCTGAA GAAGGTGGCT 1080
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CAAGAACTGT GA

Seq ID NO: 475 Protein sequence
Protein Accession #: NP_003652.1

1 11 21 31 41 51
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75 KEKVSTQNL LLLTDNEAWN GPVAAELPR NEADELRKAL DNLRQMIMK DKNWHDKQGG 120
YRNWFLKEFP RLKSELEDNI RRLRALADGV QKVHKGTTIA NVVSGSLSSS SGILTLVGMG 180
LAFTEGGSL VLEPEGMELG ITAALTGITS STMDYGKKWW TQAQAHDLVI KSLDKLKEVR 240
80 EPLGENISNF LSLAGNTYQL TRGIGKDIRA LRRARANLQS VPHASASRPR VTEPISAESG 300
EQVERVNEPS ILEMSRGVKL TDVAPVSFFL VLDVYLVYE SKHLHEGAKS ETAELKQVA 360
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Seq ID NO: 476 DNA sequence
Nucleic Acid Accession #: NM_014452.1
Coding sequence: 1..1968

1 11 21 31 41 51

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5	GCTCAGCCAG	AACAGAAAGGC	CTCGAATCTC	ATTGGCACAT	ACGCCCATGT	TGACCGTGCC	180
	ACCGGCCAGG	TGCTAACCTG	TGACAAGTGT	CCAGCAGGAA	CCTATGTCTC	TGAGCATGTG	240
	ACCAACACAA	GCCTGCGCGT	CTGCAGCAGT	TGCCCTGTGG	GGACCTTTAC	CAGGCATGAG	300
	AATGGCATAG	AGAAATGCCA	TGACTGTAGT	CAGCCATGCC	CATGGCCAAT	GATTGAGAAA	360
	TTACCTTTGTG	CTGCCCTTGAC	TGACCGAGAA	TGCATTTGCC	CACCTGGCAT	GTTCCAGTCT	420
10	AACGCTACCT	GTGCCCCCCA	TACGGTGTGT	CCTGTGGGTT	GGGGTGTGCG	GAAGAAAGGG	480
	ACAGAGACTG	AGAGAGTGGG	GTGTAAAGCAG	TGTGCTCGGG	GTACCTTCTC	AGATGTGCCT	540
	TCTAGTGTGA	TGAAATGCAA	AGCATACACA	GACTGTCTGA	GTCAGAACTT	GGTGGTGATC	600
	AAGCCGGGGA	CCAAGGAGAC	AGACAACGTC	TGTGGCACAC	TCCCGTCCTT	CTCCAGCTCC	660
	ACCTCACCTT	CCCTCGGACG	AGCCATCTTT	CCACGCCCTG	AGCACATGGA	AACCCATGAA	720
15	GTCCCTTCTT	CCACTTATGT	TCCCAAAGGC	ATGAACCTCA	CAGAACTCAA	CTCTTCTGCC	780
	TCTGTTAGAC	CAAAGGTACT	GAGTAGCATC	CAGGAAGGGA	CAGTCCCTGA	CAACACAAGC	840
	TCAGCAAGGG	GGAAGGAAGA	CGTGAACAAG	ACCCTCCCAA	ACCTTCAGGT	AGTCAACCAC	900
	CAGCAAGGCC	CCCAACACAG	ACACATCCTG	AAGCTGCTGC	CGTCCATGGA	GGCCAAGTGG	960
	GGCGAGAAAT	CCAGCAGCGC	CATCAAGGGC	CCCAAGAGGG	GACATCCTAG	ACAGAACTTA	1020
20	CACAAGCATT	TTGACATCAA	TGAGCATTTG	CCCTGGATGA	TTGTGCTTTT	CCTGCTGCTG	1080
	GTGCTTGTGG	TGATTGTGGT	GTGCAGTATC	CGGAAAGCT	CGAGGACTCT	GAAAAAGGGG	1140
	CCCCGGGAGG	ATCCAGTGC	CATTGTGGAA	AAGGCAGGGC	TGAAGAAATC	CATGACTCCA	1200
	ACCCAGAAAC	GGGAGAAATG	GATCTACTAC	TGCAATGGCC	ATGGTATCGA	TATCTGAAG	1260
	CTTGTAGCAG	CCCAAGTGGG	AAGCCAGTGG	AAAGATATCT	ATCAGTTTCT	TTGCAATGCC	1320
	AGTGAGAGGG	AGGTTGCTGC	TTTCTCCAAT	GGGTACACAG	CCGACCACGA	GCGGGCTTAC	1380
25	GCAGCTCTGC	AGCACTGGAC	CATCCGGGGC	CCCGAGGCCA	GCCTCGCCCA	GCTAATTAGC	1440
	GCCCTGCGCC	AGCACCGGAG	AAACGATGTT	GTGGAGAAGA	TTCGTGGGCT	GATGGAAGAC	1500
	ACCACCCAGC	TGGAAACTGA	CAAACTAGCT	CTCCCGATGA	GCCCCAGCCC	GCTTAGCCCG	1560
	AGCCCCATCC	CCAGCCCCAA	CGGAAACTT	GAGAAATCCG	CTCTCTTAC	GGTGGAGCCT	1620
	TCCCCACAGG	ACAAGAACAA	GGGCTTCTTC	GTGGATGAGT	CGGAGCCCCC	TCTCCGCTGT	1680
30	GACTCTACAT	CCAGCGGCTC	CTCCGCGCTG	AGCAGGAACG	GTTCCTTTAT	TACCAAAGAA	1740
	AAGAAGGACA	CAGTGTGTGG	GCAGGTACGC	CTGGACCCCT	GTGACTTGCA	GCCTATCTTT	1800
	GATGACATGC	TCCACTTTCT	AAATCCTGAG	GAGCTGCGGG	TGATTGAAGA	GATTCCCCAG	1860
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35	CAGACCTCC	TGGACTCTGT	TTATAGCCAT	CTTCTGACC	TGCTGTAG		

Seq ID NO: 477 Protein sequence
Protein Accession #: NP_055267.1

	1	11	21	31	41	51	
40	MGTSPPSSSTA	LASCSRIARR	ATATMIAGSL	LLGLFLSTTT	AQPEQKASNL	IGTYRHVDRA	60
	TGQVLTCDKC	PAGTYVSEHC	TNTSLRVCS	CPVGTFRHE	NGIEKCHDCS	QPCPWPMEIK	120
	LPCAALTDRE	CTCPPGMFQS	NATCAPHTVC	PVGWGVRRKG	TETEDVRCKQ	CARGTFSDVP	180
45	SSVMKCKAYT	DCLSQLNVVI	KPGTKETDNV	CGTLPSPFSS	TSPSPGTAIF	PRPEHMETHE	240
	VPSSTYVPKG	MNSTESNSSA	SVRPKVLSSI	QEGTVPDNTS	SARGKEDVNK	TLPNLQVNVH	300
	QQGPHRHIL	KLLPSMEATG	GEKSSSTPIK	PKRGHPRQNL	HKHFDINEHL	PWMIVLFLLL	360
	VLVVIVVCSI	RKSSRTLKKG	PRQDPSAIVE	KAGLKKSMTP	TQNRKWIYY	CNGHGIDILK	420
	LVAQVGSQW	KDIYQFLCNA	SEREVAAFSN	GYTADHERAY	AALQHWITRG	PEASLAQLIS	480
	ALRQHRNDV	VEKIRGLMED	TTQLETDKLA	LPMSPSPLSP	SPIPSNPAKL	ENSALLTVEP	540
50	SPQDKNKGF	VDESEPLLRC	DSTSSGSSAL	SRNGSFITKE	KKDTVLRQVR	LDPCLQPIF	600
	DDMLHFLNPE	ELRVIEEIPQ	AEDKLDRLF	IIGVKSQEAS	QTLDSVYSH	LPDLL	

Seq ID NO: 478 DNA sequence
Nucleic Acid Accession #: XM_044533
Coding sequence: 238..2751

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	GGAGGCGGGG	GCCCCCGGGG	CGACTCGGGG	GCGGACCGCG	GGGCGGAGCT	GCCGCCCGTG	180
	AGTCCGGCCG	AGCCACCTGA	GCCCCAGCCG	CGGGACACCG	TGCTCTCTGC	TCTCCGAATG	240
	CTCGCACCCG	CGATGGGCGT	GAGGAGCTGG	CTCGCCGCCC	CATGGGGCGC	GCTGCCGCTC	300
	CGGCCACCGC	TGCTGCTGCT	CCTGCTGCTG	CTGCTCTGCT	TGCAGCCGCC	GCCTCCGACC	360
65	TGGGCGCTCA	GCCCCCGGAT	CAGCCTGCGT	CTGGGCTCTG	AAGAGCGGCC	ATTCTCTAGA	420
	TTCGAAGCTG	AACACATCTC	CAACTACACA	GCCCTTCTGC	TGAGCAGGGA	TGGCAGGACC	480
	CTGTACTGTG	GTGCTCGAGT	GGCCCTCTTT	GCACTCAGTA	GCAACCTCAG	CTTCTGCCA	540
	GGCGGGGAGT	ACCAGGAGCT	GCTTTGGGGT	GCAGACGCGG	AGAAGAAACA	GCAGTGCAGC	600
	TTCAAGGGCA	AGGACCCACA	GCGCGACTGT	CAAAACTACA	TCAAGATCCT	CCTGCCGCTC	660
70	AGCGGCAGTC	ACCTGTTCAC	CTGTGGCACA	GCAGCCTTCA	GCCCCATGTG	TACCTACATC	720
	AACATGGAGA	ACTTCACCTT	GGCAAGGGAC	GAGAAGGGGA	ATGTCCTCCT	GGAAGATGGC	780
	AAGGGCCGTT	GTCCCTTCGA	CCCGAATTTT	AAGTCCAATG	CCCTGGTGGT	TGATGGCGAG	840
	CTCTACACTG	GAACAGTCAG	CAGCTTCCAA	GGGAATGACC	CGGCCATCTC	GCGGAGCCAA	900
75	AGCCTTGGCC	CCACCAAGAC	CGAGAGCTCC	CTCAACTGGC	TGCAAGACCC	AGCTTTTGTG	960
	GCCTCAGCCT	ACATTCTCTA	GAGCCTGGGC	AGCTTGCAAG	GCGATGATGA	CAAGATCTAC	1020
	TTTTTCTTCA	GCGAGACTGG	CCAGGAATTT	GAGTTCTTTG	AGAACACCAT	TGTGTCCCGC	1080
	ATTGCCCGCA	TTTGCAAGGG	CGATGAGGGT	GGAGAGCGGG	TGCTACAGCA	GCGCTGGACC	1140
	TCCTTCTCTA	AGGCCAGGCT	GCTGTGCTCA	CGGCCCGACG	ATGGCTTCCC	CTTCAACGTC	1200
80	CTGCAGGATG	TCTTACAGCT	GAGCCCCAGC	CCCCAGGACT	GGCGTGACAC	CCTTTCTTAT	1260
	GGGGTCTTCA	CTTCCCAGTG	GCACAGGGGA	ACTACAGAAG	GCTCTGCCGT	CTGTGTCTTC	1320
	ACAATGAAGG	ATGTGCAGAG	AGTCTTCAGC	GGCCTCTACA	AGGAGGTGAA	CCGTGAGACA	1380
	CAGCAGTGGT	ACACCGTGAC	CCACCCGGTG	CCCACACCCC	GGCCTGGAGC	GTGCATCACC	1440
	AACAGTCCCC	GGGAAAGGAA	GATCAACTCA	TCCCTGCAGC	TCCAGACCCG	CGTGGCTGAA	1500
	TTCTCAAGG	ACCACTTCTT	GATGGACGGG	CAGGTCCGAA	GCCGCATGCT	GCTGCTGCAG	1560
85	CCCCAGGCTC	GCTACCAAGC	CGTGGCTGTA	CACCGCGTCC	CTGGCCTGCA	CCACACCTAC	1620
	GATGTCTCTT	TCCTGGGCAC	TGGTGACGGC	CGGCTCCACA	AGGCAGTGAG	CGTGGGCCCC	1680
	CGGGTGACCA	TCATTGAGGA	GCTGCAGATC	TTCTCATCGG	GACAGCCCGT	GCAGAACTGT	1740

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 5 ACCAGGCCGT GGATCCAGGA CATCGAGGA GCCAGCGCA AGGACCTTTG CAGCGCTCT 1980
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 20 GGCCAGCTGG CCGTGTGCTC TCCAGTCAAG TAGCGAAGCT CCTACCACCC AGACACCCAA 2940
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 CAGGACCCAG TTGGGCTGCG TGGCTTCTGC CTTGCGAGTC AGCCGAGGAT GTAGTTGTG 3300
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 30 CAGGGAAGAG ACTGTGCGCT GCCTTCTCC GTTGTGCGT GAGAACCCGT GTGCCCTTC 3540
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 TCAACACTGC CCAGCACAGG GGCCCTGAAT TTATGTGGTT TTTATACATT TTTAATAAG 3720
 35 ATGCACCTTA TGTCTTTTT TAATAAAGTC TGAAGAATTA CTGTTT

Seq ID NO: 479 Protein sequence
 Protein Accession #: XP_044533.3

1 11 21 31 41 51
 40 | | | | |
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 RFEAHISNY TALLLSRDRG TLYVGAREAL FALSSNLSFL PGGEYQELLW GADAEKKQQC 120
 SFKGDQPDQR CQNYIKILF LSGSHLFTCG TAAFSPPMCTY INMENFTLAR DEKGNVLLED 180
 45 GKRCPPDPN FKSTALVVDG ELYTGVVSSP QGNDPAISRS QSLRPTKTES SLNWLQDPAF 240
 VASAYIPESL GSLQGGDDKI YFFFSETGQE FEFFENTIVS RIARICKGDE GGERVLQQRW 300
 TSFLKAQLLC SRPDDGFPPN VLQDVPTLSP SPQDWRDTLP YGVFTSQWHR GTTEGSAVCV 360
 FTMKDQVRVF SGLYKEVNR E QQWYTVTHP VPTPRPGACI TNSARERKIN SSLQLPDRVL 420
 NFLKDHFLMD GQVRSRMLLL QPQARYQRYA VHRVPGLHHT YDVLFLGTGD GRLHKAHSV 480
 50 PRVHIIEELQ IFSSGQPVQN LLLDTHRGLL YAASHSGVVQ VPMANCSLYR SCGDCLLARD 540
 FYCAWSGSSC KHVSLYQPL ATRPWIQDIE GASAKDLCSA SSVSPSPFVP TGEKPCEQVQ 600
 PQPNTVNTLA CPLLSNLATR LWLRNGAPVN ASASCHVLPT GDLLLVGTQQ LGFQCNSLE 660
 EGQQLVASY CPEVVEDGVA DQDDEGGSVP VIISTSRVSA PAGGKASWA DRSYWKFLV 720
 MCTFLVLAFL LPVFLLYRH RNSMKVFLKQ GECASVHPKT CPVVLPPETR PLNLGPPST 780
 55 PLDHRGYSLS SDSPPGSRVF TESEKRPLSI QDSFVEVSPV CPRPRVRLGS EIRDSVV

Seq ID NO: 480 DNA sequence
 Nucleic Acid Accession #: NM_004217.1
 Coding sequence: 58..1092

1 11 21 31 41 51
 60 | | | | |
 GGCCGGGAGA GTAGCAGTGC CTTGGACCCC AGCTCTCCTC CCCCTTTCTC TCTAAGGATG 60
 GCCCAGAAAG AGAACTCCTA CCCCTGGCCC TACGGCCGAC AGACGGCTCC ATCTGGCCTG 120
 AGCACCTGTC CCCAGCGAGT CCTCCGGAAG GAGCCTGTCA CCCCATCTGC ACTTGTCTCT 180
 65 ATGAGCCGCT CCAATGTCCA GCCCACAGCT GCCCTTGCC AGAAGGTGAT GGAGAATAGC 240
 ATGCGGACAC CCGACATCTT AACCGGGCAC TTCACAAATG ATGACTTTGA GATTGGGCGT 300
 CCTCTGGGCA AAGCGAAGTT TGGAAACGTC TACTTGGCTC GGGAGAAGAA AAGCCATTTC 360
 ATCGTGGCGC TCAAGTCTCT CTTCAAGTCC CAGATAGAGA AGGAGGGCGT GGAGCATCAG 420
 70 CTGCGCAGAG AGATCGAAAT CCAGGCCAC CTGCACCATC CCAACATCCT GCGTCTCTAC 480
 AACTATTTTT ATGACCGGAG GAGGATCTAC TTGATTCTAG AGTATGCCCC CCGCGGGGAG 540
 CTCTACAAGG AGCTGCAGAA GAGCTGCACA TTGACGAGC AGCGAACAGC CACGATCATG 600
 GAGGAGTTGG CAGATGCTCT AATGTACTGC CATGGGAAGA AGGTGATTCA CAGAGACATA 660
 AAGCCAGAAA ATCTGCTCTT AGGGCTCAAG GGAGAGCTGA AGATTGTGTA CTTGGGCTGG 720
 75 TCTGTGCATG CGCCCTCCCT GAGGAGGAAG ACAATGTGTG GCACCTGGA CTACCTGCCC 780
 CCAAGATGA TTGAGGGGCG CATGCACAA TGAAGAAGTGG ATCTGTGGTG CATTTGAGTG 840
 CTTTGTCTATG AGCTGCTGGT GGGGAACCCA CCCTTTGAGA GTGCATCACA CAACGAGACC 900
 TATCGCCGCT TCGTCAAGGT GGACCTAAAG TTCCCGCTT CTGTGCCAC GGGAGCCAG 960
 80 GACCTCATCT CCAAACTGCT CAGGCATAAC CCCTCGGAAC GGCTGCCCTT GGCCAGGTC 1020
 TCAGCCACCT CTTGGGTCGG GGCCTCACTCT CGGAGGGTGC TGCCCTCCCTC TGCCCTTCAA 1080
 TCTGTGCGCT GATGGTCCCT GTCAATCACT CGGGTGGTGT TGTGTGTATG TCTGTGTATG 1140
 TATAGGGGAA AGAAGGGATC CTTAATCTGT CCCTTATCTG TTTTCTACCT CCTCCTTTGT 1200
 TTAATAAAGG CTGAAGCTTT TTGT

Seq ID NO: 481 Protein sequence
 Protein Accession #: NP_004208

1 11 21 31 41 51

MAQKENSYPW	PYGRQTAPSG	LSTLPQVRVLR	KEPVTPSALV	LMSRSNVQPT	AAPGQKVMEN	60
SSGTPDILTR	HFTIDDFEIG	RPLGKGKFGN	VYLAREKKSH	FIVALKVLFPK	SQIEKEGVEH	120
QLRREIEIQA	HLHHPNLRRL	YNYFYDRRRI	YLILEYAPRG	ELYKELQKSC	TFDEQRTATI	180
MEELADALMY	CHGKKVIHRD	IKPENLLLGL	KGELKIADFG	WSVHAPSLRR	KTMCGTLDYL	240
PPEMIEGRMH	NEKVDLWCTG	VLCYELLVGN	PPFESASHNE	TYRRIVKVDL	KFPASVPTGA	300
QDLISKLLRH	NPSERLPLAQ	VSAHPWVRAN	SRRVLPPSAL	QSV		

Seq ID NO: 482 DNA sequence
Nucleic Acid Accession #: AK055663
Coding sequence: 38..1423

1	11	21	31	41	51	
AGAACGGCTT	COGGCGGGAG	CTGTGCAGCT	CCTTATCATG	GGGACAATTC	ATCTCTTTCC	60
AAAACCACAA	AGATCCTTTT	TTGGCAAGTT	GTTACGGGAA	TTTAGACTTG	TAGCAGCTGA	120
CCGAAGGTCC	TGGAAGATAC	TGCTCTTTGG	TGTAATAAAC	TTGATATGTA	CTGGCTTCCT	180
GCTTATGTGG	TGCAGTTCTA	CTAATAGTAT	AGCTTTAACT	GCCTATACTT	ACCTGACCAT	240
TTTGTATCTT	TTTAGTTTAA	TGACATGTTT	AATAAGTTAC	TGGGTAACAT	TGAGGAAACC	300
TAGCCCTGTC	TATTCATTGG	GGTTTGAAAG	ATTAGAAGTC	CTGGCTGTAT	TTGCCCTCCAC	360
AGTCTTGGCA	CAGTTGGGAG	CTCTCTTTAT	ATTAAGAGAA	AGTGCAGAAC	GCTTTTGGGA	420
ACAGCCCGAG	ATACACACGG	GAAGATTATT	AGTTGGTACT	TTTGTGGCTC	TTTGTTTCAA	480
CCTGTTACAG	ATGCTTTCTA	TTCCGAATAA	ACCTTTTGCT	TATGCTCAG	AAGCTGCTAG	540
TACGAGCTGG	CTTCAAGAGC	ATGTTGCAGA	TCTTAGTCTG	AGCTTGTGTG	GAATTATTCC	600
GGGACTTAGC	AGTATCTTCC	TTCCCCGAAT	GAATCCATTT	GTTTTGATTG	ATCTTGCTGG	660
AGCAITTTGCT	CTTTGTATTA	CATATATGCT	CATTGAAATT	AATAATTATT	TTGCCGTAGA	720
CACCTGCCTCT	GCTATAGCTA	TTGCCCTGAT	GACATTTGGC	ACTATGTATC	CCATGAGTGT	780
GTACAGTGGG	AAAGTCTTAC	TCCAGACAAC	ACCACCCCAT	GTTATTGGTC	AGTTGGACAA	840
ACTCATCAGA	GAGGTATCTA	CCTTAGATGG	AGTTTATAGG	GTCCGAAATG	AACATTTTGG	900
GACCCTAGGT	TTTGGCTCAT	TGGCTGGATC	AGTGCATGTA	AGAATTGAC	GAGATGCCAA	960
TGAACAAATG	GTCTTGTCTC	ATGTGACCAA	CAGGCTGTAC	ACTCTAGTGT	CTACTCTAAC	1020
TGTTCAAAT	TTCAAGGATG	ACTGGATTAG	GCCTGCCTTA	TTGTCTGGGC	CTGTGTCAGC	1080
CAATGTCCTA	AACTTTTCAG	ATCATCACGT	AATCCCAATG	CCTCTTTTAA	AGGGTACTGA	1140
TGATTTGAAC	CCAGTTACAT	CAACTCCAGC	TAAACCTAGT	AGTCCACCTC	CAGAATTTTC	1200
ATTTAAACACT	CCTGGGAAAA	ATGTGAACCC	AGTTATTCTT	CTAAACACAC	AAACAAGGCC	1260
TTATGGTTTT	GGTCTCAATC	ATGGACACAC	ACCTTACAGC	AGCATGCTTA	ATCAAGGACT	1320
TGGAGTTCCA	GGAATTTGGG	CAACTCAAGG	ATTGAGGACT	GGTTTATCAA	ATATACCAAG	1380
TAGATATGGA	ACTAATAATA	GAATTGGACA	ACCAAGACCA	TGATAGACTC	TAACATTATT	1440
TTATAAGGAA	TATTGACTCC	TTGGCTTCCA	ATTTATTTAG	TAATCCAAC	TTGCATTGAC	1500
TGTTTAAATCA	TTTACTCTAA	ATGTTAGATA	ATAGTAGTCT	TGTTCACTAT	TCATGAAACC	1560
TATGAAACTA	TATTTTGTGA	AAATGTATTT	GTGACAGTGA	AATCCTCGTA	AATGTTAAAG	1620
GCTTTAAATA	GGCTTCTCTT	AGAAAATGTG	TTTCTTTAAA	TTTGGATTTT	GGTATCTTTG	1680
GTTTTGTAGT	TGACTGTCAGT	GTGATGTGAC	CTTACCTTTA	TAAGAGCCAC	TTGATGGAGT	1740
AGATCTGTCA	CTTACTTAAG	ATACGATATT	TCTTTTTTTT	TCCGAGACGG	AGTCTTCTCT	1800
TGCCACTGTG	CCCGGCCAAT	ACATTATTAT	TAACCTAAGG	CTGTACTTTA	TTAAGGCTTC	1860
CTTAGTTTTT	GTTTTGTGTT	GTTTTTTGAG	ATGGAGTCTC	ACTCTGTGCG	CCAGGCTGGA	1920
ATGCAGTGGC	ATGATCTCAG	CTCACTGCAA	CCTCTGCTCT	CTGAGTTCAA	ATGATTCTCC	1980
TGCCTCAGCC	TCCCGAGTAG	CTGGGATTAC	AGGCACCTGC	CACCACGCCC	AGCTAATTTT	2040
TGTATTTTAA	GTAAAGACGG	GGGATTTTCA	CATGTTGGCC	AGGCTGTGCT	TGAACCTCTG	2100
ACCTCATGAT	CCACCCACTC	TAGCCTCCCA	AAGTGTGGG	ATTAGGTGTG	AGCCACCGCA	2160
CCTGGCCGAT	ATTTTCTTTA	ATGAAATTTA	TAAATATGCT	TCTTGAATAA	TACACATTTT	2220
GGGAAAGGGA	AAAATGCTTG	TTCAAAAAGT	AAAGGTCTCT	TTTATAGCTT	TTCCAAAAC	2280
AAATTGCTAA	TTTTTCTTTG	AGGTTCTCCT	GAATTATGTC	TTACAAACTA	AAAGCAAAAA	2340
TTTTTAGCAG	AAATTTTGGA	ATACATTCTA	TCTAGCACAA	TTTGAATTTT	TAATTATCAA	2400
GATTTTGTGT	AAAGTTTCTC	TCCTTTAAAA	ATTTTAGTAC	ATTTGTAAT		

Seq ID NO: 483 Protein sequence
Protein Accession #: BAB70980.1

1	11	21	31	41	51	
MGTIHLFRKP	QRSFFGKLLR	EFRLVAADRR	SWKILLFGVI	NLICTGFLLM	WCSSTNSIAL	60
TAYTYLTIFD	LFSMLTCLIS	YWVTLRKPS	VYSFGFERLE	VLAFASTVL	AQLGALFILK	120
ESAERFLEQP	EHTGRLLVVG	TFVALCFNLF	TMLSIRNKPF	AYVSEAASTS	WLQEHVADLS	180
RSLCGIIPGL	SSIFLPRMNP	FVLIDLAF	ALCITYMLIE	INNYFAVDTA	SAIAIALMTF	240
GTMYPMVSYS	GKVLQTPP	HVIGQLDKLI	REVSTLDGVL	EVRNEHFWTL	GFGSLAGSVH	300
VRIRRDANEQ	MVLAHVNTNL	YTLVSTLTQ	IFKDDWIRPA	LLSGPVAANV	LNFSDDHVIP	360
MPLLKGTDDL	NPVTSTPAKP	SSPPPEFSFN	TPGKNVNPVI	LLNTQTRPYG	FGLNHHGHTPY	420
SSMLNQLGLV	PGIGATQGLR	TGFTNIPSR	GTNNRIGQPR	P		

Seq ID NO: 484 DNA sequence
Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 1..900

1	11	21	31	41	51	
ATGCGCGCGC	GGGAGCTGAG	CGAGGCGGAG	CCGCCCCCGC	TCCGGGCCCC	GACCCCTCCC	60
CCGCGGCGGC	GAGCGCGGCC	CCCAGAGCTG	GGCATCAAGT	GCGTGCTGGT	GGGCGACGGC	120
GCCGTGGGCA	AGAGCAGCCT	CATCGTCAGC	TACACCTGCA	ATGGGTACCC	CGCGCGCTAC	180
CGGCCCACTG	CAGCTGGACAC	CTTCTCTGGT	ACGTACGTTT	AATCGCCCGT	GCGGCGCGCT	240
GGCTGCGGCG	GGGCTGTGCA	CCGGGAGGCT	GGGCGGGGCG	TCTCGGCGGG	AGGGCGCAGA	300
GGACCCCGGG	GAGGAGACTG	GAGCAGGCCC	CGAGGTGGCG	CTGGTGGCGG	CCAGGACGCT	360
CTTCTTAAC	CAGGCTCTCC	CCGCCCGGCC	CCTGCAGTGC	AAGTCTGGT	GGATGGAGCT	420
CCGGTGGCGA	TTGAGCTCTG	GGACACAGCG	GGACAGGAGG	ATTTTGACCG	ACTTCGTTCC	480
CTTTGCTACC	CGGATACCGA	TGTCTTCTTG	GCGTGCTTCA	GCGTGGTGCA	GCCAGCTCC	540
TTTCAAAAGA	TACAGAGGAA	ATGGCTGCC	GAGATCCGCA	CGCACACCC	CCAGGCGCTC	600
GTGCTGCTGG	TGGGCACCCA	GGCCGACCTG	AGGACGATG	TCAACGTACT	AATTCAGCTG	660

GACCAGGGGG GCGGGGAGGG CCCCGTGCCC CAACCCAGG CTCAGGGTCT GGCCGAGAAG 720
 ATCCGAGCCT GCTGTACCT TGAGTGCTCA GCCTTGACGC AGAAGAACTT GAAGGAAGTA 780
 TTGACTCGG CTATTCTCAG TGCCATTGAG CACAAAGCCC GGCTGGAGAA GAAACTGAAT 840
 GCCAAAGGTG TGCACACCT CTCGCGCTGC CGCTGGAAGA AGTTCCTCTG CTCGTTTGA

Seq ID NO: 485 Protein sequence
 Protein Accession #: PGENESH predicted

1 11 21 31 41 51
 | | | | |
 MPPRELSEAE PPPLRAPTPP PRRRSAPPEL GIKCVLVGDG AVKGSSSLIVS YTCNGYPARY 60
 RPTALDTFSG TVVQSPVRRP GCGGAVHRGA GAGVSAGGRR GPRGGDWSRP RGGAGAAQDA 120
 LPNSGSPRPA PAVQVLVDGA PVRIELWDTA GQEDFDRLLS LCYPDTDVFL ACFSVVQPSS 180
 FQNIETKMLP EIRTHNPQAP VLLVGTQADL RDDVNVLIQL DQGGREGPVP QPQAQGLAEK 240
 IRACCYLECS ALTQNLKEV FDSAILSIAIE HKARLEKKLN AKGVRTL SRC RWKKFFCFV

Seq ID NO: 486 DNA sequence
 Nucleic Acid Accession #: XM_063832.2
 Coding sequence: 1..711

1 11 21 31 41 51
 | | | | |
 ATGCCGCGCG GGGAGCTGAG CGAGGCCGAG CCGCCCCCGC TCCGGGCCCC GACCCCTCCC 60
 CCGCGGCGCG GTAGGCGCGC CCCAGAGCTG GGCATCAAGT GCGTGTCTGT GGGCGACGGC 120
 GCGGTGGGCA AGAGCAGCCT CATCGTCAGC TACACCTGCA ATGGGTACCC CGCGCGCTAC 180
 CGGCCCACTG CGCTGGACAC CTTCTCTGTG CAAGTCCTGG TGGATGGAGC TCCGGTGC GC 240
 ATTGAGCTCT GGGACACAGC GGGACAGGAG GATTTTGACC GACTTCGTTC CTTTGTCTAC 300
 CCGGATACCG ATGTCTTCTT GGCCTGCTTC AGCGTGGTGC AGCCCACTC CTTTCAAAAC 360
 ATCACAGAGA AATGGCTGCC CGAGATCCGC ACGCACAACC CCCAGGCGCC TGTGCTGCTG 420
 GTGGGCACCC AGGCCGACCT GAGGACGAT GTCAACGTAC TAATTAGCT GGACCAAGGG 480
 GGCGGGGAGG GCGCCGTGCC CCAACCCAG GCTCAGGGTC TGGCCGAGAA GATCCGAGCC 540
 TGTGCTACCT TTGAGTGCTC AGCCTTGACG CAGAAGAACT TGAAGGAAGT ATTTGACTCG 600
 GCTATTCTCA GTGCCATTGA GCACAAAGCC CGGCTGGAGA AGAACTGAA TGCCAAAGGT 660
 GTGCGCACCC TCTCCGCTG CCGCTGGAAG AAGTCTTCT GCTTCGTTTG A

Seq ID NO: 487 Protein sequence
 Protein Accession #: XP_063832.1

1 11 21 31 41 51
 | | | | |
 MPPRELSEAE PPPLRAPTPP PRRRSAPPEL GIKCVLVGDG AVKGSSSLIVS YTCNGYPARY 60
 RPTALDTFSV QVLVDGAPVR IELWDTAGQE DFDRRLSLCY PDTDVFLACF SVVQSSSFQN 120
 ITEKWLPEIR THNPQAPVLL VGTQADLRDD VNVLIQLDQG GREGPVPQPO AQGLAEKIRA 180
 CCYLECSALT QKNLKEVFDS AILSAIEHKA RLEKKLNAGK VRTL SRCRWK KFFCFV

Seq ID NO: 488 DNA sequence
 Nucleic Acid Accession #: NM_014398.1
 Coding sequence: 64..1314

1 11 21 31 41 51
 | | | | |
 GGCACCGATT CGGGGCTGCG CCGGACTTCG CCGCACGCTG CAGAACCTCG CCCAGCGCCC 60
 ACCATGCCCC GGCAGCTCAG CGCGCGGCGC GCGCTCTTCG CGTCCCTGGC CGTAATTTTG 120
 CACGATGGCA GTCAAATGAG AGCAAAAGCA TTTCCAGAAA CCAGAGATTA TTCTCAACCT 180
 ACTGCAGCAG CAACAGTACA GGACATAAAA AAACCTGTCC AGCAACACAGC TAAGCAAGCA 240
 CCTCACCAA CTTTAGCAGC AAGATTCATG GATGGTCATA TCACCTTTCA AACAGCGGCC 300
 ACAGTAAAAA TTCCAACAAC TACCCAGCA ACTACAAAAA ACTGTCAAC CACCAGCCCA 360
 ATTACCTACA CCCTGGTCAC AACCCAGGCC ACACCCAAACA ACTCACACAC AGCTCCTCCA 420
 GTTACTGAAG TTACAGTCGG CCTAGCTTA GCCCTTATT CACTGCCACC CACCATCACC 480
 CCACCACTC ATACAGCTGG AACCACTTCA TCAACCGTCA GCCACACAAC TGGGAACACC 540
 ACTCAACCCA GTAACCAAG CACCTTCCA GCAACTTTAT CGATAGCACT GCACAAAAGC 600
 ACAACCGGTC AGAAGCTGGA TCAACCCACC CATGCCCCAG GAACAACGGC AGCTGCCACC 660
 AATACCAACC GCACAGCTGC ACCTGCCCTCC ACGGTTCTCG GGCCACCCCT TGCACCTCAG 720
 CCATCGTCAG TCAAGACTGG AATTATCAG GTTCTAAACG GAAGCAGACT CTGTATAAAA 780
 GCAGAGATGG GGATACAGCT GATTGTTCAA GACAAGGAGT CGGTTTTTTC ACCTCGGAGA 840
 TACTTCAACA TCGACCCCAA CGCAACGCAA GCCTCTGGGA ACTGTGGCAC CCGAAAATCC 900
 AACCTTCTGT TGAATTTTCA GGGCGGATTT GTGAATCTCA CATTTACCAA GGATGAAGAA 960
 TCATATTATA TCAGTGAAGT GGGAGCCTAT TTGACCGTCT CAGATCCAGA GACAGTTTAC 1020
 CAAGGAATCA AACATGCGGT GGTGATGTTT CAGACAGCAG TCGGGCATT CTTCAAGTGC 1080
 GTGAGTGAAC AGAGCCTCCA GTTGTGAGCC CACCTGCAGG TGAACCAAC CGATGTCCAA 1140
 CTTCAAGCCT TTGATTTTGA AGATGACCAC TTTGGAAATG TGGATGAGTG CTCGTCTGAC 1200
 TACACAATTG TGCTTCTGT GATTGGGGCC ATCGTGGTTG GTCTCTGCCT TATGGGTATG 1260
 GGTGTCTATA AAATCCGCTT AAGGTGTCAA TCATCTGGAT ACCAGAGAAT CTAATTGTTG 1320
 CCGGGGGGGA ATGAAAATTA TGAATTTAG AGAAGCTTTT CATCCCTTCC AGGATGGATG 1380
 TTGGGAAATT CCCTCAGAGT GTGGGTCTTT CAAACAATGT AAACCAACAT CTTCTATTCA 1440
 AATGAAGTGA GTCATGTGTG ATTTAAGTTC AGGCAGCACA TCAATTTCTA AATACTTTTT 1500
 GTTATTTTGA TGAAGATAT AGTGAGCTGT TTATTTTCTA GTTCTCTTGA GAATATTTA 1560
 GCCACTCAAA GTCAACATTT GAGATATGTT GAATTAACAT AATATATGTA AAGTAGAATA 1620
 AGCCTTCAAA TTATAAACCA AGGTCATATT GTAACATAA CTACTGTGTG TGCATTGAAG 1680
 ATTTTATTTT ACCCTTGATC TTAACAAGC CTTTGCTTTG TTATCAAAATG GACTTTCATG 1740
 GCTTTTACTA TCTGTGTTTT ATGGTTTCAT GTAACATACA TATTCCTGGT GTAGCACTTA 1800
 ACTCCTTTTC CACTTTAAAT TTGTTTTTGT TTTTGTAGAC GGAGTTTAC TCTTGTCAAC 1860
 CAGGCTGGAG TACAGTGCCA CGATCTCGGC TTATGGCAAC CTCGCGCTCC CGGGTTCAAG 1920
 TGATTCTCCT GCTTCAGCTT CCCGAGTAGC TGGGATTACA GGCACACACT ACCAGCCTG 1980
 GCTAATTTT GTATTTTAT TATGAGCGGG TTTCAACATG TTGGCCAGAC TGGTCTTGAA 2040
 CTCTTGACCT CAGGTGATCC ACCCACTCA GCCTCCCAA GTGCTGGAT TACAGGCATG 2100
 AGCCATTCGG CCCGCTTAA AATGTTTTT TTAATCATCA AAAAGAACA CATATCTCAG 2160

GTTGTCTAAG TGTTTTATG TAAACCAAC AAAAGAACA AATCAGCTTA TATTTTTAT 2220
 CTTGATGACT CCTGCTCCAG AATGCTAGA CTAAGAATTA GGTGGCTACA GATGGTAGAA 2280
 CTAACAATA AGCAAGAGAC AATAATAATG GCCCTTAATT ATTAACAAAG TGCCAGAGTC 2340
 TAGGCTAAGC ACTTTATCTA TATCTCATTT CATCTCACA ACTTATAAGT GAATGAGTAA 2400
 ACTGAGACTT AAGGGAACCT AATCACTTAA ATGTCACCTG GCTAACTGAT GGCAGAGCCA 2460
 GAGCTTGAAT TCATGTTGGT CTGACATCAA GGTCTTTGGT CTCTCCCTA CACCAAGTTA 2520
 CCTACAAGAA CAATGACACC ACACCTGCGC TGAAGGCTCA CACCTCATAC CAGCATACGC 2580
 TCACCTTACA GGGAAATGGG TTTATCCAGG ATCATGAGAC ATTAGGGTAG ATGAAAGGAG 2640
 AGCTTTGCGA ATAAACAAAT AGCCTATCCT TAATAAATCC TCCACTCTCT GGAAGGAGAC 2700
 TGAGGGGCTT TGTAAACAT TAGTCAGTTG CTCATTTTGA TGGGATTGCT TAGCTGGGCT 2760
 GTAAAGATGA AGGCATCAAA TAAACTCAAA GTATTTTAA ATTTTGTGA TAATAGAGAA 2820
 ACTTCGTAA CCAACTGTTT TTTCTTGAGT GTATAGCCCC ATCTTGTGGT AACTTGCTGC 2880
 TTTCTGCACTT CATGCTGTTT TTTCTTATTG TTCACTTTAT TCTGTAGAGC AGCCTGCCAA 2940
 GAATTTTATT TCTGCTGTTT TTTTGTCTGC TAAAGAAAG AACTAAGTCA GGATGTTAAC 3000
 AGAAAAGTCC ACATAACCTT AGAATCTCTA GTCAAGGAAT AATTCAAGTC AGCCTAGAGA 3060
 CCATGTTGAC TTTCTCATG TGTTCCTCTA TGACTCAGTA AGTTGGCAAG GTCCTGACTT 3120
 TAGTCTTAAT AAAACATTGA ATTGTAGTAA AGGTTTTTGC AATAAAACT TACTTTGG

Seq ID NO: 489 Protein sequence
 Protein Accession #: NP_055213.1

1 11 21 31 41 51
 | | | | |
 MPRQLSAAAA LFASLAVILH DGSQMRKAF PETRDYSQPT AAATVQDIKK PVQPAKQAP 60
 HQTLAARFMD GHITFQTAAT VKIPTTTPAT TKNTATTSPI TYTLVTQAT PNNSHAPPV 120
 TEVTVGPSLA PYSLPPTITP PAHTAGTSSS TVSHHTGNNT QPSNQTTLPA TSLIALHKST 180
 TGQKPDQPTH APGTTAAAHN TTRTAAPAST VPGPTLAPQP SSVKGTGIYQV LNSRLCTKA 240
 EMGIQLIVQD KESVFSPPRY FNIDPNATQA SGNCGTRKSN LLLNFQGGFV NLTPTKDEES 300
 YYISEVGAYL TVSDPETVYQ GIKHAVVMFQ TAVGHSHFCV SEQSLQLSAH LQVKTTDVQL 360
 QAFDFEDDHF GNVDECSSDY TIIVLPVIGAI VVGLCLMGMG VYKIRLRQCS SGYQRI

Seq ID NO: 490 DNA sequence
 Nucleic Acid Accession #: NM_005409.3
 Coding sequence: 94..378

1 11 21 31 41 51
 | | | | |
 TTCCTTTTCT GTTCAGCATT TCTACTCCTT CCAAGAAGAG CAGCAAAGCT GAAGTAGCAG 60
 CAACAGCACC AGCAGCAACA GCAAAAAACA AACATGAGTG TGAAGGGCAT GGCTATAGCC 120
 TTGGCTGTGA TATTGTGTGC TACAGTTGTT CAAGGCTTCC CCATGTTCAA AAGAGGACGC 180
 TGTCTTTGCA TAGGCCCTGG GGTAAAGCA GTGAAAGTGG CAGATATTGA GAAAGCCTCC 240
 ATAATGTACC CAAGTAACAA CTGTGACAAA ATAGAAGTGA TTATTACCCT GAAAGAAAAAT 300
 AAAGGACAAC GATGCCTAAA TCCCAATCG AAGCAAGCAA GGCTTATAAT CAAAAAGTT 360
 GAAAGAAAGA ATTTTAAAA ATATCAAAAC ATATGAAGTC CTGAAAAGG GCATCTGAAA 420
 AACCTAGAAC AAGTTTAACT GTGACTACTG AAATGACAAG AATTCTACAG TAGGAAACTG 480
 AGACTTTTCT ATGGTTTTGT GACTTTCAAC TTTTGTACAG TTATGTGAAG GATGAAAGGT 540
 GGGTGAAGG ACCAAGAACG GAAATACAGT CTTCCTGAAT GAATGACAAT CAGAATTCCA 600
 CTGCCCAAAG GAGTCCAGCA ATTAATGGA TTTCTAGGAA AAGCTACCTT AAGAAAGGCT 660
 GGTACCATC GAGTGTACAA AAGTGCTTTC ACGTTCCTAC TTGTGTATT ATACATTCAT 720
 GCATTCTTAG GCTAGAGAGC CTCTAGATT TGATGCTTAC AACTATTCTG TTGTGACTAT 780
 GAGAACATTT CTGTCTCTAG AAGTTATCTG TCTGTATTGA TCTTTATGCT ATATTACTAT 840
 CTGTGGTTAC AGTGAGAGCA TTGACATTAT TACTGGAGTC AAGCCCTTAT AAGTCAAAAG 900
 CATCTATGTG TCGTAAAGCA TTCTCAAAC ATTTTTCAT GCAAAATACAC ACTTCTTTCC 960
 CCAATATCA TGTAGCAGAT CAATATGTAG GGAACATTC TTATGCATCA TTTGGTTTGT 1020
 TTTATAACCA ATTCATTAAA TGTAATTCAT AAAATGTACT ATGAAAAAA TTATACGCTA 1080
 TGGGATACCT GCAACAGTGC ACATATTCA TAACCAAAT AGCAGCACCG GTCTTAATTT 1140
 GATGTTTTTC AACTTTTATT CATTGAGATG TTTTGAAGCA ATTAGGATAT GTGTGTTTAC 1200
 TGTACTTTTT GTTTGTATCC GTTTGTATAA ATGATAGCAA TATCTTGGAC ACATTGAAA 1260
 TACAAAATGT TTTTGTCTAC CAAGAAAAA TGTGTAAAAA TAAGCAAAATG TATACCTAGC 1320
 AATCACTTTT ACTTTTGTG ATTCTGTCTC TTAGAAAAAT ACATAATCTA ATCAATTTCT 1380
 TTGTTTCATGC CTATATACTG TAAATTTTAG GTATACICAA GACTAGTTTA AAGAATCAAA 1440
 GTCAATTTTT TCTCTAATAA ACTACCACAA CCTTCTTTT TAAAAAAA AAA

Seq ID NO: 491 Protein sequence
 Protein Accession #: NP_005400.1

1 11 21 31 41 51
 | | | | |
 MSVKGMAL AVILCATVVQ GPFMPKRGRC LCIGPGVKAV KVADIEKASI MYPSNNCDKI 60
 EVIITLKENK GQRCLNPKSK QARLIKKVE RKNF

Seq ID NO: 492 DNA sequence
 Nucleic Acid Accession #: NM_000577.1
 Coding sequence: 41..520

1 11 21 31 41 51
 | | | | |
 GGCACGAGGG GAAGACCTCC TGTCTATCA GGCCCTCCCC ATGGCTTTAG AGACGATCTG 60
 CCGACCTCTT GGGAGAAAAT CCAGCAAGAT GCAAGCCTTC AGAATCTGGG ATGTTAACCA 120
 GAAGACCTTC TATCTGAGGA ACACCAACT AGTTGCCGGA TACTTGCAAG GACCAATGT 180
 CAATTTAGAA GAAAAGATAG ATGTGGTACC CATTGAGCCT CATGCTCTGT TCTTGGGAAT 240
 CCATGGAGGG AAGATGTGCC TGTCTGTGT CAAGCTGGT GATGAGACCA GACTCCAGCT 300
 GGAGGACGTT AACATCTCTG ACCTGAGCGA GAACAGAAAG CAGGACAAAG GCTTCGCTT 360
 CATCCGCTCA GACAGTGCC CCACCACCAG TTTTGTGCTT GCCGCTGCC CCGGTTGGTT 420
 CCTCTGCACA GCGATGGAAG CTGACCAGCC CGTCAGCCTC ACCAATATGC CTGACGAAGG 480
 CGTCATGGTC ACCAAATCT ACTTCCAGGA GGACGAGTAG TACTGCCAG GCCTGCTGT 540
 TCCCATCTT GCATGGCAAG GACTGCAGGG ACTGCCAGTC CCCTGCCCC AGGGCTCCCG 600

GCTATGGGGG CACTGAGGAC CAGCCATTGA GGGGTGGACC CTCAGAAGGC GTCACAACAA 660
 CCTGGTCACA GGACTCTGCC TCCTCTTCAA CTGACCAGCC TCCATGCTGC CTCCAGAATG 720
 GTCTTTCTAA TGTGTGAATC AGAGCACAGC AGCCCTTGCA CAAAGCCCTT CCATGTGCGC 780
 TCTGCATTCA GGATCAAAAC CCGACCACTG GCCCAACCTG CTCTCTCTT GCCATGCCT 840
 CTTCCCTCCCT CATTCCACCT TCCCATGCCG TGGATCCATC AGGCCACTTG ATGACCCCA 900
 ACCAAGTGGC TCCCACACCC TGTTTTACAA AAAAGAAAAG ACCAGTCCAT GAGGGAGGTT 960
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 GAAGGAGAGC CTTTCATTG GAGATTATGT TCTTTCGGGG AGAGGCTGAG GACTTAAAT 1080
 ATTCTGTCAT TTGTGAAATG ATGGTGAAAG TAAGTGGTAG CTTTTCCTT CTTTTCCTC 1140
 TTTTTCCTG ATGTCCCAAC TTGTAAAAAT TAAAGTTAT GGTACTATGT TAGCCCATG 1200
 ATTTTTCCTT TCCTTTTAAA ACACCTCCAT AATCTGGACT CCTCTGCCA GGCCTGCTG 1260
 CCCAGCTCC CAGCTCCATC TCCACTCCAG ATTTTTCATA GCTGCTGCA GTACTTTACC 1320
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 TCTTCCTCTG CTGAAGGAAT AAATTGCTCC TTGACATTGT AGAGCTTCTG GCCTTGGAG 1440
 ACTTGATAGA AAGATGGCTG TGCTCTGCC TGTCTCCCC ACCAGGCTGG GAGCTCTGCA 1500
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 CTCTTGGCAG CTGATCAGCG AATGAATGCT GTATATGTTG GGTGCAAAAG TCCCTACTTC 1620
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 AAAAAAAA AAAAAAAA AAAAAAAA AAAAAA

Seq ID NO: 493 Protein sequence
 Protein Accession #: NP_000568.1

1 11 21 31 41 51
 MALETICRPS GRKSSKMQAF RIWDVNQKTF YLRNNQLVAG YLQGPVNLE EKIDVVPPIEP 60
 HALFLGIHGG KMCLSCVKSG DETRLQLEAV NITDLSNRK QDKRPAFIRS DSGPTTSPES 120
 AACPGWFLCT AMEADQPVSL TNMPDEGVMV TKFYFQEDE

Seq ID NO: 494 DNA sequence
 Nucleic Acid Accession #: NM_002081.1
 Coding sequence: 222..1898

1 11 21 31 41 51
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 AGAGCGCGCG GCGGGTGGCC GGGGCGCGCG CCGGCCCCGC CATGGAGCTC GGGGCGCGAG 240
 GCTGGTGGCT GCTATGTGCG GCGCAGCGCG TGGTGGCTG CCGCGCGCGG GACCGCGCCA 300
 GCAAGAGCGG GAGCTCGGCG GAGGTCCGCC AGATCTACGG AGCCCAAGGC TTCAGCCTGA 360
 GCGACGTGCC CCAGGCGGAG ATCTCGGGTG AGCACCTGCG GATCTGTCCC CAGGGCTACA 420
 CCTGCTGCAC CAGCGAGATG GAGGAGAACC TGGCCAACCG CAGCCATGCC GAGCTGGAGA 480
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 AGCTGCGCGT GTACTACCGG GGTGCCAACC TGCACTGGA GGAGACGCTG GCCGAGTCT 720
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CTGGACGGGC CCTCCTTCCC TCCTGTGCCC CAGCTGCCAG GTGGCCCTGG GGAGGGGTGG 3180
 TGTGGTGTGG GGAAGGGGTC CTGCAGGGGG AGGAGGACTT GGAGGGTCTG GGGGCAGCTG 3240
 TCCTGAACCG ACTGACCCTG AGGAGGGCGC TTAGTGCTGC TTGTCTTTTC ATCACCCTCC 3300
 CGCACAGTGG ACGGAGGTCC CCGGTTGCTG GTCAGGTCCC CATGGCTTGT TCTCTGGAAC 3360
 CTGACTTTAG ATGTTTTGGG ATCAGGAGCC CCCAACACAG GCAAGTCCAC CCCATAATAA 3420
 CCTTGCCAGT GCCAGGGTGG GCTGGGGACT CTGGCACAGT GATGCCGGGC GCCAGGACAG 3480
 CAGCACTCCC GCTGCACACA GACGGCCTAG GGGTGGCGCT CAGACCCAC CCTACGCTCA 3540
 TCTCTGGAAG GGCAGCCCT GAGTGGTCAC TGGTCAGGGC AGTGGCCAAG CCTGCTGTGT 3600
 CCTTCTCTCA CAAGGTCCTC CCACCGCTCA GTGTACGGCG GTGACGTGTG TTCTTTTGAG 3660
 TCCTTGTATG AATAAAAGGC TGGAAACCTA AA

Seq ID NO: 495 Protein sequence
 Protein Accession #: NP_002072.1

1 11 21 31 41 51
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 ICPOGYTCTT SEMEENLANR SHAELETALR DSSRVLQAML ATQLRSFDDH FQHLLNDSER 120
 TLQATFFGAF GELYTONARA FRDLYSELRL YVRGANLHLE ETLAEFWARL LERLFKQLHP 180
 QLLLPDDYLD CLGKQAEALR PFGEAPRELRL LRATRAFVAA RSFVQGLGVA SDVVRKVAQV 240
 PLGPECSRVA MKLVYCAHCL GVPGARPCPD YCRNVKLGCL ANQADLDAEW RNLLDSMVL I 300
 TDKFWGTSGV ESIVIGSVHTW LAEAINALQD NRDTLTAKVI QGCGNPKVNP QGPGPEEKRR 360
 RGKLAPRERP PSGTLEKLVS EAKAQLRDVQ DFWISLPGTL CSEKMALSTA SDDRCWNGMA 420
 RGRYLPVVMG DGLANQINNP EVEVDITKPD MTIRQQIMQL KIMTNRLRSA YNGNDVDFQD 480
 ASDDGSGSGS

Seq ID NO: 496 DNA sequence
 Nucleic Acid Accession #: NM_001650.2
 Coding sequence: 40.1011

1 11 21 31 41 51
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 GGGGTCTGGA CTCAAGCTTT CTGGAAAGCA GTCACAGCGG AATTCTGGC CATGCTTATT 180
 TTTGTTCTCC TCAGCCTGGG ATCCACCATC AACTGGGGTG GAACAGAAAA GCCTTTACCG 240
 GTCGACATGG TTCTCATCTC CCTTTGCTTT GGACTCAGCA TTGCAACCAT GGTGCAGTGC 300
 TTTGGCCATA TCAGCGGTGG CCACATCAAC CTGCGAGTGA CTGTGGCCAT GGTGTGCACC 360
 AGGAAGATCA GCATCGCCAA GTCTGTCTTC TACATCGCAG CCCAGTGCCT GGGGGCCATC 420
 ATGGAGCAGG GAATCCTCTA TCTGGTCACA CCTCCAGTG TGGTGGGAGG CCGGGAGTGC 480
 ACCATGGTTC ATGGAATCTT TACCGCTGGT CATGGTCTCC TGGTTGAGTT GATAATCACA 540
 TTTCAATGGG TGTTTACTAT CTTTGCCAGC TGTGATTCCA AACGGACTGA TGTCACTGGC 600
 TCAATAGCTT TAGCAATTGG ATTTCTGTT GCAATTGGAC ATTTATTTGC AATCAATTAT 660
 ACTGGTGCCA GCATGAATCC CGCCCGATCC TTTGGACCTG CAGTTATCAT GGGAAATTGG 720
 GAAAACCATT GGATATATTG GGTGTGGCCC ATCATAGGAG CTGTCTCTCG TGGTGGCCTT 780
 TATGAGTATG TCTTCTGTCC AGATGTTGAA TTCAAACGTC GTTTTAAAGA AGCCTTCAGC 840
 AAAGCTGCCC AGCAAACAAA AGGAAGCTAC ATGGAGGTGG AGGACAACAG GAGTCAGGTA 900
 GAGACGGATG ACCTGATTCT AAAACCTGGA GTGGTGATG TGATTGACGT TGACCGGGGA 960
 GAGGAGAAGA AGGGGAAGA CCAATCTGGA GAGGTATTGT CTTAGTATG ACTAGAAGAT 1020
 CGCACTGAAA GCAGACAAGA CTCCTTAGAA CTGTCCTCAG ATTTCTCTCC ACCCATTAAG 1080
 GAAACAGATT TGTATATAAT TAGAAATGTG CAGGTTTGTG GTTTCATGTC ATATTACTCA 1140
 GTCTAAACAA TAAATTTTTC ATAATTACA AAGGAGGAAC GGAAGAAACC TATTGTGAAT 1200
 TCCAAATCTA AAAAAAGAAA TATTTTAAAG ATGTTCTTAA GCAATATATAT ACCTATTTTA 1260
 TCTAGTTACC TTTCATTAAC AACCAATTTT AACCGTGTGT CAAGATTGGG TTAAGTCTTG 1320
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Seq ID NO: 497 Protein sequence
 Protein Accession #: NP_001641.1

1 11 21 31 41 51
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 AQCLGAIIGA GILYLVTPPS VVGGLGVMTV HGNLTAGHGL LVELIITFQL VFTIFASCD 180
 KRTDVTGSIA LAIGFSAVIG HLFAINYTGA SMNPARSFGP AVIMGNWENH WIYVVGPIIG 240
 AVLAGGLYEF VFCPDVEFKR RFKEAFSKAA QQTGKSYMEV ZDNRSQVETD DLILKPGVVH 300
 VIDVDRGEK KGDQSGEVL SSV

Seq ID NO: 498 DNA sequence
 Nucleic Acid Accession #: AB020684.1
 Coding sequence: 1..1744

1 11 21 31 41 51
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 TGCTTGCTTT TATGTTGCTG TAATTTTAT TTTAAATGGA CTAATGATGG CATTATTCTT 240
 CATATATGGC ACATATTTAA GTGGCAGCCG ATTAGGAGGC CTGGTTACAG TGTGTGCTT 300
 CTTTTTCAAT CATGGAGAGT GTACCCGTGT AATGTGGACA CCACCTCTCC GTGAAAGCTT 360
 CTCATATCCA TTCTTTGTTC TTCAGATGTT GCTAGTGACT CATATTCTCA GGGCTACAAA 420
 ACTTTATAGA GGAAGCTTGA TTGCACTCTG CATTTCGAAT GTATTTTCA TGCTTCCTTG 480
 CGAGTTTGCT CAGTTTGTAT TTCTTACTCA GATTGCATCA TTATTTCAG TATATGTTGT 540
 GCGGTACATT GATATATGTA AATTACGGAA GATCATTAT ATACACATGA TTTCTCTTGC 600
 ACTTTGTTTT GTTTTGTATG TTGGGAACCT AATGTTATTA ACTTCTTATT ATGCTTCTTC 660
 TTTGGTAATT ATTTGGGGTA TTCTGGCAAT GAAACACAT TTCCTGAAA TAAATGTTAT 720

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TGAACCTAGT TTATGGGTGA TTCAAGGATG TTTTGGTTA TTTGGAACGT TCATACCTTAA 780
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 ATCAAAATTC TTTAGTTATA AGGATTTTGA TACTTTATTG TATACCTGTG CAGCGGAGTT 900
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 GAAAGTATGT ATCAGGAATA AAGTGATATT GCATAGGAGT ATTGTATTTT TATGAATTTT 4380
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Seq ID NO: 499 Protein sequence
 Protein Accession #: BAA74900.1

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75
80

1 11 21 31 41 51
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 SYPFLVLQML LVTHILRATK LVRGSLIALC ISNVFFMLPW QFAQFVLLTQ IASLFAVYVV 180
 GYIDICKLRK IYIHMISLA LCFVLMFGNS MLLTSYYASS LVIIWILAM KPHFLKINVS 240
 ELSLWVIQGC PNLFGTVILK YLTSKIFGIA DDAHIGNLLT SKFFSYKDFD TLLYTCAAEP 300
 DFMKEETPLR YTKTLLLPVV LVVFVAIVRK IISDMWGLA KQKTHVRKHQ FDHGLVYHA 360
 LQLLAYTALG ILIMRLKLF LTPHMCVMASL ICSRQLFGWL FCKVHPGAIV FAILAAMSIQ 420
 GSNALQQTWN IVGEFNLNPQ EELIEWIKYS TKPDVAFAGA MPTMASVKLS ALRPIVNHHPH 480
 YEDAGLRART KIVYSMYSRK AAEVVKRELI KLKVNYYILE ESWCVRRSKP GCSMP EIWDV 540
 EDPANAGKTP LCNLLVKDSK PHFTTVFQNS VYKVLVVEKE

Seq ID NO: 500 DNA sequence
 Nucleic Acid Accession #: NM_001276.1
 Coding sequence: 127..1278

85

1 11 21 31 41 51
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	TGCTCTGCAT	ACAACTGGT	CTGCTACTAC	ACCAGCTGGT	CCCAGTACCG	GGAAGGCGAT	240
	GGGAGCTGCT	TCCCAGATGC	CCTTGACCGC	TTCTCTGTA	CCCACATCAT	CTACAGCTTT	300
5	GCCAATATAA	GCAACGATCA	CATCGACACC	TGGGAGTGGG	ATGATGTGAC	GCTCTACGGC	360
	ATGCTCAACA	CACTCAAGAA	CAGGAACCCC	AACCTGAAGA	CTCTCTTGTC	TGTGGGAGGA	420
	TGGAACCTTG	GGTCTCAAAG	ATTTTCCAAG	ATAGCCTCCA	ACACCCAGAG	TCGCGGAGAT	480
	TTCATCAAGT	CAGTACCGCC	ATTCTGCGC	ACCCATGGCT	TTGATGGGCT	GGACCTTGCC	540
	TGGCTCTACC	CTGGACGGAG	AGACAAACAG	CATTTTACCA	CCCTAATCAA	GGAATGAAG	600
10	GCCGAATTTA	TAAAGGAAGC	CCAGCCAGGG	AAAAAGCAGC	TCCTGCTCAG	CGCAGCACTG	660
	TCGTGGGGGA	AGGTCACCAT	TGACAGCAGC	TATGACATTG	CCAAGATATC	CCAACACCTG	720
	GATTTTCATTA	GCATCATGAC	CTACGATTTT	CATGGAGCCT	GGCGTGGGAC	CACAGGCCAT	780
	CACAGTCCCC	TGTTCCGAGG	TCAGGAGGAT	GCAAGTCCTG	ACAGATTGAG	CAACACTGAC	840
	TATGCTGTGG	GGTACATGTT	GAGGCTGGGG	GCTCCTGCCA	GTAAGCTGGT	GATGGGCATC	900
15	CCCACTTCG	GGAGGAGCTT	CACCTTGGCT	TCTTCTGAGA	CTGGTGTGGG	AGCCCCAATC	960
	TCAGGACCGG	GAATTCACAG	CCGGTTCACC	AAGGAGGCAG	GGACCCCTGC	CTACTATGAG	1020
	ATCTGTGACT	TCCTCCGCGG	AGCCACAGTC	CATAGAACCC	TCGGCCAGCA	GGTCCCCTAT	1080
	GCCACCAAGG	GCAACCAAGT	GTTAGGATAC	GACGACCAAG	AAAGCGTCAA	AAGCAAGGTG	1140
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20	TTCCAGGGCT	CCTTCTGCGG	CCAGGATCTG	CGCTTCCCTC	TCACCAATGC	CATCAAGGAT	1260
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	GCCTCAGTCT	CCCTCCCTTG	GGGCCTATGC	AGAGGTCCAC	AACACACAGA	TTTGAGCTCA	1440
	GCCTCTGTGG	GGAGTAGAGT	AGGGATGGGG	CTGTGGGGAT	AGTGAGGCAT	CGCAATGTAA	1500
25	GACTCGGGAT	TAGTACACAC	TGTGTGATGA	TTAATGGAAA	TGTTTACAGA	TCCCCAAGCC	1560
	TGGCAAGGGA	ATTTCTTCAA	CTCCCTGCCC	CCTAGCCCTC	CTTATCAAAG	GACACCATT	1620
	TGGCAAGCTC	TATCAACAAG	GAGCCAAACA	TCCTACAAGA	CACAGTGACC	ATACTAATTA	1680
	TACCCCTGTC	AAAGCCAGCT	TGAAACCTTC	ACTTAGGAAAC	GTAATCGTGT	CCCCTATCCT	1740
	ACTTCCCTCT	CCTAATTCCA	CAGCTGCTCA	ATAAAGTACA	AGAGTTTAA	AGTGTGTTGG	1800
30	CGCTTTGCTT	TGCTCTCATC	TTGAGCGCCC	ACTAGACCCA	CTGGAATCAC	CTCCCCATC	1860
	TCCTCTGGGT	TCCTTCTCT	GAGCCTTGGG	ACCCCTGAGC	TTGAGAGAT	GAAGGCCGCC	1920
	ATGTT						

Seq ID NO: 501 Protein sequence
Protein Accession #: NP_001267.1

35	1	11	21	31	41	51	
	MGVKASQTGF	VVLVLLQCCS	AYKLVCYYTS	WSQYREGDGS	CFPDALDRFL	CTHIIYSFAN	60
40	ISNDHIDTWE	WMDVTLYGML	NTLKNRNPNL	KTLLSVGGWN	PGSQRFSKIA	SNQSRRTFI	120
	KSVPPPLRTH	GFDGLDLAWL	YPRRDQKHQF	TTLIKEMKAE	FIKEAQPGKK	QLLLSAALSA	180
	GKVTIDSSYD	IAKISQHLDF	ISIMTYDFHG	AWRGTTGHHS	PLFRGQEDAS	PDRFSNTDYA	240
	VGVMRLRLGAP	ASKLVMGIPT	FGRSFTLASS	ETGVGAPISG	PGIPGRFTKE	AGTLAYEIE	300
	DFLRGATVHR	TLGQQVPYAT	KGNQWVGYYD	QESVSKSVQY	LKDRQLAGAM	VWALDLDDFQ	360
45	GSFCGQDLRF	PLTNAIKDAL	AAT				

Seq ID NO: 502 DNA sequence
Nucleic Acid Accession #: NM_006474.1
Coding sequence: 181..669

50	1	11	21	31	41	51	
	GCTGCCTAGG	GTCTGGAAAG	CTCGGGCACC	CTCCCTCTCC	GGGGCTCCTG	CTCCCACCCC	60
	TCGGGCCCCC	CCACGTCGCG	GCTCTCTCCAG	GCTGGGCTCG	TGGCCGCGGT	GCTTTTAATT	120
55	TTCCCCCAGC	TCAGAATCTT	GCTGCTCGGC	CCCCAGGAGA	GCAACAACTC	AACGGGAACG	180
	ATGTGGAAGG	TGTCAGCTCT	GCTCTTCGTT	TTGGGAAGCG	CGTCGCTCTG	GGTCTGGGCA	240
	GAAGGAGCCA	GCACAGGCCA	GCCAGAAGAT	GACACTGAGA	CTACAGGTTT	GGAAGGCGGC	300
	GTTGCCATGC	CAGGTGCCGA	AGATGATGTG	GTGACTCCAG	GAACCAGCGA	AGACCGCTAT	360
	AAGTCTGGCT	TGACAACTCT	GGTGGCAACA	AGTGTCAACA	GTGTAACAGG	CATTGCGATC	420
60	GAGGATCTGC	CAACTTCAGA	AAGCAAGTC	CACGCGCAAG	AACAAAGTCC	AAGCGCCACA	480
	GCCTCAAACG	TGGCCACCAG	TCACTCCACG	GAGAAAGTGG	ATGGAGACAC	ACAGACAACA	540
	GTTGAGAAAG	ATGTTTGTG	AACAGTGACC	CTGGTTGGAA	TCATAGTTGG	GGTCTTACTA	600
	CCCATCGGTT	TCATTGGTGT	AATCATCGTT	GTGGTTATGC	GAAAAATGTC	GGGAAGGTAC	660
	TCGCCCTAAA	GAGCTGAAGG	GTTACGCCCT	GCTTGCCAAC	GTGCTTTAAA	AAAAGACCGT	720
65	TTCTGACTCT	GTGGCCCTGT	CCCTGAGCTC	GTGGGGAGAA	GATGACCCCTG	GGAACATTTG	780
	CGGGCCCATC	CAGATTCCAC	GGTGACTTTC	CGTTTGCCAA	ATTAACCGAG	GAAAGACCTT	840
	TCACCAGATT	TGTTCTTTAA	ACTTT				

Seq ID NO: 503 Protein sequence
Protein Accession #: NP_006465.1

70	1	11	21	31	41	51	
	MWKVSALLFV	LGSASLWVLA	EGASTGQPED	DTETTGLEGG	VAMPGAEDDV	VTPGTSEDYR	60
75	KSLGTLTVAT	SVNSVTGIRI	EDLPTSESTV	HAQEQSPSAT	ASNVTASHST	EKVDGDTQTT	120
	VERDGLSTVT	LVGIIVGVLL	AIGFIGGIIV	VVMRMSGRY	SP		

Seq ID NO: 504 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 62..895

80	1	11	21	31	41	51	
	CACGTGCTCTG	AGAATTGTGT	AGCAGCCCCCT	AACAGGCTGT	TACTTCACTA	CAACTGACGA	60
85	TATGATCATC	TTAATTTACT	TATTTCTCTT	GCTATGGGAA	GACACTCAAG	GATGGGGATT	120
	CAAGGATGGA	ATTTTTCATA	ACTCCATATG	GCTTGAACGA	GCAGCCGGTG	TGTACCACAG	180
	AGAAGCACGG	TCTGGCAAAAT	ACAAGCTCAC	CTACGCAGAA	GCTAAGGCGG	TGTGTGAATT	240
	TGAAGGCGGC	CATCTGCGAA	CTTACAAGCA	GCTAGAGGCA	GCCAGAAAAA	TTGGATTCTA	300

5
10
15
20

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TGCTCTGTCT GCTGGATGGA TGGCTAAGGG CAGAGTTGGA TACCCCATGT TGAAGCCAGG 360
GCCCCAATGT GGATTGGGAA AACTTGGCAT TATTGATTAT GGAATCCGTC TCAATAGGAG 420
TGAAGATGAG GATGCTCTATT GCTACAACCC ACAACGAAAG GAGTGTGGTG GCGTCTTTAC 480
AGATCCAAAG CAAATTTTAA AATCTCCAGG CTTCCCAAAT GAGTACGAAG ATAACCAAAT 540
CTGCTACTGG CACATTAGAC TCAAGTATGG TCAGCGTATT CACCTGAGTT TTTTAGATTT 600
TGACCTTGAA GATGACCCAG GTTGCTTGCC TGATTATGTT GAAATATATG ACAGTTACGA 660
TGAATGCCAT GGCCTTGTGG GAAGATACG TGGAGATGAG CTTCCAGATG ACATCATCAG 720
TACAGGAAAT GTCATGACCT TGAAGTTTCT AAGTGATGCT TCAGTGACAG CTGGAGGTTT 780
CCAAATCAA TATGTTGCAA TGGATCCTGT ATCCAAATCC AGTCAAGGAA AAAATACAAG 840
TACTACTTCT ACTGGAATA AAAACTTTT AGCTGGAAGA TTAGCCACT TATAAAAAAA 900
AAAAAAGGA TGATCAAAC ACACAGTGT TATGTTGGA TCTTTTGGAA CTCCTTTGAT 960
CTCACTGTTA TTATTAACAT TTATTATTA TTTTCTAAA TGTGAAAGCA ATACATAATT 1020
TAGGGAATAA TGGAATAATA AGGAACTTT AAACGAGAAA ATGAAACCTC TCATAATCCC 1080
ACTGCATAGA AATAACAAGC GTTAACATTT TCATATTTTT TTCTTTCAGT CATTTTCTA 1140
TTTGTGGTAT ATGTATATAT GTACCTATAT GTATTGCGT TTGAAATTTT GGAATCCGTC 1200
TCTATGTACA GTTTTGTATT ATACTTTTAA AATCTTGAAC TTTATAAACA TTTTCTGAAA 1260
TCATTGATTA TTCTACAAA ACATGATTTT AAACAGCTGT AAAATATTCT ATGATATGAA 1320
TGTTTTATGC ATTATTAAAG CCTGCTCTA TTGTTGGAAT TTCAGGTCAT TTTCATAAAT 1380
ATTGTTGCAA TAAATATCCT TGAACACACA AAAAAAAAAA AA

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Seq ID NO: 505 Protein sequence
Protein Accession #: Eos sequence

25
30

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1 11 21 31 41 51
| | | | |
MIILYLFLL LWEDTQGWGF KDGIFHNSIW LERAAGVYHR EARSQKYKLT YAEAKAVCEF 60
EGGHLATYKQ LEAARKIGHF VCAAGWMAKG RVGYPIVKPG PNCQPGKGTGI IDYGIRLNRS 120
ERWDAYCYNP HAKECGGVFT DPKQIFKSPG FPNEYEDNQI CYWHIRLKYG QRIHLSFLDF 180
DLEDDPGCLA DYVEIYDSYD DVHGFVGRYC GDELPDDIIS TGNVMTLKFL SDASVTAGGF 240
QIKYVAMPDV SKSSQGNKNTS TTSTGNKNFL AGRFSLH

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Seq ID NO: 506 DNA sequence
Nucleic Acid Accession #: NM_007115.1
Coding sequence: 69..902

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40
45
50
55
60

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1 11 21 31 41 51
| | | | |
GAATTCGCAC TGCTCTGAGA ATTTGTGAGC AGCCCTTAAC AGGCTGTTAC TTCACTACAA 60
CTGACGATAT GATCATCTTA ATTTACTTAT TTCTCTTGCT ATGGGAAGAC ACTCAAGGAT 120
GGGGATTCAA GGATGGAATT TTTTCAACT CCATATGGCT TGAACGAGCA GCCCGTGTGT 180
ACCAAGAGAG AGCACGGTCT GGCATAATACA AGCTCACCTA CGCAGAAAGCT AAGGCGGTGT 240
GTGAATTGGA AGGCGGCCAT CTCGCAACTT ACAAGCAGCT AGAGGCAGCC AGAAAAATTG 300
GATTTCATGT CTGTGCTGCT GGATGGATGG CTAAGGGCAG AGTTGGATAC CCCATTGTGA 360
AGCCAGGGCC CAATGATGAT TTTGAAAAAA CTGGCATTAT TGATTATGGA ATCGTCTCA 420
ATAGGAGTGA AAGATGGGAT GCCTATTGCT ACAACCCACA CGCAAAGGAG TGTGGTGGCG 480
TCTTTACAGA TCCAAAGCGA ATTTTAAAT CTCCAGGCTT CCCAAATGAG TACGAAGATA 540
ACCAAATCTG CTACTGGCAC ATTAGACTCA AGTATGGTCA CGGTATTACAC CTGAGTTTTT 600
TAGATTTTGA CCTTGAAGAT GACCCAGGTT GCTTGGCTGA TTATGTTGAA ATATATGACA 660
GTTACGATGA TGTCCATGGC TTTGTGGGAA GATACTGTGG AGATGAGCTT CCAGATGACA 720
TCATCAGTAC AGGAAATGTC ATGACCTTGA AGTTTCTAAG TGATGCTTCA GTGACAGCTG 780
GAGGTTTCCA AATCAAATAT GTTGCAATGG ATCCTGTATC CAAATCCAGT CAAGGAAAAA 840
ATACAAGTAC TACTTCTACT GGAAATAAAA ACTTTTATAG TGGAAAGATT AGCCACTTAT 900
AAAAAAAAAA AAGGATGATG AAAACACACA GTGTTTATGT TGGAAATCTT TGGAACTCCT 960
TTGATCTCAC TGTTATTATT AACATTTATT TATTATTTT CTAAATGTGA AAGAAATACA 1020
TAATTTAGGG AAAATTGGAA AATATAGGAA ACTTTAAACG AGAAAAATGAA ACCTCTCATA 1080
ATCCCACTGC ATAGAAATGA CAAGCGTTAA CATTTTCATA TTTTCTTCT TCAAGTCATT 1140
TTGTATTTGT GGTATATGTA TATATGTACC TATATGTATT TGCATTTGAA ATTTTGGAA 1200
CTCTGCTCTAT GTACAGTTTT GTATTATACT TTTTAAATCT TGAACCTTAT GAACATTTTC 1260
TGAAATCATT GATTATTCTA CAAAACATG ATTTTAAACA GCTGTAAAAT ATTCTATGAT 1320
ATGAATGTTT TATGCATTAT TTAAGCCTGT CTCTATTGTT GGAATTTTCA GTCATTTTCA 1380
TAAATATTGT TGCAATAAAT ATCCTTCGGA ATTC

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Seq ID NO: 507 Protein sequence
Protein Accession #: NP_009046.1

65
70

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1 11 21 31 41 51
| | | | |
MIILYLFLL LWEDTQGWGF KDGIFHNSIW LERAAGVYHR EARSQKYKLT YAEAKAVCEF 60
EGGHLATYKQ LEAARKIGHF VCAAGWMAKG RVGYPIVKPG PNXXFGKGTGI IDYGIRLNRS 120
ERWDAYCYNP HAKECGGVFT DPKRIFKSPG FPNEYEDNQI CYWHIRLKYG QRIHLSFLDF 180
DLEDDPGCLA DYVEIYDSYD DVHGFVGRYC GDELPDDIIS TGNVMTLKFL SDASVTAGGF 240
QIKYVAMPDV SKSSQGNKNTS TTSTGNKNFL AGRFSLH

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Seq ID NO: 508 DNA sequence
Nucleic Acid Accession #: NM_001044.1
Coding sequence: 129..1991

80
85

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1 11 21 31 41 51
| | | | |
ACCGCTCCGG AGCGGGAGGG GAGGCTTCGC GGAACGCTCT CGGCGCCAGG ACTCGCGTGC 60
AAAGCCCAGG CCGGGGCGGC CAGACCAAGA GGAAGAAGC ACAGAATTCC TCAACTCCCA 120
GTGTGCCAT GAGTAAGAGC AAATGCTCCG TGGGACTCAT GTCTTCCGTG GTGGCCCCGG 180
CTAAGGAGCC CAATGCCGTG GGGCCGAAGG AGGTGGAGCT CATCTTGTG AAGGAGCAGA 240
ACGGAGTGCA GCTCACCAGC TCCACCTCA CCAACCCGCG GCAGAGCCCC GTGGAGGCCC 300
AGGATCGGGA GACCTGGGGC AAGAAGATCG ACTTCTCCT GTCCGTCAAT GGCCTTGTCT 360
TGGACCTGGC CAACGTCTGG CGGTTCCCTT ACCTGTGCTA CAAAAATGGT GCGCGTGCCT 420

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	TCCTGGTCCC	CTACCTGCTC	TTTCATGGTCA	TTGCTGGGAT	GCCACTTTTC	TACATGGAGC	480
	TGGCCCTCGG	CCAGTTCAAC	AGGGAAGGGG	CCGCTGGTGT	CTGGAAGATC	TGCCCCATAC	540
	TGAAAGGTGT	GGGCTTCACG	GTTCATCCTCA	TCTCACTGTA	TGTGGGCTTC	TTCTACAACG	600
5	TCATCATGCG	CTGGGCGCTG	CACATATCTCT	TCTCCTCCTT	CACCACGGAG	CTCCCTTGGG	660
	TCCACTGCAA	CAACTCTCGG	AACAGCCCCA	ACTGCTCGGA	TGCCCCATCT	GGTGACTCCA	720
	GTGGAGACAG	CTCGGGCCTC	AACGACACTT	TTGGGACCAC	ACCTGCTGCC	GAGTACTTTG	780
	AACGTGGCGT	GCTGCACCTC	CACCAGAGCC	ATGGCATCGA	CGACCTGGGG	CCTCCGCGGT	840
	GGCAGCTCAC	AGCCTGCGTG	GTGCTGGTCA	TCGTGCTGCT	CTACTTCAGC	CTCTGGAAGG	900
10	GGGTGAAGAC	CTCAGGGAAG	GTGGTATGGA	TCACAGCCAC	CATGCCATAC	GTGGTCTCTCA	960
	CTGCCCTGCT	CCTGCGTGGG	GTACCCCTCC	CTGGAGCCAT	AGACGGCATC	AGAGCATACC	1020
	TGAGCGTTGA	CTTCTACCGG	CTCTGCGAGG	CGTCTGTTTG	GATTGACGCG	GCCACCCAGG	1080
	TGTGCTTCTC	CCTGGGCGTG	GGGTTGCGGG	TGCTGATCGC	CTTCTCCAGC	TACAACAAGT	1140
	TCACCAACAA	CTGCTACAGG	GACGCGATTG	TCACCACCTC	CATCAACTCC	CTGACGAGCT	1200
15	TTCTCTCCGG	CTTCGTCTGT	TTCTCCTTCC	TGGGGTACAT	GGCACAGAAG	CACAGTGTGC	1260
	CCATCGGGGA	CGTGGCCAAG	GACGGGCCAG	GGCTGATCTT	CATCATCTAC	CCGGAAGCCA	1320
	TGCGCACGCT	CCCTCTGTCC	TCAGCCTGGG	CCGTGGTCTT	CTTCATCATG	CTGCTCAGCC	1380
	TGGGTATCGA	CAGCGCCATG	GTGGTATGGA	AGTCAGTATG	CACCGGGCTC	ATCGATGAGT	1440
	TCCAGCTGCT	GCACAGACAC	CGTGAGCTCT	TCACGCTCTT	CATCGTCTGT	GCGACCTTCC	1500
20	TCCTGTCCCT	GTTCGTGCTG	ACCAACGGTG	GCATCTACGT	CTTCACGCTC	CTGGACCATT	1560
	TTGCAGCCCG	CACGCTCCAT	CTCTTTGGAG	TGCTCATCGA	AGCCATCGGA	GTGGCCCTGGT	1620
	TCTATGGTGT	TGGGCAAGTT	AGCGACGACA	TCCAGCAGAT	GACCGGGCAG	CGGCCAGGCC	1680
	TGTACTGGCG	GCTGTGCTGG	AAGCTGGTCA	GCCCTGCTT	TCTCCTGTTC	GTGGTCTGTG	1740
	TCAGCATTGT	GACCTTCAGA	CCCCCCACT	ACGGAGCCTA	CATCTTCCCC	GACTGGGCCA	1800
25	ACGCGCTGGG	CTGGGTCTAT	GCCACATCCT	CCATGGCCAT	GGTGCCCATC	TATGCGGCCT	1860
	ACAAGTTCTG	CAGCCTGCTT	GGGTCTCTTC	GAGAGAAACT	GGCCTACGCC	ATTGCACCCG	1920
	AGAAGGACCG	TGAGCTGGTG	GACAGAGGGG	AGGTGCGCCA	GTTCAAGCTC	CGCCACTGGC	1980
	TCAGGTGTGA	GAGGGAGCAG	AGACGAAGAC	CCCAGGAAGT	CATCTGCAA	TGGGAGAGAC	2040
	ACGAACAAC	CAAGGAATC	TAAGTTTCGA	GAGAAAGGAG	GGCAACTTCT	ACTCTTCAAC	2100
30	CTCTACTGAA	AACACAAACA	ACAAAGCAGA	AGACTCCTCT	CTTCTGACTG	TTTACACCTT	2160
	TCCGTGCCGG	GAGGCGACCT	CGCCGTGTCT	TGTGTTGCTG	TAATAACGAC	GATGATCTGT	2220
	GACGCGAGGT	CCACCCCGTT	GTGTGCTCTG	CAGGGCAGAA	AAACGTCTAA	CTTCATGCTG	2280
	TCGTGTGAG	GCTCCTCTCC	TCCCTGCTCC	CTGCTCCCGG	CTCTGAGGCT	GCCCCAGGGG	2340
	CACGTGTGTT	TCAGGCGGGG	ATCAGCATCC	TTGTAGACGC	ACCTGCTGAG	AATCCCGGTG	2400
35	CTCACAGTAG	CTTCTAGAC	CATTACTTTT	GCCCATATTA	AAAAGCCAAG	TGCTCTGCTT	2460
	GGTTTAGCTG	TGCAGAAAGT	GAAATGGAGG	AAACCAAAA	TTTCATGCAA	GTCTTTTCCC	2520
	GATGCGTGGC	TCCCAGCAGA	GGCCGTAAAT	TGAGCGTTCA	GTTGACACAT	TGCACACACA	2580
	GTCTGTTTCA	AGGCATTGGA	GGATGGGGGT	CCTGGTATGT	CTCACCAGGA	AATTCTGTTT	2640
	ATGTTCTTGC	AGCAGAGAGA	AATAAACTC	CTTGAAACCA	GCTCAGGCTA	CTGCCACTCA	2700
40	GGCAGCCTGT	GGGTCTCTGT	GGTGTAGGGA	ACGGCCTGAG	AGGAGCGTGT	CCTATCCCCG	2760
	GACGCATGCA	GGGCCCCCAC	AGGAGCGTGT	CCTATCCCCG	GACGCATGCA	GGGCCCCCAC	2820
	AGGAGCATGT	CCTATCCCTG	GACGCATGCA	GGGCCCCCAC	AGGAGCGTGT	ACTACCCCGG	2880
	AACGCATGCA	GGGCCCCCAC	AGGAGCGTGT	ACTACCCCGG	GACGCATGCA	GGGCCCCCAC	2940
	TGGAGCGTGT	ACTACCCCGG	GACGCATGCA	GGGCCCCCAC	AGGAGCGTGT	CCTATCCCCG	3000
45	GACCGGACGC	TGCGAGCGTG	CCCAAGGAG	CGTGTACTAC	CCCAAGGAGC	ATGCAGGGCC	3060
	CCCAAGGAG	CGTGTACTAC	CCCAAGGAGC	ATGCAGGGCC	CCCAAGGAG	CGTGTACTAC	3120
	CCCAAGGAGC	ATGCAGGGCC	CCCAAGGAGC	ATGCAGGGCC	CCCAAGGAGC	ATGCAGGGCC	3180
	TGAGCCGTGA	CCTCAGGAGG	GGGACCCAC	TGGAATTTTA	TTTCTCTCAG	GTGCGTGCCA	3240
	CATCAATAAC	AACAGTTTTT	ATGTTTGCGA	ATGGCTTTTT	AAAATCATAT	TTACCTGTGA	3300
50	ATCAAAACAA	ATTCAAGAA	GCAGTATCCG	CGAGCCTGCT	TGCTGATATT	GCAGTTTTTG	3360
	TTTCAAGAA	TAATAGCAA	TACTAGTGA	AGGATGTTGG	CCAAAAGCTG	CTTTCCATGG	3420
	CACACTGCCC	TCTGCCACTG	ACAGGAAAGT	GGATGCCATA	GTTTGAATTC	ATGCCTCAAG	3480
	TCGGTGGGCC	TGCCTACGTG	CTGCCGAGG	GCAGGGGCGG	TGCAGGGCCA	GTCATGGCTG	3540
	TCCCTGCAA	GTGGACGTGG	GCTCCAGGGA	CTGGAGTGTA	ATGCTCGGTG	GGAGCCGTCA	3600
55	GCCTGTGAAC	TGCCAGGCAG	CTGCAGTTAG	CACAGAGGAT	GGCTTCCCCA	TTGCCTTCTG	3660
	GGGAGGGACA	CAGAGGACGG	CTTCCCCATC	GCCTTCTGGC	CGCTGCAGTC	AGCACAGAGA	3720
	GCGGCTTCCC	CATTGCTTTC	TGGGAGGGA	CACAGAGGAC	AGTTTCCCCA	TGCGCTTCTG	3780
	GTGTGTTAAG	ACAGCACAGA	GAGCGGCTTC	CCCATCGCCT	TCTGGGGAGG	GGCTCGGTGT	3840
	AGCAACCCAG	GTGTTGTCCG	TGTCTGTTGA	CCAATCTCTA	TTCAGCATCG	TGTGGGTCCC	3900
60	TAAGCACAAT	AAAAGACATC	CACAATGGAA	AAAAAAAAG	GAATTC		

Seq ID NO: 509 Protein sequence
Protein Accession #: NP_001035.1

65	1	11	21	31	41	51	
	MSKSKCSVGL	MSSVVAPAKE	PNAVGPKEVE	LILVKEQNGV	QLTSSTLTNP	RQSPVEAQDR	60
	ETWKKIDFL	LSVIGFAVDL	ANVVRFPYLC	YKNGGGAFLV	PYLLFMVIAG	MPLPFYMEAL	120
	GQFNREGAAG	VWKICPILKG	VGFTVILISL	YVGFFYNVII	AWALHYLFSS	FTTELPWIHC	180
70	NNSWNSPNC	DAHPSDSSGD	SSGLNDTFGT	TPAAEYFERG	VLHLHQSHGI	DDLGPFRWQL	240
	TACLVLVIVL	LYFSLWKGVK	TSGKVWVITA	TMPIVVLTA	LLRGVTLPGA	IDGIRAYLSV	300
	DFYRLCEASV	WIDAATQVCA	SLGVGFGLI	AFSSYNKFTN	NCYRDAIVTT	SINSLTSFSS	360
	GFVVFSLFLY	MAQKHSVPIG	DVAKDGPGLI	PIIYPEAIAT	LPLSSAWAVV	FFIMLLTLGI	420
	DSAMGMESV	ITGLIDEFQL	LHRHRELFTL	FIVLATFLLS	LFCVTNGGIY	VFTLLDHFAA	480
75	GTSILFGLV	EAIGVAVFYG	VGQFDDIQQ	MTGQRPSLYW	RLCWKLVSFC	FLFVIVVSI	540
	VTFRPPHYGA	YIFPDWANAL	GWVIATSSMA	MVPIYAAKYP	CSLPGSPREK	LAYAIAPKED	600
	RELVDREVR	QFTLRHWLV					

Seq ID NO: 510 DNA sequence
Nucleic Acid Accession #: NM_001216.1
Coding sequence: 43..1422

85	1	11	21	31	41	51	
	GCCCCGTACAC	ACCGTGTGCT	GGGACACCCC	ACAGTCAGCC	GCATGGCTCC	CCTGTGCCCC	60
	AGCCCCCTGGC	TCCCTCTGTT	GATCCCGGCC	CCTGCTCCAG	GCCTCACTGT	GCAACTGCTG	120
	CTGTCACTGC	GCCTTCTGAT	GCTGTCCAT	CCCCAGAGGT	TGCCCGGAT	GCAGAGGAT	180
	TCCCCCTTGG	GAGGAGGCTC	TTCTGGGAA	GATGACCCAC	TGGCGAGGA	GGATCTGCC	240

AGTGAAGAGG ATTACCCAG AGAGGAGGAT CCACCCGGAG AGGAGGATCT ACCTGGAGAG 300
 GAGGATCTAC CTGGAGAGGA GGATCTACCT GAAGTTAAGC CTAATCAGA AGAAGAGGGC 360
 TCCTGAAAGT TAGAGGATCT ACCTACTGTT GAGGCTCCTG GAGATCCTCA AGAACCCAG 420
 AATAATGCCC ACAGGGACAA AGAAGGGGAT GACCAGAGTC ATTGGCGCTA TGGAGGCGAC 480
 CGCCCTGGC CCGGGGTGTC CCCAGCCTGC GCGGGCGCT TCCAGTCCCC GGTGGATATC 540
 CGCCCCAGC TCGCCGCTT CTGCCCGGCC CTGCCGCCCT TGGAACTCCT GGGCTTCCAG 600
 CTCCCGCGC TCCAGAACT GCGCCTGCGC ACAAATGGCC ACAGTGTGCA ACTGACCCTG 660
 CTCTCTGGG TAGAGATGGC TCTGGGTCCC GGGCGGGAGT ACCGGGCTCT GCAGCTGCAT 720
 CTGCACTGGG GGGCTGCAGG TCGTCCGGGC TCGGAGCACA CTGTGGAAGG CCACCGTTTC 780
 CTTGCCGAGA TCCACGTGCT TCACCTCAGC ACCGCTTTG CCAGAGTTGA CGAGGCCTTG 840
 GGGCGCCCGG GAGGCTTGGC CGTGTGGCC GCTTTCTGG AGGAGGGCCC GGAAGAAAAC 900
 AGTGCCTATG AGCAGTTGCT GTCTCGCTTG GAAGAAATCG CTGAGGAAGG CTCAGAGACT 960
 CAGGTCCAG GACTGGACAT ATCTGCACTC CTGCCCTCTG ACTTCAGCCG CTACTTCCAA 1020
 TATGAGGGGT CTCTGACTAC ACCGCCCTGT GCCCAGGGTG TCATCTGGAC TGTGTTTAAAC 1080
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 GGTGACTCTC GGCTACAGCT GAACTTCCGA GCGACGCAGC CTTTGAATGG GCGAGTGATT 1200
 GAGGCTCTCT TCCTCTGCTG AGTGGACAGC AGTCTCTGGG CTGTGAGGCC AGTCCAGCTG 1260
 AATTCTCGCC TGCTGCTGCG TGACATCCTA GCCCTGGTTT TTGGCCTCCT TTTTGCTGTC 1320
 ACCAGCGTCG CGTTCCTTGT GCAGATGAGA AGGCAGCACA GAAGGGGAAC CAAAGGGGGT 1380
 GTGAGCTACC GCCCAGCAGA GGTAGCCGAG ACTGGAGCCT AGAGGCTGGA TCTTGAGAGAA 1440
 TGTGAGAGAG CAGCCAGAGG CATCTGAGGG GGAGCCGGTA ACTGTCTCTG CTGCTCATT 1500
 ATGCCACTTC CTTTAACTG CCAAGAAATT TTTTAAATA AATATTATA AT

Seq ID NO: 511 Protein sequence
Protein Accession #: NP_001207.1

1 11 21 31 41 51
 MAPLCPSWPL PLLIPAPAPG LTVQLLSLL LLMPVHPQRL PRMQEDSPLG GGSSGEDDPL 60
 GEEDLPSEED SPREEPPGGE EDLPGEEDLP GEEDLPEVKP KSEEEGLSLK EDLPTVEAPG 120
 DPQEPQNNAH RDKEGDDQSH WRYGGDPPWP RVSPACAGRF QSPVDIRPQL AAPCPALRPL 180
 ELLGFQLPPL PELRLRNNGH SVQLTLPPGL EMALGPREGY RALQLHLHWG AAGRPGSEHT 240
 VEGHRFPAEI HVVHLSTAFAP RVDEALGRPG GLAVLAAFL EGPENSAYE QLLSRLBEIA 300
 EEGSETQVPG LDISALLPSD FSRYPQYEGS LTPPCAQGV INTVFNQTVM LSAQLHTLS 360
 DTLWGPDSR LQLNFRATQP LNRVIEASF PAGVDSPPRA AEPVQLNSCL AAGDILALVF 420
 GLLFAVTSVA FLVQMRQRH RGTGKGVSYR PAEVAETGA

Seq ID NO: 512 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..3978

1 11 21 31 41 51
 ATGGTGGGTG AAGGACCCTA CTTATCTCA GATCTGGACC AGCGAGGCCG GCGGAGATCC 60
 TTTGCAGAAA GATATGACCC CAGCCTGAAG ACCATGATCC CAGTGGCACC CTGTGCAAGG 120
 TTAGCACCCA ACCCGGTGGA TGATGCCGGG CTACTCTCCT TCGCCACATT TTCTGGCTC 180
 ACGCGGTGA TGGTGAAGG CTACCGGCAA AGGCTGACCG TAGACACCCT GCCCCATTG 240
 TCGACATATG ACTCATCTGA CACCAATGCC AAAAGATTTC GAGTCTTTG GATGAAGAG 300
 GTAGCAAGGG TGGGTCTCTG GAAGGCTCT CTGAGCCACG TGGTGTGGAA ATTCCAGAGG 360
 ACACGCGTGT TGTGTCGATC CGTGGCCAAC ATCCTGTGCA TCATCATGGC AGCCATAGGG 420
 CCGACAGTTC TCATTACCA AATCCTCCAG CAGACTGAGA GGACCTCTGG GAAAGTCTGG 480
 GTTGGCATTG GACTGTGCAT AGCCCTTTT GCCACCGAGT TTACCAAGT CTCTTTTGG 540
 GCCCTTGCCT GGGCCATCAA CTACCGCAGC GCCATCCGGT TGAAGGTGGC GCTCTCCACC 600
 TTGTTTATTG AAAACCTAGT GTCTTCAAG ACATTGACCC ACATCTCTGT TGGCGAGGTG 660
 CTCAATATAC TGTCAGTGA TAGCTATTCT TTGTTGAAG CTGCCTTGT TTGTCCTTG 720
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 GCCAAGCTCA ATTACGCTTT CCGAAGGTCA GCAATTTTGG TGACAGACAA GCGAGTTTCA 900
 ACAATGAATG AGTTTCTGAC CTGCATCAGG CTGATCAAAA TGTATGCCCT GGAGAAATCT 960
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 10 CGAACGGGAA CAGAGACGCA AGCCAAATTC ACCTCCGTGG AGCTGCTCAG GGAATACATT 3180
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 20 TCAAAGATCA TTCTCCTTGA TGAAGCCACC GCCTCTATGG ACTCCAAGAC TGACACCCCTG 3780
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25 Seq ID NO: 513 Protein sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 30 MVGEGPYLIS DLDQRGRRRS FAERYDPSLK TMIPVRPCAR LAPNPVDDAG LLSFATPSWL 60
 TPVMVKGYRQ RLTVDTLPPL STYDSSDTNA KRFRVLWDEE VARVGPEKAS LSHVVKPQR 120
 TRVLMDIVAN ILCIIMAAIG PTVLIHQILQ QTERTSGKVM VGIGLCIALF ATEFTKVFFW 180
 ALAWAINYRT AIRLKVALLST LVFENLVSEK TLTHISVGEV LNILSSDSYS LFEAALFCPL 240
 35 PATIPILMFV CAAYAFFILG PTALIGISVY VIFIPVQFMF AKLNSAFRRS AILVTDKRVQ 300
 TMNEFLTICR LTKMYAWEKS FTNTIQDIRR RERKLEKAG FVQSGNSALA PIVSTIAIVL 360
 TLSCHILLRR KLTAPVAFSV IAMFNVMKFS IAILPFSSIA MAEANVSLRR MKKILIDKSP 420
 PSYITQPEDP DTVLLLANAT LTWEHEASRK STPKKLQNK RHLCKQRSE AYSESPPAK 480
 40 GATGPEEQSD SLKSVLHSIS FVVRKLCRYP EAQLLAWRWP AVFVGRIIRG YRPHGFSAD 540
 KDESRLLLTW PQEVDRTORA AKYLKILGI CGNVGSGKSS LLAALLGQM LQKGVVAVNG 600
 TLAYVSQQA IFHGNVRENI LFGKYDHQR YQHTVRVCG LKDLNLDPY DLTETGERGL 660
 NLSGGQRQRI SLARAVYSDR QLYLLDDPLS AVDAHVGKHV FECCIKTTLR GKTVVVLVTHQ 720
 LQPLESCDEV ILLEDEIGE KGTHELMEE RGRYAKLIHN LRGLQFKDPE HLYNAAMVEA 780
 FKESPAEREE DAGIIGYLLS LFTVFLFLM IGSAAFSNWW LGLWLDKGSR MTCGPQGNRT 840
 45 MCEVGAFLAD IQGHVYQWVY TASMVFLVF GVTKGFFVTK TTLMASSSLH DTVFDKILKS 900
 PMSFFDTTPT GRLLMNRFSK MDELDRVLEF HAENFLQOFF MVVFILVILA AVFPAVLLV 960
 ASLAVGFFIL LRIPHRGVQE LKKVENVSRS PWFTHITSSM QGLGIHAYG KKESCITYTS 1020
 SKGLSLSYII QLSGLLQVCV RTGTETQAKF TSVELLREYI STCVPECTHP LKVGTCPKWD 1080
 50 PSCGEITFRD YQMRVDRNTP LVLDLNLNI QSGQTVGIVG RTGSGKSSLG MALFRLVEPA 1140
 SGTIFIDEVD ICILSLEDLR TKLTVIPQDP VLFVGTVRYN LDPFESHTDE MLWQVLERTF 1200
 MRDTIMKLEP LKQAEVTENG ENFSVGERQL LCVARALLRN SKIILLDEAT ASMSDKTDTL 1260
 VQNTIKDAFK GCTVLTIAHR LNTVLNCDHV LVMENGKIVIE FDKPEVLAEK PDSAFAMLLA 1320
 AEVRL

55 Seq ID NO: 514 DNA sequence
 Nucleic Acid Accession #: Z31560
 Coding sequence: 1-966

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 CGCAAGATGG CCCAGAGAAA CCCCAAGATG CACAACCTCG AGATCAGCAA GCGCCTGGGC 240
 65 GCCGAGTGA AACTTTTGTC GGAGACGGAG AAGCGGCGGT TCATCGACGA GGCTAAGCGG 300
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 ATGAACGGCT CGCCCACTCA CAGCATGTCC TACTCGCAGC AGGGCACTCC TGGCATGGCT 720
 CTTGGCTCCA TGGGTTCCGT GGTCAAGTCC GAGGCCAGCT CCAGCCCCC TGTGTTTACC 780
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 75 TATCTCCCGC GCGCGAGGAT GCCGGAACCC GCCGCCCCCA GCAGACTTCA CATGTCCAG 900
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80 Seq ID NO: 515 Protein sequence
 Protein Accession #: CAA83435

1 11 21 31 41 51
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 KTLMKDKYKT LPGGLLAPGG NSMASGVGVG AGLGAGVNQR MDSYAHMNGW SNGSYSMMQD 180

QLGYPOHPGL NAHGAAQMQP MHRVDVLSAQ YNSMTSSQTY MNGSPTYSMS YSQQGTGMA 240
 LGSMGSSVVK EASSSPFVVT SSSHSRAPCQ AGDLRDMISM YLPGAEPPEP AAPSRHMSQ 300
 HYQSGFVPGT AINGTLPLSH M

5 Seq ID NO: 516 DNA sequence
 Nucleic Acid Accession #: U91618
 Coding sequence: 29..541

10 1 11 21 31 41 51
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 15 TCCTCTTGG AAGATGACTC TGCTAAATGT TTGCAGTCTT GTAAATAATT TGAACAGCCC 240
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 TGCTTTAGAT GGCTTTAGCT TGAAGCAAT GTTGACAATA TACCAGCTCC ACAAATCTG 360
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 TGACAAAAT GGAAAGGAAG AAGTCATAAA GAGAAAAAT CCTTATATTC TGAACCGCA 480
 20 GCTGTATGAG AATAAACCCA GAAGACCCTA CATACTCAA AGAGATTCTT ACTATTACTG 540
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25 Seq ID NO: 517 Protein sequence
 Protein Accession #: AAB50564

30 1 11 21 31 41 51
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 LIQEDILDTG NDKNGKEEVI KRKIPYILKR QLYENKPRRP YILKRDSSYY

35 Seq ID NO: 518 DNA sequence
 Nucleic Acid Accession #: NM_006536.2
 Coding sequence: 109..2940

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 GAACTCCCAT TCCTGGGAGC TGGAGTACAG CTTCAGACA ATGGGTATAA TGGATTGCTC 240
 45 ATTGCAATTA ATCCTCAGGT ACCTGAGAAT CAGAACCTCA TCTCAAACAT TAAGGAAATG 300
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 TCATATGAAA AGCAAAATGT CAATGTGACT GACTGGTATG GGGCACATGG AGATGATCCA 480
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 80 CCACATGCA AATATTGA CTTGGAAGCT GTAAAAGTAG AAGAGGAAT GACCCTATCT 2460
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 85 ACCAATGGAC CTGAACATCA GCCAAATGGA GAAACACATG AAAGCCACAG AATTTATGTT 2700
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Seq ID NO: 519 Protein sequence
 Protein Accession #: NP_006527.1

1 11 21 31 41 51
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 KPFYINGQNO IKVTRCSSDI TGIFVCEKGP CPQENCIISK LFKEGCTFIY NSTQNATASI 240
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 TFSLVQAGDK VVCLVLDVSS KMAEADRLQ LQQAEPYLM QIVEIHTFVG IASFDSKGEI 360
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Seq ID NO: 520 DNA sequence
 Nucleic Acid Accession #: NM_000228.1
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 CAGTCCCTGC CTCAGAGGCC TAATGCACGC CTAATGGGG GGAAGGTCCA ACTTAACCTT 660
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 Protein Accession #: NP_000219.1

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Protein Accession #: NP_001935.1

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	TG	CA	TG	AT	GA	TC	TG	AA	GC	AT	TT	TG	CA	GC	TA	GC	AG	TC	GA	TC	GG	TG	GC	AG	A	4620			
5	AG	GC	CA	TT	CA	T	GG	AA	TT	TG	TT	GT	TT	AT	CT	CT	GC	CC	TC	TC	GG	GC	CA	TA	AG	A	4680		
	CT	AT	GA	AA	TT	AA	GC	CT	AT	CT	GA	TT	CT	CT	CT	CA	TT	TC	TC	TC	TC	TC	TC	TC	TC	A	4740		
	TG	AC	CC	TA	AAA	AT	CT	AT	GT	TT	TG	AC	TA	CT	TA	CT	TC	TC	TC	TC	TC	TC	TC	TC	TC	T	4800		
	TT	GA	AC	GC	GA	TC	TC	GC	CT	CA	GC	CA	GC	AG	TC	GG	AG	TC	GA	TC	GG	TC	TC	TC	TC	T	4860		
	CT	GA	AA	AG	TC	GC	CT	CC	CG	GT	TC	CA	TC	GC	CA	TC	CT	CT	CT	CT	CT	CT	CT	CT	CT	T	4920		
	G	AC	TA	AC	GC	GC	CC	AC	CC	AC	GC	CC	GC	CT	AA	TT	TT	TT	TT	TT	TT	TT	TT	TT	TT	T	4980		
10	TT	CA	CT	TG	TT	TG	CC	AG	GC	AT	GC	TC	GC	AT	TC	TC	GC	AG	TC	TC	GC	TC	TC	TC	TC	T	5040		
	T	CC	CA	AA	AG	TC	TC	GG	AT	TC	AG	GC	AT	GC	CA	CC	GC	TC	CC	GC	CT	TG	TT	T	TC	CG	TT	5100	
	GT	CG	TC	TC	TC	TT	TA	AT	GT	TC	CA	TT	TT	TC	GA	TC	GA	TC	GA	TC	AG	TT	TC	GA	TC	AG	A	5160	
	T	CA	AT	TG	TA	AA	TA	CT	CA	AC	AA	AG	CA	GC	TC	GA	AG	GC	AG	GC	GC	GC	GC	GC	GC	GC	T	5220	
15	GC	CA	CA	AA	AA	TT	GG	TC	TG	AG	AA	TG	GA	AT	TC	GA	AA	GC	TA	GT	TG	CT	GA	AA	TC	TC	T	5280	
	TC	T	AA	CC	GA	TC	AA	GC	AG	TC	TT	TC	TC	TC	TC	TC	TC	TC	TC	TC	TC	TC	TC	TC	TC	TC	T	5340	
	CC	CA	CT	C	ACC	CA	AA	AG	TC	GC	TA	CT	CA	CC	AA	GC	TC	TC	TC	TC	TC	TC	TC	TC	TC	TC	T	5400	
	T	CA	AA	AG	GA	TC	CA	AG	TA	TC	CT	CC	CT	GT	TC	TA	AA	AA	CC	TC	TA	AA	CC	TC	TC	TC	T	5460	
	TG	AC	AT	GC	TC	GA	AA	CC	AC	TC	TG	CT	TC	GC	AT	TC	GC	CC	GA	AT	TC	GC	CC	GA	AT	TC	T	5520	
20	AA	AT	G	AA	AA	TT	AA	TT	TT	AG	GC	AT	TC	CA	TT	CT	AT	AT	TT	TC	AT	AT	TT	TC	AT	AT	TC	T	5580
	TC	CT	T	AT	AT	TC	TG	TA	AG	GT	GA	AT	TC	TC	TC	TC	TC	TC	TC	TC	TC	TC	TC	TC	TC	TC	T	5640	
	AG	CT	TT	CT	CA	TT	TT	CC	CC	CA	TC	TG	AT	GA	TT	AG	AT	TT	TT	TC	AT	GA	AT	TC	TC	TC	T	5700	
	TT	TT	CT	CT	TA	TT	TA	AG	GA	GC	AT	GC	TC	TC	TC	TC	TC	TC	TC	TC	TC	TC	TC	TC	TC	TC	T	5760	
	TT	TA	AA	CA	GA	GT	TT	TA	GT	AT	TG	CT	AT	TA	AA	AG	AT	TC	TC	TC	TC	TC	TC	TC	TC	TC	T	5820	
25	CT	GC	TT																										

Seq ID NO: 527 Protein sequence
Protein Accession #: NP_077741.1

	1	11	21	31	41	51	
50	MAAAGPRRSV	RGAVCLHLLL	TLVIFSRDGE	ACKKVILNVP	SKLEADKIIG	RVNLEECFRS	60
	ADLIRSSDDP	FRVLNDGGSVY	PARMAQENSLK	KRSFTIWLSD	KRKQTKQEV	VLLEHQKQVS	120
	KTRHRTETVL	RAKRWRWAPI	PCSAVENSQDG	PFPLFLQQVE	SDAAQNYTVF	YSISRGVDK	180
	EPLNLFYIER	DTGNLFCRPI	VDREYDVDF	LIAAYASTAD	YSADGLPLP	IRVEDENDNH	240
55	PVFTEAIYNP	EVLESSRPGT	TGVGVCAATR	DEPDTMHLRT	KYSILQQTPT	SPGLFSVHP	300
	TGVITTVSHY	LDREVVDKFS	LIMKVQMDQF	QDFFLGITST	CIITVDSND	NAPPTRONAY	360
	EAFVEENAFN	VEILRIPIED	KDLINTANWR	VNPTILKGV	NGHFKISTDK	ETNEGVLVSV	420
	KPLNYEENRQ	VNLEIGVNNE	APFARDIPRV	TALNRALVT	HVRDLDEGPE	CTPAAQYVRI	480
	KENLAVGSKI	NGYKAYDPEN	RNGNGLRYKK	LHDPKGWITI	DEISGSITS	KILDREVBTP	540
60	KNELNYITVL	ALDKDRSRTG	GTLAVNIEDV	NDNPPPEILQ	YVVIKCKPKG	YTDLDVADPD	600
	EPVHGAPYFF	SIDPSTPEIS	RLWSLTKVND	TAARLSYQKN	AGFOETIPI	VTDKRAGQAA	660
	TKLLRVNLCE	CTHPQCRAT	SRSTGVILKG	WAILAILLGI	ALLFSVLLTL	VCGVFGATKG	720
	KRPFPEDLAQ	NLIISNTEAP	GDDRVCSSAG	FMFTQTTNNS	QGFCTMGSSG	KMGSGQETIE	780
	MMKGGNQTLE	SCRGAGHHHT	LDSRCRGHTE	VONCRVTYSE	WHSFTQPRLG	EESIRGHTG	

Seq ID NO: 528 DNA sequence
Nucleic Acid Accession #: NM_001941.2
Coding sequence: 64..2754

70	1	11	21	31	41	51	
	GGCAGGTCCTC	GCTCTCGGCA	CCCTCCCGGC	GCCCGCGTTC	TCCTGGCCCT	GCCCGGCATC	60
	CGATGGCCG	CCGCTGGGCC	CCGGCGCTCC	GTGCGCGGAG	CCGTCTGCCT	GCATCTGCTG	120
	CTGACCCCTCG	TGATCTTCAG	TCGTGATGGT	GAAGCTCGCA	AAAAGGCTAT	ACTTAATGTA	180
75	CCTTCTAAAC	TAGAGGCGAGA	CAAAATAATT	GGCAGAGTTA	ATTTTGAAGA	GTGCTTCAGG	240
	TCTGTCAGACC	TCATCCGGCT	AAGTGACTCT	GATTTCAGAT	TTCTAAATGA	TGGGTCAGTG	300
	TACACAGCCA	GGGCTGTTGC	CGTGTCTGAT	AAGAAAAGAT	CATTTTACAT	ATGGCTTTCT	360
	GACAAAAGGA	AACACAGACA	GAAAGAGGTA	ACTGTGCTGC	TAGAACATCA	GAAAGAAGTA	420
80	TCGAAGACAA	GACACACTAG	AGAAACTGTT	CTCAGGCGTG	CCAAGAGGAG	ATGGGCACCT	480
	ATTCTCTGCT	CATGCAAGA	GAATTCCTGT	GGCCCTTTCC	CATTGTTTCT	TGCAACAGTT	540
	GAATCTGATG	CAGACACAGA	CTATCTGTCT	TTTACTACTA	TAAGTGGACG	TCGAATGAT	600
	AAAGAACCTT	TAAATTTGTT	TTATATAGAA	AGAGACACTG	GAATCTATT	TTGCACTCGG	660
	CCTGTGGATC	TGAGAAGATA	TGATGTTTTT	GATTTGATTG	CTTATGCGTG	AACCTGCAGAT	720
85	GGATATTGAG	CAGATCTGCC	CCTCCCACTA	CCCATCAGGG	TAGAGGATGA	AAATGCACAAC	780
	CACCCTGTTT	TCACAGAAGC	AATTTATAAT	TTTGAAGTTT	TGGAAAGTAG	TAGACCTGGT	840
	ACTACAGATGG	GGGTGGTTTG	TGCCACAGAC	AGAGATCAAC	CCGACACAAT	GCATACGGCG	900
	CTGAATAACTA	GCAATTTTGA	GCAGACACCA	AGGTCACTGC	GGCTCTTTTC	TGTGCATCCC	960

	AGCACAGGCG	TAATCACCAC	AGTCTCTCAT	TATTTGGACA	GAGAGGTGT	AGACAAGTAC	1020
	TCATTGATAA	TGAAAGTACA	AGACATGGAT	GGCCAGTTTT	TTGGATTGAT	AGGCACATCA	1080
	ACTTGTATCA	TAACAGTAAC	AGATTCAAAT	GATAATGCAC	CCACTTTTCAG	ACAAAAATGCT	1140
5	TATGAAGCAT	TTGTAGAGGA	AAATGCATTTC	AATGTGGAAA	TCTTACGAAT	ACCTATAGAA	1200
	GATAAGGATT	TAATTAACAC	TGCCAATTGG	AGAGTCAATT	TTACCATTTT	AAAGGGAAAT	1260
	GAATAATGGAC	ATTTCAAAAT	CAGCACAGAC	AAAGAAACTA	ATGAAGGTGT	TCTTTCTGTT	1320
	GTAAAGCCAC	TGAATTATGA	AGAAAAACCGT	CAAGTGAACC	TGGAAATTGG	AGTAAACAAT	1380
	GAAGCGCCAT	TTGCTAGAGA	TATTTCCAGA	GTGACAGCCT	TGAACAGAGC	CTTGGTTACA	1440
10	GTTCATGTGA	GGGATCTGGA	TGAGGGGCCT	GAATGCATCT	CTGCAGCCCA	ATATGTGCGG	1500
	ATTAAAGAAA	ACTTAGCAGT	GGGGTCAAAG	ATCAACGGCT	ATAAGGCATA	TGACCCCGAA	1560
	AATAGAAATG	GCAATGGTIT	AAGGTACAAA	AAATTGCATG	ATCCTAAAGG	TTGGATCACC	1620
	ATTGATGAAA	TTTCAGGGTC	AATCATAACT	TCCAAAATCC	TGGATAGGGA	GGTTGAAACT	1680
	CCCAAAAATG	AGTTGTATAA	TATTACAGTC	CTGGCAATAG	ACAAAGATGA	TAGATCATGT	1740
15	ACTGGAACAC	TTGCTGTGAA	CATTGAAGAT	GTAATGATA	ATCCACCAGA	AATACCTCAA	1800
	GAATATGTAG	TCATTTCGAA	ACCAAAAATG	GGGTATACCG	ACATTTTAGC	TGTTGATCCT	1860
	GATGAACCTG	TCCATGGAGC	TCCATTTTAT	TTCAGTTTGC	CCAATACCTC	TCCAGAAATC	1920
	AGTAGACTGT	GGAGCTCTAC	CAAGGTTAAT	GATACAGCTG	CCCGTCTTTC	ATATCAGAAA	1980
	AATGTCTGGAT	TTCAAGAATA	TACCATTCTT	ATTACTGTAA	AAGACAGGGC	CGGCCAAGCT	2040
	GCAACAAAAT	TATTGAGAGT	TAATCTGTGT	GAATGTACTC	ATCCAACTCA	GTGTCGTGCG	2100
20	ACTTCAAGGA	GTACAGGGTT	AATACTTGGA	AAATGGGCAG	TCCTTGCAAT	ATTACTGGGT	2160
	ATAGCACTGC	TCTTTTCTGT	ATTGCTAACT	TTAGTATGTG	GAGTTTITGG	TGCAACTAAA	2220
	GGGAAACGTT	TTCTGGAAGA	TTTAGCAGAG	CAAAACTTAA	TTATATCAAA	CACAGAAGCA	2280
	CCTGGAGACG	ATAGAGTGTG	CTCTGCCAAT	GGATTATGGA	CCCAAACTAC	CAACAACTCT	2340
	AGCCAAGGTT	TTTGTGGTAC	TATGGGATCA	GGAATGAAAA	ATGGAGGGCA	GGAACCATT	2400
25	GAATATGATG	AAGGAGGAAA	CCAGACCTTG	GAATCCTGCC	GGGGGGCTGG	GCATCATCAT	2460
	ACCTCGGACT	CCTGAGGGG	AGGACACACG	GAGGTGGACA	ACTGCAGATA	CACCTTACTCG	2520
	GAGTGGCACA	GTTTTACTCA	ACCCCGTCTC	GGTAAAAAT	TGCATCGATG	TAATCAGAAT	2580
	GAAGACCGCA	TGCCATCCCA	AGATTATGTC	CTCACTTATA	ACTATGAGGG	AAGAGGATCT	2640
	CCAGCTGGTT	CTGTGGGCTG	CTGCAGTGAA	AAGCAGGAAG	AAGATGGCCT	TGACTTTTTA	2700
30	AATAATTGG	AACCCAAATT	TATTACATTA	GCAGAAGCAT	GCACAAAGAG	ATAATGTCTC	2760
	ATGCTACAAA	TTAGGTCTTT	GTGAGACATT	CTGGAGGTTT	CCAAAAATAA	TATTGTAAAG	2820
	TTCAATTTC	ACATGTATGT	ATATGATGAT	TTTTTCTCTA	ATTTTGAATT	ATGCTACTCA	2880
	CCAATTTATA	TTTTTAAAGC	CAGTTGTGTC	TTATCTTTTC	CAAAAAGTGA	AAAATGTTAA	2940
	AACAGACAAC	TGGTAAATCT	CAAACTCCAG	CACCTGGAAT	AAGGTCTCTA	AAGCATCTGC	3000
35	TCTTTTTTTT	TTTTTCAGAT	ATTTTAGTAA	TAAATATGCT	GGATAAATAT	TAGTCCAACA	3060
	ATAGCTAAGT	TATGCTAATA	TCACATTATT	ATGTATTAC	TTTAAGTGAT	AGTTTAAAAA	3120
	ATAAACCAAG	AATATTGAGT	ATCATTATGT	GAAGAAAGTT	TTGGAAAAGA	AACAATGAAG	3180
	ACTGAATTA	ATTAAAAATG	TTGCAGCTCA	TAAAGAATTG	GGACTCACCC	CTACTGCAC	3240
40	ACCAAAATCA	TTTGACTTTG	GAGGCAAAAT	GTGTGAAGT	GCCCTATGAA	GTAGCAATTT	3300
	TCATATAGGA	TATAGTTGGA	AATAAATGTG	TGTGTGTATA	TTATTATTAA	TCAATGCAAT	3360
	ATTTAAAAAT	AAATAGAGAA	AAAGAGGAAA	ATGGTAAAAA	CTTGAAATGA	GGCTGGGGTA	3420
	TAGTTTGTCC	TACAATAGAA	AAAAGAGAGA	GCTTCTTAGG	CCTGGGCTCT	TAAATGCTGC	3480
	ATTATAACTG	AGTCTATGAG	GAATAGTTTC	CTGTCCAATT	TGTGTAATTT	GTTTAAAAAT	3540
45	GTAATAAAT	TAACTTTTTC	TGGTTTCTGT	GGGAAGGAAA	TAGGGAATCC	AATGGAACAG	3600
	TAGCTTTGCT	TTGCAGTCTG	TTTCAAGATT	TCTGCATCCA	CAAGTTAGTA	GCAAACTGGG	3660
	GAATACTCGG	TGCAGCTGGG	GTTTCCCTGCT	TTTTGGTAGC	AAGGGTCCAG	AGATGAGGTG	3720
	TTTTTTTCGG	GGAGCTGTG	ACAAAACAT	TTTAAACTTT	ACCTTTACTG	AAGTTAAATC	3780
	CTCTATTGCT	GTTTCTATTCT	TCTCTTATAG	TGACCAACAT	CTTTTTAATT	TAGATCCAAA	3840
	TAACCATGCT	CTCCTAGAGT	TTAGAGGCTA	GAGGGAGCTG	AGGGGAGGAT	CTTACTGAAA	3900
50	GCACCTGGG	GAGATTGATT	GTCTTTAAAC	CTAAGCCCCA	CAAACTTGAC	ACCTGATCAG	3960
	GTCTGGGAGC	TACAAAATTT	CATTTTCTCT	CTCACTGCCC	TTCTTCTGAG	TGGCAITGGC	4020
	CTGAATCAAG	GAAAGCCAGG	CCTTGTGGGC	CCCCTTCTTT	CGGCTTCTG	CTAAAGCAAC	4080
	ACCTCCAGCA	GAGATTCCCT	TAAGTGACTC	CAGGTTTTCC	ACCATCCTTC	AGCTGTAATT	4140
55	AATTTTTAAT	CAGTTTGCCT	TCTCCAGAGA	AATTTTAAAA	TAATAGAAGA	AATAGAAATT	4200
	TTGAATGTAT	AAAAGAAAAA	GATCAAGTTG	TCATTTTAGA	ACAGAGGGAA	CTTTGGGAGA	4260
	AAGCAGCCCA	GATAGTTATT	TTGTACAGTC	AGAGGGCAAC	AGGAAGATGC	AGGCCCTCAA	4320
	GGGCAAGGAG	AGGCCACAAG	GAATATGGGT	GGGAGTAAAA	GCAACATCGT	CTGCTTCATA	4380
	CTTTTTCTTA	GGCTTGGCAC	TGCTTTTCC	TTTCTCAGGC	CAATGGCAAC	TGCCATTGTA	4440
60	GTCCGGTGAG	GGATCAGCCA	ACCTCTTCTC	TATGGCTCAC	CTTATTGGA	GTGAGAAATC	4500
	AAGGAGACAG	AGCTGACTGC	ATGATGAGTC	TGAAGGCATT	TGCAGGATGA	GCCTGAACTG	4560
	TTTGTGCAGA	ACAAACAAGG	CATTATGGG	AATTGTTGTA	TTCTTCTGCG	AGCCCTCCTT	4620
	CTGGGCACTA	GGAAGGTCTA	TGAATTAAT	GCCTATCTAA	AATCTGATT	TATCTCTACA	4680
	TTTTCTGTTT	TCTAATTGGA	CCCTAAAATC	TATGTGTTTT	AGACTTAGAC	TTTTTATTGC	4740
65	CCCCCCCCCT	TTTTTTTTTG	AGACGGAGTC	TCGCTCTGAC	GCACAGGCTG	GAGTGCAGTG	4800
	GCTCCGATCT	CTGCTCACTG	AAAGCTCCGC	CTCCCGGGTT	CATGCCATTC	TCCTGCCTCA	4860
	GCCTCCTGAG	TAGCTGGGAC	TACAGGCGCC	CACCACCACG	CCCGGCTAAT	TTTTTGTATT	4920
	TTTAATAGAG	ACGGGGTTTT	ACTGTGTTAG	CCAGGATGGT	CTCGATCTCC	TGACCTCGTG	4980
	ATCCGCCTGC	CTCGGCTCC	CAAAAGTGCTG	GGATTACAGG	CATGACCCAC	CGCTCCCGGC	5040
70	CTTGTTTTCC	GTTTAAAGTC	GTCTTCTTTT	AATGTAATCA	TTTTGAACAT	GTGTGAAAGT	5100
	TGATCATACG	AATTGGATCA	ATCTTGAAAT	ACTCAACCAA	AAGACAGTCG	AGAAGCCAGG	5160
	GGGAGAAAGA	ACTCAGGGCA	CAAAATATTG	GTCTGAGAAT	GGAATTCTCT	GTAAGCCTAG	5220
	TTGCTGAAAT	TTCTGCTGT	AACCAGAAGC	CAGTTTTATC	TAACGGCTAC	TGAACACCCC	5280
	ACTGTGTTTT	GCTCACTCCC	TCACTCACCG	ATCAAAACCT	GCTACCTCCC	CAAGACTTTA	5340
75	CTAGTGCCGA	TAAACTTTCT	CAAGAGCAAA	CCAGTATCAC	TTCCCTGTTT	ATAAAACCTC	5400
	TAACCATCTC	TTTGTCTTTT	GAACATGCTG	AAAACCACCT	GGTCTGCATG	TATGCCCGAA	5460
	TTTGTAAATC	TTTTCTCTCA	AATGAAAATT	TAAATTTAGG	GATTCAATTC	TATATTTTCA	5520
	CATATGTAGT	ATTATTTATT	CCTTATATGT	GTAAGGTGAA	ATTTATGGTA	TTTGAGTGTG	5580
	CAAGAAAATA	TATTTTAAAA	GCTTTCATTT	TTCCCCCAGT	GAATGATTTA	GAATTTTTTA	5640
	TGTAATATAT	CAGAATGTTT	TTTTTACTTT	TTATAAGGAA	GCAGCTGTCT	AAAATGCAGT	5700
80	GGGGTTTGT	TTGCAATGTT	TTAAACAGAG	TTTTAGTATT	GCTATTAAAA	GAGTTACTTT	5760
	TGCTTTTAAA	GAAACTTGGC	TGCTTAAAAA	AAGCAAAAAT	TGGATGCATA	AAGTAATATT	5820
	TACAGATGTG	GGGAGATGTA	ATAAAACAAAT	ATTAACCTGG	TTTCTTGTTT	TTGCTGTATT	5880
	TAGAGATTAA	ATAATTTCTA	GATGATCACT	TTGCAAAAAT	ATGCTTATGG	CTGGCATGGA	5940
	AATAGAAAATA	CTCAATTATG	TCTTTGTTGT	ATTAATGGGG	AATATTTTGG	ACAATGTTTC	6000
85	ATTATCAAAT	TGTCGACATC	ATTAATATAT	ATTGTAATGT	TGGGAAGAGA	TCACTATTTT	6060
	GAAGCACAGC	TTTACAGATG	AGTATCTATG	ATACATATGT	ATAATAAAT	TTGATCGGGT	6120
	ATTAAGAGTA	TTAGAAGGTG	GTTATAATTG	CAGAGTATTC	CATGAATAGT	ACACTGACAC	6180

AGGGGTTTAA CTTTGAGGAC CAGTGTAGTC AAGGGAAAAC ATGAGTTAAA AAGAAAAGCA 6240
 GGCAATATTG CAGTCTTGAT TCTGCCACTT ACAGGATAGA TAATGCCTGA ACTTTAATGA 6300
 CAAGATGATC CAACCATAAA GGTGCTCTGT GCTTCACAGT GAATCTTTTC CCCATGCGAG 6360
 AGTGTGCTCC CCTACAAACG TTAAGACTGA TCATTTCAAA AATCTATTAG CTATATCAAA 6420
 AGCCTTACAT TTTAATATAG GTTGAACCAA AATTTCAATT CCAGTAACCTT CTATTGTAAC 6480
 CATTATTTTT GTGTATGTCT TCAAGAATGT TCATTGGATT TTTGTTTGTG ATAGTAAAAT 6540
 ACCGGATACA TTTACAGTGT CCTTCAGTAT TGATTGGTT GAATATTGGG TCATAATGGT 6600
 TGAGAAGCAT GGACACTAGA GCCAGAATGC TTGGATATGA ATCCTGGATC TGTCACTTAC 6660
 TTCTGTGTGA CCTTTGAAAG GCTACTTATT TCCTCTCTTA GCTTTCTCAT TAAAATCAAT 6720
 GAACAATGCC AGCCTCATGG GGTGTTGAA TGATTAAAT AGTTAATATA CCTAAAGTAC 6780
 ATAGAACACT GCCTGCACAT AGTAAAGAA TTATAAGTGT GAGGTAGTTG GTAAATATAT 6840
 GTAGTTGGAT ATACTACCGA ACAATATCTA ATCTCTTTT AGGGAAATAA AGTTTGTGCA 6900
 TATATATAAT CCCGAAACAT G

Seq ID NO: 529 Protein sequence
 Protein Accession #: NP_001932.1

1 11 21 31 41 51
 MAAAGPRRSV RGAUCLHLLL TLVIFSRDGE ACKKVILNVP SKLEADKIIG RVNLEECFRS 60
 ADLIRSDPD FRVLNDGSVY TARAVALS DK KRSFTIWLSD KRKQTQKEVT VLEHQKKVS 120
 KTRHRETVL RRAKRRWAPI PCSMQENSLG PFPLFLQQVE SDAQNYTVF YSISGRGVDK 180
 EPLNLFYIER DTGNLFCTRP VDREYDVFD LIAYASTADG YSADLPLPLP IRVEDENDNH 240
 PVFTEATYNP EVLESSRPGT TVGVVCAADR DEPDTHMTRL KYSILQQTTPR SPGLFSVHPS 300
 TGWITTVSHY LDREVVQDKYS LIMKVQDMOG QFFGLIGTST CIITVTDSDN NAPTFRQNAV 360
 EAFVEENAFN VEILRIPIED KDLINTANWR VNFTILKGNE NGHFKISTDK ETNEGVLVSV 420
 KPLNYEENRQ VNLEIGVNNP APPARDIPRV TALNRALVTV HVRDLDEGPE CTPAAQYVRI 480
 KENLAVGSKI NGYKAYDPEN RENGGLRYKK LHDPKGWITI DEISGSIITS KILDREVETP 540
 KNELYNITVL AIDKDRSCT GTLAVNIEDV NDNPPPEILQE YVICKPKMG YTDILAVDPD 600
 EPVHGAPFFY SLNPTSPEIS RLWSLTKVND TAARLSYQKN AGFQETIPI TVKDRAGQAA 660
 TKLLRVNLCE CTHPTQCRAT SRSTGVILGK WAILAILLGI ALLFSVLLTL VCGVFGATKG 720
 KRFPEDLAQQ NLIISNTEAP GDDRVCSSANG FMTQTNNSS QGFCGTMGSG MKNGGQETIE 780
 MMKGGNQTLE SCRGAGHHHT LDSCRGGHTE VDNCRYTYSE WHSFQPRLG EKLHRCNQNE 840
 DRMPSEQYVL TYNYEGRGSP AGSVGCCSEK QEEDGLDFLN NLEPKFITLA EACTKR

Seq ID NO: 530 DNA sequence
 Nucleic Acid Accession #: NM_016583.2
 Coding sequence: 72..842

1 11 21 31 41 51
 GGAGTGGGGG AGAGAGAGGA GACCAGGACA GCTGCTGAGA CCTCTAAGAA GTCCAGATAC 60
 TAAGAGCAAA GATGTTTCAA ACTGGGGGCC TCATTGTCTT CTACGGGCTG TTAGCCAGCA 120
 CCATGGCCCA GTTTGAGGCG CTGCCCGTGC CCCTGGACCA GACCTGCCCC TTGAATGTGA 180
 ATCCAGCCCT GCCCTTGAGT CCCACAGGTC TTGCAGGAAG CTTGACAAAT GCCCTCAGCA 240
 ATGGCCTGCT GTCTGGGGGC CTGTTGGGCA TTCTGGAATA CCTTCGCTC CTGGACATCC 300
 TGAAGCCTGG AGGAGGTACT TCTGTTGGCC TCCTTGGGGG ACTGCTTGGG AAAGTGACGT 360
 CAGTGATTCC TGGCCTGAAC AACATCATTG ACATAAAGGT CACTGACCCC CAGCTGCTGG 420
 AACTTGGCCT TGTGCAGAGC CCTGATGGCC ACCGTCTCTA TGTCAACATC CCTCTCGGCA 480
 TAAAGCTCCA AGTGAATACG CCCTGGTTCG GTGCAAGTCT GTTGAGGCTG GCTGTGAAGC 540
 TGGACATCAC TGCAGAAATC TTAGCTGTGA GAGATAAGCA GGAGAGGATC CACCTGGTCC 600
 TTGGTGACTG CACCCATTCC CTGGAAGGCC TGCAAATTC TCTGCTTGAT GGACTTGGCC 660
 CCCTCCCCAT TCAAGTCTT CTGGACAGCC TCACAGGGAT CTTGAATAAA GTCTGCTCTG 720
 AGTTGGTTCA GGGCAACGTG TGCCCTCTGG TCAATGAGGT TCTCAGAGGC TTGGACATCA 780
 CCCTGGTGCA TGACATTGTT AACATGCTGA TCCACGGACT ACAGTTTGTG ATCAAGTCTT 840
 AAGCCTTCCA GGAAGGGGCT GGCCTCTGCT GAGCTGCTTC CCAGTGCTCA CAGATGGCTG 900
 GCCCATGTGC TGAAGATGA CACAGTTGCC TTCTCTCCGA GGAACCTGCC CCTCTCCTT 960
 TCCACACAGG CGTGTGTAAC ATCCCATGTG CCTCACCTAA TAAATAGGCT CTTCTCTGTC 1020
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA

Seq ID NO: 531 Protein sequence
 Protein Accession #: NP_057667.1

1 11 21 31 41 51
 MFQTGGLIVF YGLLAQTMAG FGGLPVPLDQ TLPLNVNPAI PLSPTGLAGS LTNALSNGLL 60
 SGGLLGILEN LPLLDILKPG GGTSGLLGGL LLGKVTSPVP GLNNIIDIKV TDPQLLELGL 120
 VQSPDGHRLY VTIPGLIKLP VNTPLVGASL LRLAVKLDIT ABILAVRDKQ ERIHLVLGDC 180
 THSPGSLQIS LLDGLGLPLPI QGLDLSLTGI LNKVLPPLVQ GNVCPVNEV LRGLDITLVH 240
 DIVNMLIHGL QFVIKV

Seq ID NO: 532 DNA sequence
 Nucleic Acid Accession #: NM_004363.1
 Coding sequence: 115..2223

1 11 21 31 41 51
 CTCAGGGCAG AGGGAGGAAG GACAGCAGAC CAGACAGTCA CAGCAGCCTT GACAAAACGT 60
 TCCTGGAACT CAGCTCTTTC TCCACAGAGG AGGACAGAGC AGACAGCAGA GACCATGGAG 120
 TCTCCCTCGG CCCTCTCCCA CAGATGGTGC ATCCCTCTGGC AGAGGCTCCT GCTCACAGCC 180
 TCACTTCTAA CCTTCTGGAA CCGGCCACCC ACTGCCAAGC TCACTATTGA ATCCACGCCG 240
 TTCAATGTGC CAGAGGGGAA GGAGGTGCTT CTACTTGTCC ACAATCTGCC CCAGCATCTT 300
 TTTGGCTACA GCTGGTACAA AGGTGAAAGA GTGGATGGCA ACCGTCAAAT TATAGGATAT 360
 GTAATAGGAA CTCAACAAGC TACCCACAGG CCCGCATACA GTGGTCGAGA GATAATATAC 420
 CCCAATGCAT CCTGTCTGAT CCAGAACATC ATCCAGAATG ACACAGGATT CTACACCTTA 480

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CAGTTCATAA AGTCAGATCT TGTGAATGAA GAAGCAACTG GCCAGTTCGG GGTATACCCG 540
GAGCTGCCCA AGCCCTCCAT CTCCAGCAAC AACTCCAAAC CCGTGGAGGA CAAGGATGCT 600
GTGGCCTTCA CTGTGGAACC TGAGACTCAG GACGCAACCT ACCTGTGGTG GGTAAACAAT 660
CAGAGCCTCC CGGTCACTCC CAGGCTGCAG CTGTCCAATG GCAACAGGAC CCTCACTCTA 720
TTCAATGTCA CAAGAAATGA CACAGCAAGC TACAAATGTG AAACCCAGAA CCCAGTGAGT 780
GCCAGGCGCA GTGATTCACT CATCTGTAAT GTCCTCTATG GCCCGGATGC CCCACCATT 840
TCCCTCTCAA ACACATCTTA CAGATCAGGG GAAAATCTGA ACCTCTCTCTG CCACGCAGCC 900
TCTAACCCAC CTGCACAGTA CTCTTGGTTT GTCAATGGGA CTTTCCAGCA ATCCACCCAA 960
GAGCTCTTTA TCCCCAACAT CACTGTGAAT AATAGTGGAT CCTATACGTG CCAAGCCCAT 1020
AACTCAGACA CTGGCCTCAA TAGGACCACA GTCACGACGA TCACAGTCTA TGCAGAGCCA 1080
CCCAAACCTT TCATCACCAG CAACAACTCC AATCCCGTGG AGGATGAGGA TGCTGTAGCC 1140
TTAACCTGTG AACCTGAGAT TCAGAACACA ACCTACCTGT GGTGGGTAAA TAATCAGAGC 1200
CTCCCGGTCA GTCCAGGGCT GCAGCTGTCC AATGACAACA GGACCCCTAC TCTACTCAGT 1260
GTCAACAAGG ATGATGTAGG ACCCTATGAG TGTGGAATCC AGAACGAATT AAGTGTGAC 1320
CAGAGCGACC CAGTCACTCT GAATGTCTCT TATGGCCAGC ACGACCCAC CATTTCCCCC 1380
TCATACACCT ATTACGCTCC AGGGGTGAAC CTCAGCCTCT CTGCCCATGC AGCCTCTAAC 1440
CCACCTGCAC AGTATTCTTG GCTGATTGAT GGGAAACATCC AGCAACACAC ACAAGAGCTC 1500
TTTATCTCCA ACATCACTGA GAAGAACAGC GGACTCTATA CCTGCCAGGC CAATAACTCA 1560
GCCAGTGGCC ACAGCAGGAC TACAGTCAAG ACAATCACAG TCTCTGCGGA GCTGCCAAG 1620
CCCTCCATCT CCAGCAACAA CTCCAAACCC GTGGAGGACA AGGATGCTGT GGCCTTCACC 1680
TGTGAACCTG AGGCTCAGAA CACAACCTAC CTGTGGTGGG TAAATGGTCA GAGCCTCCCA 1740
GTCACTCCCA GGCTGCAGCT GTCCAATGGC AACAGGACCC TCACTCTATT CAATGTCACA 1800
AGAAATGAGC CAAGAGCCTA TGTATGTGGA ATCCAGAACT CAGTGAGTGC AAACCCGAGT 1860
GACCCAGTCA CCTGGATGT CTCTATGGG CCGGACACCC CCATCATTTT CCCCCAGAC 1920
TCGTCTTACC TTTCCGGAGC GAACCTCAAC CTCTCTGCC ACTCGGCTC TAACCATCC 1980
CCGAGTATT CTGTGGCTAT CAATGGGATA CCGCAGCAAC ACACACAAGT TCTCTTTATC 2040
GCCAAATCA CGCCAAATAA TAAACGGGACC TATGCCTGTT TTGTCTCTAA CTGGGTACT 2100
GGCCGCAATA ATTCCATAGT CAAGAGCATC ACAGTCTCTG CATCTGGAAC TTCTCTGGT 2160
TCTCAGCTG CGGCACCTGT CGGCATCATG ATTGGAGTGC TGGTGGGGT TGCTCTGATA 2220
TAGCAGCCCT GGTGTAGTTT CTTCAATTTA GGAAGACTGA CAGTGTGTTT GCTTCTTCT 2280
TAAAGCATT GCAACAGTCA CAGTCTAAAA TTGCTTCTTT ACCAAGGATA TTTACAGAAA 2340
AGACTCTGAC CAGAGATCGA GACCATCTTA GCCAACATCG TGAAACCCCA TCTCTACTAA 2400
AAATACAAAA ATGAGCTGGG CTGTGTGGCG CGCACCTGTA GTCCCACTTA CTGGGAGGC 2460
TGAGGCAGGA GAATCGCTTG AATCCGGGAG GTGGAGATTG CAGTGAGCCC AGATCGCACC 2520
ACTGCACTCC AGTCTGGCAA CAGAGCAAGA CTCCATCTCA AAAAGAAAAG AAAAGAGAGC 2580
TCTGACCTGT ACTCTGAAT ACAAGTTTCT GATACCACTG CACTGTCTGA GAATTTCCAA 2640
AACTTTAATG AACTAACTGA CAGCTTCATG AAAGTGTCCA CCAAGATCAA GCAGAGAAAA 2700
TAATTAATTT CATGGACTA AATGAACATA TGAGGATTGC TGATTTCTTA AATGTCTTGT 2760
TTCCAGATT TCAGGAAACT TTTTCTTT TAAGCTATCC ACTCTTACAG CAATTTGATA 2820
AAATATACTT TTGTGAACAA AAATTGAGAC ATTTACATTT TCTCCCTATG TGGTCGCTCC 2880
AGACTGGGA AACTATTCTA GAATATTAT ATGTATGGT AATATAGTTA TTGCACAAGT 2940
TCAATAAAAA TCTGCTCTTT GTATAACAGA AAAA

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Seq ID NO: 533 Protein sequence
Protein Accession #: NP_004354.1

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60

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1 11 21 31 41 51
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MESPSAPPHR WCIPWQRLLL TASLLTFWNP PTTAKLTIES TPFNVAEKGE VLLLVHNLPO 60
HLFGYSWYKG ERVDGNRQII GYVIGTQQAT PGPAYSGREI IYPNASLLIQ NIIQNDTGFY 120
TLHVIKSDLV NEEATGQFRV YPELPKPSIS SNNSKPVEDK DAVAFTEPE TQDATYLWVV 180
NNQSLPVSFR LQLSNGNRTL TLFNVTRNDT ASYKCETQNP VSARRSDSVI LNVLYGPDAP 240
TISPLNTSYR SGENLNLSCA AASNPPAQYS WFNVTGTFQS TQELFIPNIT VNNSGYSYTCQ 300
AHNSDTGLNR TTVTTITVYA EPPKPFITSN NSNPVEDEDA VALTCEPEIQ NTTYLWVWVN 360
QSLPVSFRLQ LSNDRNLTL LSVTRNDVGP YECGIQNELS VDHSDPVILN VLYGPDPTI 420
SPSYTYRPG VNLSSLSCAA SNPPAQYSWL IDGNIQHTQ ELFISNITEK NSGLYTCQAN 480
NSASGHSRRT VKTITVSABL KPSSISSNNS KPVEDKDAVA FTCEPEAQNT TYLWVWNGQS 540
LPVSPRLQLS NGNRTLTLFN VTRNDARAYV CGIQNSVSAN RSDPVTLDVL YGPDPTIISP 600
PDSSYLSGAN LNLSCASAN PSPQYSWRIN GIPQHTQVL FIAKITPNNN GTYACFVSNL 660
ATGRNNSIVK SITVSASGTS PGLSAGATVG IMIGVLVGVA LI

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Seq ID NO: 534 DNA sequence
Nucleic Acid Accession #: NM_006952.1
Coding sequence: 11..793

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70
75
80

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1 11 21 31 41 51
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AATCCCGACA ATGGCGAAAG ACAACTCAAC TGTTCTGTGC TTCCAGGGCC TGCTGATTTT 60
TGAAATGTG ATTATTGGTT GTTGGGCGAT TGCCCTGACT GCGGAGTGCA TCTTCTTTGT 120
ATCTGACCAA CACAGCCTCT ACCCACTGCT TGAAGCCACC GACAACGATG ACATCTATGG 180
GGCTGCCTGG ATCGCATAT TTGTGGGCAT CTGCCTCTTC TGCTGTCTG TTCTAGGCAT 240
TGTAGGCATC ATGAAGTCCA GCAGGAAAT TCTTCTGGCG TATTTCAATC TGATGTTTAT 300
AGTATATGCC TTTGAAGTGG CATCTTGAT CACAGCAGCA ACACAACGAG ACTTTTTCAC 360
ACCAACCTCT TTCTGGAAGC AGATGCTAGA GAGGTACCAA AACACAGCC CTCCAAACAA 420
TGATGACCAG TGGAAAAACA ATGGAGTCAC CAAACCTGG GACAGGCTCA TGCTCCAGGA 480
CAATTGCTGT GGCCTAAATG GTCCATCAGA CTGGCAAAAA TACACATCTG CCTTCCGGAC 540
TGAGAATAAT TTCTGGAAGC ATCCCTGGCC TCGTCAATGC TGTGTTATGA ACAATCTTAA 600
AGAACCTCTC AACCTGGAGG CTTGTAAACT AGGCGTGCCT GGTTTTATC ACAATCAGGG 660
CTGCTATGAA CTGATCTCTG GTCCAATGAA CCGACACGCC TGGGGGGTTG CTGGTTTGG 720
ATTTGCCATT CTCTGCTGGA CTTTGTGGGT TCTCTGGGT ACCATGTTCT ACTGGAGCAG 780
AATTGAATAT TAAGAA

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Seq ID NO: 535 Protein sequence
Protein Accession #: NP_008883.1

85

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1 11 21 31 41 51
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MAKDNSTVRC FQGLLIFGNV IIGCCGIALT AECIFFVSDQ HSLYPLLEAT DNDDIYGAHW 60
 IGIFVIGICLP CLSVLGIVGI MKSSRKILLA YFILMFIVYA FEVASCITAA TQRDFPTPNL 120
 FLKQMLERYQ NNSPNNDDQT WKNNGVTKTW DRLMLQDNCC GVNGPSDWQK YTSAFRTENN 180
 DADYPWPRQC CVMNNLKEPL NLEACKLGVP GFYHNQGCYE LISGPMNRHA WGVAWFGFAI 240
 LCWTFWVLLG TMFYWSRIEY

Seq ID NO: 536 DNA sequence
 Nucleic Acid Accession #: NM_002638.1
 Coding sequence: 120..473

1 11 21 31 41 51
 CAATACAGCT AAGGAATTAT CCCTTGTAAG TACCACAGAC CCGCCCTGGA GCCAGGCCAA 60
 GCTGGACTGC ATAAAGATTG GTATGGCCTT AGCTCTTAGC CAAACACCTT CCTGACACCA 120
 TGAGGGCCAG CAGCTTCTTG ATCGTGGTGG TGTTCCTCAT CGCTGGGACG CTGGTTCTAG 180
 AGGCAGCTGT CACGGGAGTT CCTGTTAAAG GTCAAGACAC TGTCAAAGGC CGTGTTCAT 240
 TCAATGGACA AGATCCCGTT AAAGGACAAG TTTCAAGTAA AGGTCAAGAT AAAGTCAAAG 300
 CGCAAGAGCC AGTCAAAGGT CCACTCTCCA CTAAGCCTGG CTCTGCCCCC ATTATCTTGA 360
 TCCGGTGGC CATGTTGAAT CCCCCTAACC GCTGCTTGA AGATACTGAC TGCCAGGAA 420
 TCAAGAAGTG CTGTGAAGGC TCTTGCGGGA TGGCCTGTTT CGTCCCCCAG TGAAGGGAGC 480
 CGGTCTCTGC TGCACCTGTG CCGTCCCCAG AGCTACAGGC CCCATCTGGT CCTAAGTCCC 540
 TGCTGCCTT CCCCCTCCA CACTGTCCAT TCTTCTCTCC ATTCAAGATG CCCACGGCTG 600
 GAGCTGCCTC TCTCATCCAC TTTCAATAA A

Seq ID NO: 537 Protein sequence
 Protein Accession #: NP_002629.1

1 11 21 31 41 51
 MRASSFLIVV VFLIAGTLVL EAAVTGVPVK GQDTVKGKRP FNGQDPVKGQ VSVKGQDKVK 60
 AQEPVKGPVS TKPGSCPIL IRCAMLNPPN RCLKDTDCPG IKKCEGSCG MACFPVQ

Seq ID NO: 538 DNA sequence
 Nucleic Acid Accession #: NM_001793.2
 Coding sequence: 71..2560

1 11 21 31 41 51
 AAAGGGGCAA GAGCTGAGCG GAACACCGGC CCGCCGTGCG GGCAGCTGCT TCACCCCTCT 60
 CTCTGCAGCC ATGGGGCTCC CTCGTGGACC TCTCGCGTCT CTCCTCTCTC TCCAGGTTTG 120
 CTGGCTGCAG TCGCGGGCCT CCGAGCCGTG CCGGGCGGTC TTCAGGGAGG CTGAAAGTGC 180
 CTTGGAGGCG GGAGGCGCGG AGCAGGAGCC CGGCCAGGCG CTGGGGAAAG TATTCTAGGG 240
 CTGCCCTGGG CAAGAGCCAG CTCTGTTTAG CACTGATAAT GATGACTTCA CTGTGCGGAA 300
 TGGCGAGACA GTCCGAAGAA GAAGGTCACT GAAGGAAAGG AATCCATTGA AGATCTTCCC 360
 ATCCAAACGT ATCTTACGAA GACACAAGAG AGATTGGGTG GTTGCTCCAA TATCTGTCCC 420
 TGAAATGGC AAGGGTCCCT TCCCCCAGAG ACTGAATCAG CTCAGTCTA ATAAAGATAG 480
 AGACACCAAG ATTTCTTACA GCATCACGGG GCCCGGGGCA GACAGCCCCC CTGAGGGTGT 540
 CTTGCTGTGA GAGAAGGAGA CAGGCTGGTT GTTGTGAAT AAGCCACTGG ACCGGGAGGA 600
 GATTGCCAAG TATGAGCTCT TTGGCCACGC TGTGTGAGAG AATGGTGCCT CAGTGGAGGA 660
 CCCCATGAAC ATCTCCATCA TCGTAGCCGA CCAGAATGAC CACAAGCCCA AGTTTACCCA 720
 GGACACCTTC CGAGGGAGTG TCTTAGAGGG AGTCTTACCA GGTACTTCTG TGATGCAGGT 780
 GACAGCCACG GATGAGGATG ATGCCATCTA CACCTACAAT GGGGTGGTTG CTTACTCCAT 840
 CCATAGCCAA GAACCAAGG ACCCAACAGA CCTCATGTTT ACCATTACCC GGAGCACAGG 900
 CACCATCAGC GTCATCTCCA GTGGCCTGGA CCGGGAAAAA GTCCTTGAGT ACACACTGAC 960
 CATCCAGGCC ACAGACATGG ATGGGGACGG CTCCACCACC ACGGCAGTGG CAGTAGTGGA 1020
 GATCCTTGAT GCCAATGACA ATGCTCCCAT GTTTGACCCC CAGAAGTACG AGGCCCATGT 1080
 GCCTGAGAAT GCAGTGGGCC ATGAGGTGCA GAGGCTGACG GTCATGATC TGGACGCCCC 1140
 CAACTCACCA GCGTGGCGTG CCACCTACCT TATCATGGGC GGTGACGACG GGGACCATTT 1200
 TACCATCACC ACCCTCCCTG AGAGCAACCA GGGCATCTCT ACAACCAAGG AGGGTTTGGG 1260
 TTTTGAGGCC AAAAACCAGC ACACCTGTGA CGTTGAAGTG ACCAACGAGG CCCCTTTTGT 1320
 GCTGAAGCTC CCAACCTCCA CAGCCACCAT AGTGGTCCAC GTGGAGGATG TGAATGAGGC 1380
 ACCGTGTGTT GTCCACCTCG CCAAAGTCGT TGAGGTCCAG GAGGGCATCC CCACTGGGGA 1440
 GCCTGTGTGT GTCTACACTG CAGAAGACCC TGACAAGGAG AATCAAAGA TCAGCTACCG 1500
 CATCCTGAGA GACCCAGCAG GGTGGCTAGC CATGGACCCA GACAGTGGGC AGGTACAGC 1560
 TGTGGGCACC CTCGACCGTG AGGATGAGCA GTTTGTGAGG AACACATCT ATGAAGTCAT 1620
 GGTCTTGGCC ATGGACAATG GAAGCCCTCC CACCACTGGC ACGGGAACCC TTCTGCTAAC 1680
 ACTGATTGAT GTCAATGACC ATGGCCCACT CCCTGAGCCC CGTCAGATCA CCATCTGCAA 1740
 CCAAAGCCCT GTGCGCCAGG TGCTGAACAT CACGGACAAG GACCTGTCTC CCCACACCTC 1800
 CCCTTTCCAG GCCCAGCTCA CAGATGACTC AGACATCTAC TGGACGGCAG AGGTCAACGA 1860
 GGAAGGTGAC ACAGTGGTCT TGTCCCTGAA GAAGTTCCTG AAGCAGGATA CATATGACGT 1920
 GCACCTTTCT CTGTCTGACC ATGGCAACAA AGAGCAGCTG ACGGTGATCA GGGCCACTGT 1980
 GTGCGACTGC CATGGCCATG TCGAAACCTG CCCTGGACCC TGAAGGGGAG GTTTCATCCT 2040
 CCGTGTGCTG GGGGCTGTCC TGGCTCTGCT GTTCTCTCTG CTGGTGTGTC TTTTGTGGT 2100
 GAGAAAGAAG CGGAAGATGA AGGAGCCCTC CTAAGTCCCA GAAGATGACA CCGGTGACAA 2160
 CGTCTTCTAC TATGGCGAAG AGGGGGGTGG CGAAGAGGAC CAGGACTATG ACATCACCCA 2220
 GCTCCACCGA GGTCTGGAGG CCAGGCCGGA GGTGGTCTCT CGCAATGACG TGGCACCAAC 2280
 CATCATCCCG ACACCCATGT ACCGTCTCTG GCCAGCCAAC CCAGATGAAA TCGGCAACTT 2340
 TATAATTGAG AACCTGAAGG CGGCTAACAC AGACCCCA GCGCGCCCTC ACACACCCCT 2400
 CTTGGTGTTC GACTATGAGG GCAGCGGCTC CGACGCCGCG TCCCTGAGCT CCCTCACCTC 2460
 CTCGCCCTCC GACCAAGACC AAGATTACGA TTATCTGAAC GAGTGGGGCA GCGCCTTCAA 2520
 GAAGCTGGCA GACATGTACG GTGGCGGGGA GGACGACTAG CCGGCCTGCC TGCAGGGCTG 2580
 GGGACCAAAC GTGAGGCTAC AGAGCATCTC CAAGGGGTCT CAGTTCCTCC TTAGCTGAG 2640
 GACTTCGGAG CTTGTGAGG AGTGCCCGTA GCAACTTGGC GGAGACAGGC TATGAGTCTG 2700
 ACCTTAGAGT GGTGCTTCTC TTAGCCTTTC AGGATGGAGG AATGTGGGCA GTTTGACTTC 2760
 AGCACTGAAA ACCTCTCCAC CTGGGCCAGG GTTGCCCTCAG AGGCCAAGTT TCCAGAAGCC 2820
 TCTTACCTCG CTAATAATGC TCAACCCCTG GTCTGGGGCC TGGGCTGTCT GTGACTGACC 2880
 TACAGTGGAC TTTCTCTCTG GAATGGAACC TTCTTAGGCC TCCTGGTGCA ACTTAATTTT 2940

TTTTTTTAAAT GCTATCTTCA AAACGTTAGA GAAAGTCTCT CAAAAGTGCA GCCCAGAGCT 3000
 GCTGGGCCCA CTGGCCGTCC TGCATTTCTG GTTCCAGAC CCCAATGCCT CCCATTCGGA 3060
 TGGATCTCTG CGTTTTTATA CTGAGTGTGC CTAGGTGGCC CCTTATTTTT TATTTTCCCT 3120
 GTTGCCTTGC TATAGATGAA GGGTGAGGAC AATCGTGTAT ATGTACTAGA ACTTTTTTAT 3180
 TAAAGAAACT TTCCAGAA AAAAA

Seq ID NO: 539 Protein sequence
 Protein Accession #: NP_001784.2

1 11 21 31 41 51
 MGLPRGPLAS LLLLQVCWLQ CAASEPCRAV FREAEVTLEA GGAEQEPGQA LGKVPMGCPG 60
 QEPALFSTDN DDFTVRNGET VQERRSLKER NPLKIFPSKR ILRRHKRDWV VAPISVPENG 120
 KGFFPQRLNQ LKSNKDRDTK IPYSITGPGA DSPPEGVFAV EKETGWLILLN KPLDREBIAR 180
 YELFGHVAUSE NGASVEDPMN ISIIIVTDQND HKPKFTQDTF RGSVLEGVLP GTSVMQVTAT 240
 DEDDAIYTYN GVVAYSISHSQ BPKDPHDLMP TIHRSTGTIS VISSGLDREK VPEYTLTIQA 300
 TDMDGSGSTT TAVAVVEILD ANDNAPMFDQ QKYEAHVPEN AVGHEVQRLT VTDLDAPNSP 360
 AWRATYILING GDDGDHFTIT THPESNQGIL TTRKGLDFEA KNQHTLYVEV TNEAPFVLKL 420
 PTSTATIVVH VEDVNEAPVF VPPSKVVEVQ EGIPTGEPVC VYTAEDPDKE NQKISYRILR 480
 DPAGWLAMPD DSGQVAVGT LDREDEQFVR NNIYEVMLA MDNGSPPTTG TGTLLTLID 540
 VNDHGPVPEP RQITICNQSP VRQVLNITDK DLSPTSPFQ AQLTDDSDIY WTAEVNEEGD 600
 TVVLSLKKFL KQDTYDVHLS LSDHGNKEQL TVIRATVCDL HGHVETCPGP WKGGFILPVL 660
 GAVLALLFL LVLALLVRCK RKIKEPLLLP EDDTRDNVYF YGEEGGGEED QDYDITQLHR 720
 GLEARPEVVL RNDVAPTII PFMYRPRPAN PDEIGNFIIE NLKAANTDPT APPYDTLLVF 780
 DYEAGSGDAA SLSSLTSSAS DQDQDYDYLN EWGSRFKKLA DMYGGGEDD

Seq ID NO: 540 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..672

1 11 21 31 41 51
 ATGAGGCTCC AAAGACCCCG ACAGGCCCGG GCGGGTGGGA GCGCGCGGCC CCGGGGCGGG 60
 CGGGGCTCCC CTACCCGGCC AGACCCGGGG AGAGGCGCGC GGAGGCTGCG AAGGTTCCAG 120
 AAGGGCGGGG AGGGGCGCGC GCGCGCTGAC CCTCCCTGGG CACCGCTGGG GACGATGGCG 180
 CTGCTGCGCT TGCTGCTGGT CGTGGCCCTA CCGCGGGTGT GGACAGACGC CAACCTGACT 240
 GCGAGACAAC GAGATCCAGA GGACTCCAG CGAACGGACG AGGGTGACAA TAGAGTGTGG 300
 TGTGATGTTT GTGAGAGAGA AAACACTTTC GAGTGCCAGA ACCCAAGGAG GTGCAATGG 360
 ACAGAGCCAT ACTGCGTTAT AGCGGCCGTG AAAATATTTC CACGTTTTTT CATGGTTGCG 420
 AAGCAGTGCT CGCTGGTTTG TGCAGCGATG GAGAGACCCA AGCCAGAGGA GAAGCGGTTT 480
 CTCTGGAAG AGCCCATGCC CTTCTTTTAC CTCAGTGTG GTAAAAATCG CTAAGTCAAT 540
 TTAGAGGGGC CACCTATCAA CTCATCAGTG TTCAAAGAAT ATGCTGGGAG CATGGGTGAG 600
 AGCTGTGGTG GGTGTGGCT GGCCATCCTC CTGCTGCTGG CCTCCATTGC AGCCGCGCTC 660
 AGCCTGTCTT GA

Seq ID NO: 541 Protein sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 MRLQRPQAP AGRRRAPRGG RGSYPYRDPG RGARRLRRFQ KGEGEAPRAD PPWAPLGTMA 60
 LLALLLVVAL PRVWTDANLT ARQRDPEDSQ RTDEGDNRVW CHVCERENTF EQCNPRRCKW 120
 TEPYCVIAAV KIFPRFFMVA KQCSAGCAAM ERPKPEEKRF LLEPMPPFFY LKCKKIRYCN 180
 LBGPPINSSV FKEYAGSMGE SCGLWLAIL LLLASIAAGL SLS

Seq ID NO: 542 DNA sequence
 Nucleic Acid Accession #: XM_035292.2
 Coding sequence: 53..1576

1 11 21 31 41 51
 GCTCGTGGG CCGCGGCTCC CGGGTGTCCC AGGCCCGGCC GGTGCGCAGA GCATGGCGGG 60
 TGCGGGCCCG AAGCGGCGCG CGCTAGCGGC GCCGGCGGCC GAGGAGAAGG AAGAGGCGCG 120
 GGAGAAGATG CTGGCCGCCA AGAGCGCGGA CGGCTCGGCG CCGGCAGGCG AGGGCGAGGG 180
 CGTGACCCTG CAGCGGAACA TCACGCTGCT CAACGGCGTG GCCATCATCG TGGGGACCAT 240
 TATCGGCTCG GGCATCTTCG TGACGCCCAC GGGCGTGTCT AAGGAGGCAG GCTCGCCGGG 300
 GTGGGCGCTG GTGGTGTGGG CGCGTGGCG CGTCTTCTCC ATCGTGGGCG CGCTCTGCTA 360
 CGCGGAGCTC GGCACCAACA TCTCAAATC GGGCGGCGAC TACGCTACA TGCTGGAGGT 420
 CTACGGCTCG CTGCCCGCCT TCCTCAAGCT CTGGATCGAG CTGCTCATCA TCCGGCCTTC 480
 ATCGCAGTAC ATCGTGGCCC TGGTCTTTCG CACCTACCTG CTCAGCCCGC TCTTCCCCAC 540
 TGCCCGGGTG CCCGAGGAGG CAGCCAAAGCT CGTGGCCTGC CTCTGCGTGC TGCTGCTCAC 600
 GGCCGTGAAC TGCTACAGCG TGAAGGCCGC CACCCGGGTC CAGGATGCCT TTGCCCGCGC 660
 CAGCTCCTG GCCCTGGCCC TGATCATCCT GCTGGGCTTC GTCCAGATCG GAAAGGGTGA 720
 TGTGTCCAAT TAGATCCCA ACTTCTCAT TGAAGGCACC AAACCTGGATG TGGGGAACAT 780
 TGTGCTGGCA TTATACAGCG GCCTCTTTCG CTATGGAGGA TGAATTACT TGAATTTCGT 840
 CACAGAGGAA ATGATCAACC CCTACAGAAA CCTGCCCTCG GCCATCATCA TCTCCCTGCC 900
 CATCTGACG CTGGTGTACG TCTGTACCAA CCTGGCCTAC TTCAACACCC TGTCCACCGA 960
 GCAGATGCTG TCGTCCGAGG CCGTGGCCGT GGACTTCGGG AACTATCACC TGGGCGTCAT 1020
 GTCTTGATC ATCCCGCTCT TCGTGGGCTT GTCTGCTTTC GGCTCCGTCA ATGGGTCCCT 1080
 GTTCACATCC TCGAGGCTCT TCTTCTGGG GTCCCGGAA GGCCACCTGC CCTCCATCCT 1140
 CTCCATGATC CACCCACAGC TCCTCACCCC CGTGCCGTCC CTGCTGTTC CTGTGTGAT 1200
 GACGCTGCTC TACGCTTCT CCAAGGACAT CTTCTCCGTC ATCAACTTCT TCAGCTTCTT 1260
 CAACTGGCTC TGGTGGGCC TGGCCATCAT CGGCATGATC TGGCTGCGCC ACAGAAAGCC 1320
 TGAGCTTGAG CGGCCATCA AGGTGAACCT GGCCTGCGCT GTGTCTTCA TCCTGGCCTG 1380
 CCTCTTCTG ATCGCGCTCT CTTCTGGAA GACACCCGTG GAGTGTGGCA TCGGCTTCTC 1440
 CATCATCCTC AGCGGGCTGC CGTCTACTT CTTGCGGGTC TGGTGGAAAA ACAAGCCCAA 1500
 GTGGCTCCTC CAGGGCATCT TCTCCACGAC CGTCTGTGT CAGAAGCTCA TGCAGGTGGT 1560

CCCCCAGGAG ACATAGCCAG GAGGCCGAGT GGCTGCCGGA GGAGCATGC

Seq ID NO: 543 Protein sequence
Protein Accession #: XP_035292.2

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1      11      21      31      41      51
|      |      |      |      |      |
MAGAGPKRRA LAAPAAEKE EAREKMLAAK SADGSAPAGE GEGVTLQRNI TLLNGVAIIV 60
GTIIGSGIFV TPTGVLKEAG SPGLALVWVA ACGVFSIVGA LCYAEILGTTI SKSGGDYAYM 120
LEVVGSLPAP LKWIIELLII RPSSQYIVAL VFATYLLKPL FPTCFVPEEA AKLVACLCLVL 180
LLTAVNCYSV KAATRVQDAF AAKLLALAL IILLGFVQIG XGDVSNLDPN FSPEGTKLDV 240
GNIVLALYSY LFAYGWNWYL NFVTEEMINP YRNLPALIII SLPIVTLVYV LTNLAYFTTL 300
STEQMLSSAA VAVDFGNVHL GVMWIIIPVF VGLSCFGSVN GSLFTSSRLF FVGSREGHLP 360
SILSMIHPQL LTPVPSLVFT CVMTLLYAFS KDIFSVINPF SFFNWLCVAL AIIGMIWLRH 420
RKPELERPIK VNLALPVFFI LACLFLIAVS FWKTPVECGI GFTIILSLP VYFFGVWVKN 480
KPKWLLQGIF STTVLCQKLM QVVPQET

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Seq ID NO: 544 DNA sequence
Nucleic Acid Accession #: NM_005268.1
Coding sequence: 168..989

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1      11      21      31      41      51
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TAAAAAGCAA AAGAATTCGC GGCCGCGTCG ACACGGGCTT CCCCGAAAAC CTTCCTCGCT 60
TCTGGATATG AAATTCACAG TGCTTGCTGA GTCCTATTGC CGGCTGCTGG GAGCCAGGAG 120
AGCCCTGAGG AGTAGTCACT CAGTAGCAGC TGACGCGTGG GTCCACCATG AACTGGAGTA 180
TCTTTGAGGG ACTCCTGAGT GGGGTCAACA AGTACTCCAC AGCCTTTGGG CGCATCTGGC 240
TGTCCTGGT CTTCATCTTC CGCGTCTGG TGTACCTGGT GACGGCCGAG CGTGTGTGGA 300
GTGATGACCA CAAGGACCTC GACTGCAATA CTCGCCAGCC CGGCTGCTCC AACGTCTGCT 360
TTGATGAGTT CTTCCTCTGT TCCCATGTGC GCCTCTGGGC CCTGCAGCTT ATCCTGGTGA 420
CATGCCCTCT ACTGCTCGTG GTCATGCACG TGGCCTACCG GGAGGTTTCA GAGAAGAGGC 480
ACCGAGAAGC CCATGGGGAG AACAGTGGGC GCCTCTACCT GAACCCCGGC AAGAAGCGGG 540
GTGGGCTCTG GTGGACATAT GTCTGCAGCC TAGTGTCAA GGCAGCGGTG GACATCGCCT 600
TTCTCTATGT GTTCCACTCA TTCTACCCCA AATATATCCT CCTCCTGTG GTCAAGTGCC 660
ACGCAGATCC ATGTCCCAAT ATAGTGGACT GCTTCACTTC CAAGCCCTCA GAGAAGAACA 720
TTTTCACCTT CTTCATGGTG GCCACAGCTG CCATCTGCAT CCTGCTCAAC CTGTTGGAGC 780
TCATCTACCT GGTGAGCAAG AGATGCCACG AGTGCTGGC AGCAAGGAAA GCTCAAGCCA 840
TGTGCACAGG TCATCACCTC CACGGTACCA CCTCTTCTG CAAACAAGAC GACCTCCTTT 900
CGGGTGACCT CATCTTCTGT GGCTCAGACA GTCATCTCTC TCTCTTACCA GACCGCCCCC 960
GAGACCATGT GAAGAAAACC ATCTTGTTGAG GGGCTGCCTG GACTGGTCTG GCAGGTTGGG 1020
CCTGGATGGG CAGGCTCTAG CATCTCTCAT AGGTGCAACC TGAGAGTGGG GGAGCTAAGC 1080
CATGAGGTAG GGGCAGGCAA GAGAGAGGAT TCAGACGCTC TGGGAGCCAG TTCTAGTCC 1140
TCAACTCCAG CCACCTGCCC CAGCTCGACG GCACTGGGCC AGTTCCCCCT CTGCTCTGCA 1200
GCTCGGTTTC CTTTCTTAGA ATGGAATAG TGAGGGCCAA TGC

```

Seq ID NO: 545 Protein sequence
Protein Accession #: NP_005259.1

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1      11      21      31      41      51
|      |      |      |      |      |
MNWSIFEGLL SGVKNYSTAF GRIWLSLVFI FRVLVYLVT A ERVWSDHDKD FDCNTRQPGC 60
SNVCFDEFFP VSHVRLWALQ LILVTCPSLL VVMHVAYREV QEKRHREAHG ENSGRLYLNP 120
GKKRGGGLWWT YVCSLVFKAS VDIAFLYVPH SFYPKYILPP VVKCHADPCP NIVDCFISKP 180
SEKNIFTLFM VATAATCILL NLVELIYLV KRCHECLAAR KQAMCTGHH PHGTTSSCKQ 240
DDLSSGLDIF LGSDSHPLL PDRPRDHVK TIL

```

Seq ID NO: 546 DNA sequence
Nucleic Acid Accession #: NM_002391.1
Coding sequence: 26..457

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1      11      21      31      41      51
|      |      |      |      |      |
CGGGCGAAGC AGCGCGGGCA GCGAGATGCA GCACCGAGGC TTCCTCTCTC TCACCTCTCT 60
CGCCCTGCTG GCGCTCACCT CCGCGGTCCG CAAAAGAGAA GATAAGGTGA AGAAGGGCGG 120
CCCGGGGAGC GAGTGCCTG AGTGGCCCTG GGGGCCCTGC ACCCCAGCA GCAAGGATTG 180
CGGCGTGGGT TTCCGCGAGG GCACCTGCGG GGCCAGACC CAGCGCATCC GGTGCAGGGT 240
GCCCTGCAAC TGAAGAAGG AGTTTGAGC GCACTGCAAG TACAAGTTG AGAACTGGGG 300
TGCGTGTGAT GGGGGCACG GCACCAAGT CCGCCAAGGC ACCCTGAAGA AGGCGCGCTA 360
CAATGCTCAG TGCCAGGAGA CCATCCGCGT CACCAAGCCC TGCAACCCCA AGACCAAGC 420
AAAGGCCAAA GCCAAGAAAG GGAAGGGAAA GGAAGTACG CCAAGCCTGG ATGCCAAGGA 480
GCCCTGGTG TCACATGGGG CCTGGCCACG CCTCCCTCT CCCAGGCCG AGATGTGACC 540
CACCAGTGCC TTCTGTCTGC TCGTTAGCTT TAATCAATCA TGCCCTGCCT TGTCCCTCTC 600
ACTCCCCAGC CCCACCCCTA AGTGCCCAA GTGGGGAGG ACAAGGGATT CTGGGAAGCT 660
TGAGCCTCCC CCAAAGCAAT GTGAGTCCCA GAGCCCGCTT TTGTTCTTCC CCAATTTCC 720
ATTACTAAGA AACACATCAA ATAAACTGAC TTTTCCCCC CAATAAAGC TCTTCTTTT 780
TAATAT

```

Seq ID NO: 547 Protein sequence
Protein Accession #: NP_002382.1

```

1      11      21      31      41      51
|      |      |      |      |      |
MQHRGFLLLT LLALLALTS VAKKDKVKK GPGSECAEW AWGPCTPSSK DCGVGFREGT 60
CGAQTQIRIC RVPCNWKKEF GADCKYKFEN WGACDGGTGT KVRQGTLLKA RYNAQCQETI 120
RVTKPCTPKT KAKAKAKGK GKD

```

Seq ID NO: 548 DNA sequence

Nucleic Acid Accession #: NM_006783.1

Coding sequence: 1..786

```

5 1 11 21 31 41 51
| | | | | |
ATGGATTGGG GGACGCTGCA CACTTTCATC GGGGGTGTCA ACAAACACTC CACCAGCATC 60
GGGAAGGTGT GGATCACAGT CATCTTTATT TCCGAGTCA TGATCCTAGT GGTGGCTGCC 120
CAGGAAGTGT GGGGTGACGA GCAAGAGGAC TTCGTCTGCA ACACACTGCA ACCGGGATGC 180
AAAAATGTGT GCTATGACCA CTTTTCCCG GTGTCCCACA TCCGGCTGTG GGCCTCCAG 240
10 CTGATCTTGG TCTCCACCCC AGCGCTGCTG GTGGCCATGC ATGTGGCCTA CTACAGGCAC 300
GAAACCACTC GCAAGTTCAG GCGAGGAGAG AAGAGGAATG ATTTCAAAGA CATAGAGGAC 360
ATTAAAAAGC ACAAGGTTCC GATAGAGGGG TCGCTGTGGT GGACGTACAC CAGCAGCATC 420
TTTTTCCGAA TCATCTTTGA AGCAGCCTTT ATGTATGTGT TTTACTTCCT TTACAATGGG 480
15 TACCACCTGC CCTGGGTGTT GAAATGTGGG ATTGACCCCT GCCCAACCT TGTGACTGTC 540
TTTATTCTTA GGCCAACAGA GAAGACCGTG TTTACCATTT TTATGATTTC TCGCTCTGTG 600
ATTTGCATGC TGTCTAACGT GGCAGAGTTG TGCTACCTGC TGCTGAAAGT GTGTTTATAG 660
AGATCAAAGA GAGCACAGAC GCAAAAAAAT CACCCCAATC ATGCCCTAAA GGAGAGTAAG 720
CAGAATGAAA TGAATGAGCT GATTTTCAGAT AGTGGTCAAA ATGCAATCAC AGGTTTCCCA 780
AGCTAA

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Seq ID NO: 549 Protein sequence
Protein Accession #: NP_006774.1

```

25 1 11 21 31 41 51
| | | | | |
MDWGTLTHTFI GGVNKHSTSI GKVWITVIFI FRVMILVVAA QEVWGDEQED FVCNTLQPGC 60
KNVCYDHFPP VSHIRLWALQ LIFVSTPALL VAMHVAYYRH ETTRKFRRGE KRNDFKDIED 120
IKKKHVRIEG SLWWTYTSI FPRIFEAAP MYVVFYLYNG YHLPWVLKCG IDPCPNLVDK 180
FISRPTKTV FTTFMISASV ICMLLNVAEL CYLLKVCFR RSKRAQTQKN HPNHALKESK 240
30 QNEMNELISD SGQNAITGFP S

```

Seq ID NO: 550 DNA sequence
Nucleic Acid Accession #: NM_002571.1
Coding sequence: 99..587

```

35 1 11 21 31 41 51
| | | | | |
CATCCCTCTG GCTCCAGAGC TCAGAGCCAC CCACAGCCGC AGCCATGCTG TGCTCCTGTC 60
TCACCTGGGG CTGGGCCCTG GTCTGTGGTG TCCCGGCCAT GGACATCCCC CAGACCAAGC 120
40 AGGACCTGGA GCTCCCAAGG TTGGCAGGGA CCTGGCACTC CATGGCCATG GCGACCAACA 180
ACATCTCCCT CATGGCGACA CTGAAGGCCCT CTCTGAGGGT CCACATCACC TCACTGTGTC 240
CCACCCCGGA GGACAACCTG GAGATCGTTC TGCACAGATG GGAGAACAAC AGCTGTGTTG 300
AGAAGAAGGT CCTTGGAGAG AAGACTGGGA ATCCAAAGAA GTTCAAGATC AACTATACGG 360
TGCGAAACGA GGCCACGCTG CTCGATACTG ACTACGACAA TTTCTGTGTT CTCTGCCTAC 420
45 AGGACACCAC CACCCCATC CAGAGCATGA TGTGCCAGTA CCTGGCCAGA GTCCTGGTGG 480
AGGACGATGA GATCATGCAG GGATTTCATCA GGGCTTTCAG GCCCCTGCCC AGGCACCCTAT 540
GGTACTTGCT GGACTTGAAG CAGATGGAAG AGCCGTGCCG TTTCTAGCTC ACCTCCGCCT 600
CCAGGAAGAC CAGACTCCCA CCCTCCACA CCTCCAGAGC AGTGGGACTT CCTCCTGCCC 660
50 TTTCAAAGAA TAACCACAGC TCAGAAGAGC ATGACGTGGT CATCTGTGTC GCCATCCCCT 720
TCTGTCTGCA CACCTGCACC ATTGCCATGG GGAGGCTGCT CCCTGGGGGC AGAGTCTCTG 780
GCAGAGGTTA TTAATAAACC CTTGGAGCAT G

```

Seq ID NO: 551 Protein sequence
Protein Accession #: NP_002562.1

```

55 1 11 21 31 41 51
| | | | | |
MDIPQTKQDL ELPKLAGTWH SMAMATNNIS LMATLKAPLR VHITSLLPPT EDNLEIVLHR 60
WENNSCVEKK VLGEKGTGNPK KFKINYTVAN BATLLDTDYD NFLFLCLQDT TPIQSMMCQ 120
60 YLARVLVEDD EIMQGFIRAF RPLPRHLWYL LDLKQMEEPF RF

```

Seq ID NO: 552 DNA sequence
Nucleic Acid Accession #: NM_006500.1
Coding sequence: 27..1967

```

65 1 11 21 31 41 51
| | | | | |
ACTTGCCTCT CGCCCTCCGG CCAAGCATGG GGCTTCCCAG GCTGGTCTGC GCCTTCTTGC 60
TCGCGCGCTG CTGCTGCTGT CCTCGGCTCG CGGGTGTGCC CGGAGAGGCT GAGCAGCCTG 120
70 CGCCTGAGCT GGTGGAGGTG GAAGTGGGCA GCACAGCCCT TCTGAAGTGC GGCCTCTCCC 180
AGTCCCAAGG CAACCTCAGC CATGTCGACT GGTTTTCTGT CCACAAGGAG AAGCGGACGC 240
TCATCTTCCG TGTGCGCCAG GCCCAGGGCC AGAGCGAACC TGGGGAGTAC GAGCAGCGGC 300
TCAGCCTCCA GGACAGAGGG GCTACTCTGG CCTGACTCA AGTCACCCCC CAAGACGAGC 360
GCATCTTCTT GTGCCGGGC AAGCGCCCTC GGTCCCAGGA GTACCGCATC CAGCTCCGCG 420
75 TCTACAAAGC TCCGAGGAG CCAACATCC AGGTCAACCC CCTGGGCATC CCTGTGAACA 480
GTAAGGAGCC TGAGGAGGTC GCTACCTGTG TAGGGAGGAA CGGGTACCCC ATTCTCTAAG 540
TCATCTGGTA CAAGAATGGC CGGCCTCTGA AGGAGGAGAA GAACCGGGTC CACATTAGT 600
CGTCCACAGC TGTGGAGTCG AGTGGTTTGT ACACCTTGCA GAGTATTCTG AAGGCACAGC 660
78 TGGTTAAAGA AGACAAAGAT GCCCAGTTT ACTGTGAGCT CAACTACCGG CTGCCAGTGC 720
80 GGAACCATAT GAAGAGTCC AGGGAAGTCA CGTCCCTGT TTTCTACCCG ACAGAAAAAG 780
TGTGGCTGGA AGTGGAGCCC GTGGGAATGC TGAAGGAAGG GGACCGCGTG GAAATCAGGT 840
GTTTGGCTGA TGGCAACCTC CCACCACACT TCAGCATCAG CAAGCAGAAC CCCAGCACCA 900
GGGAGGCAGA GGAAGAGTCA ACCAACGACA ACGGGGTCTT GGTGCTGGAG CCTGCCGGA 960
85 AGGAACACAG TGGCGCTAT GAATGTCAGG CCTGGAACCT GGACACCATG ATATCGCTGC 1020
TGAGTGAACC ACAGGAACCT TGGTGAACT ATGTGTCTGA CGTCCGAGTG AGTCCCGCAG 1080
CCCTGAGAG ACAGGAAGGC AGCAGCCTCA CCTGACCTCA TGAGGCAGAG AGTAGCCAGG 1140
ACCTCGAGTT CAGTGGCTG AGAGAAGAGA CAGACCAGGT GCTGGAAAGG GGCCTGTGTC 1200

```

	TTCAAGTTGCA	TGACCTGAAA	CGGGAGGCAG	GAGGCGGCTA	TCGCTGCGTG	GCGTCTGTGC	1260
	CCAGCATACC	CGGCCTGAAC	CGCACACAGC	TGGTCAAGCT	GGCCATTITT	GGCCCCCTT	1320
	GGATGGCATT	CAAGGAGAGG	AAGGTGTGGG	TGAAAGAGAA	TATGGTGTG	AATCTGTCTT	1380
5	GTGAAGCGTC	AGGGCACCCC	CGGCCACCA	TCTCTGGAA	CGTCAACGGC	ACGGCAAGTG	1440
	AACAAGACCA	AGATCCACAG	CGAGTCCTGA	GCACCCTGAA	TGTCTCGTG	ACCCCGGAGC	1500
	TGTTTGAGAC	AGGTGTGTA	TGCAAGGCT	CCAACGACCT	GGGCAAAAC	ACCAGCATCC	1560
	TCTTCTGGA	GCTGTCAAT	TTAACACCC	TCACACCAGA	CTCCAACACA	ACCACTGGCC	1620
	TCAGCACTTC	CACTGCCAGT	CCTCATACCA	GAGCCAACAG	CACCTCCACA	GAGAGAAAGC	1680
10	TGCGGAGCC	GGAGAGCCGG	GGCGTGGTCA	TCGTGGCTGT	GATTGTGTGC	ATCCTGGTCC	1740
	TGGCGGTGCT	GGGCGCTGTC	CTCTATTTCC	TCTATAAGAA	GGGCAAGCTG	CCGTGCAGGC	1800
	GCTCAGGGAA	GCAGGAGATC	ACGCTGCCCC	CGTCTCGTAA	GACCGAAGCT	GATGTTGAAG	1860
	TTAAGTCAGA	TAAGCTCCCA	GAAGAGATGG	GCCTCCTGCA	GGGCGAGCAG	GGTGACAAGA	1920
	GGGCTCCGGG	AGACCAGGGA	GAGAAATACA	TCGATCTGAG	GCATTAGCCC	CGAATCACTT	1980
15	CAGCTCCCTT	CCCTGCCTGG	ACCATTCCCA	GCTCCCTGCT	CACCTCTCTC	TCAGCCAAAG	2040
	CTCTCAAAAG	GACTAGAGAG	AAGCCTCTCT	CTCCCTCAC	CTGCACACCC	CCTTTCAGAG	2100
	GGCCACTGGG	TAGGACCTTG	AGGACCTCAC	TTGGCCCTCG	AAGCCGCTTT	TCAGGGACCA	2160
	GTCCACCACC	ATCTCCTCCA	CGTTGAGTGA	AGCTCATCCC	AAGCAAGGAG	CCCCAGTCTC	2220
	CCGAGCGGGT	AGGAGAGTTT	CTTGACAGAAC	GTGTTTTTTC	TTTACACACA	TTATGGCTGT	2280
20	AAATACCTGG	CTCTGCTGG	CAGCTGAGCT	GGGTAGCCTC	TCTGAGCTGG	TTTCTGCCCC	2340
	CAAAAGGCTGG	CTTCCACCAT	CCAGGTGCAC	CACTGAAGTG	AGGACACACC	GGAGCCAGGC	2400
	GCCTGCTCAT	GTGTAAGTGC	GCTGTTCACA	CCCGCTCCGG	AGAGCACCCC	AGCGGCATCC	2460
	AGAAGCAGCT	GCAGTGTGTC	TGCCACCAAC	CTCCTGCTCG	CCTCTTCAAA	GTCTCCTGTG	2520
	ACATTTTTTC	TTTGGTCAGA	AGCCAGGAAC	TGGTGTCAAT	CCTTAAAGA	TACGTGCCGG	2580
25	GGCCAGGTGT	GGTGGCTCAC	GCCTGTAATC	CCAGCACTTT	GGGAGGCCGA	GGCGGGCGGA	2640
	TCACAAAGCT	AGGACGAGAC	CATCTGGCT	AACACGGTGA	AACCTGTCT	CTACTAAAAA	2700
	TACAAAAAAA	AATTAGCTAG	GCGTAGTGGT	TGGCACCTAT	AGTCCCAGCT	ACTCGGAAGG	2760
	CTGAAGCAGG	AGAATGGTAT	GAATCCAGGA	GGTGGAGCTT	GCAGTGAGCC	GAGACCGTGC	2820
	CACCTGCCTC	CAGCCTGGGC	AACACAGCGA	GACTCCGTCT	CGAGGAAAAA	AAAAGAAAAA	2880
30	ACGCGTACCT	GCGGTGAGGA	AGCTGGGCGC	TGTTTTCGAG	TTCAAGTGAA	TTAGCCTCAA	2940
	TCCCGTGTGT	CACTTGCTCC	CATAGCCCTC	TTGATGGATG	ACGTAAAACT	GAAAGGCAGC	3000
	GGGGAGCAGA	CAAGATGAG	GTCTACACTG	TCCTTCATGG	GGATTAAAGC	TATGTTTATA	3060
	TTAGACACCA	ACTTCTACAA	ACCAAGCTCA	GGGCCCCAAC	CCTAGAAGGG	CCCAAATGAG	3120
	AGAATGGTAT	TTAGGATGAG	AAAACGGGGC	CTGGCTAGAG	CTTCGGGTGT	GTGTGTCTGT	3180
35	CTGTGTGTAT	GCATACATAT	GTGTGTATAT	ATGGTTTTGT	CAGGTGTGTA	AATTGCAAA	3240
	TTGTTTCCTT	TATATATGTA	TGTATATATA	TATATGAAAA	TATATATATA	TATGAAAAAT	3300
	AAAGCTTAAT	TGTCAGGAA	AATCATACAT	TGCTTTTTTA	TTCTACATGG	GTACCACAGG	3360
	AACCTGGGGG	CCTGTGAAAC	TACAACCAAA	AGGCACACAA	AACCGTTTCC	AGTTGGCAGC	3420
	AGAGATCAGG	GGTTACCTCT	GCTTCTGAGC	AAATGGCTCA	AGCTCTACCA	GAGCAGACAG	3480
40	CTACCTTACT	TTTCAGCAGC	AAAACGTCCC	GTATGACGCA	GCACGAAGGG	CCTGGCAGGC	3540
	TGTTAGCAGG	AGCTATGTCC	CTTCTATCG	TTTCCGTCCA	CTT		

Seq ID NO: 553 Protein sequence
Protein Accession #: NP_006491.1

45	1	11	21	31	41	51	
	GLPRLVCAFL	LAACCCCPRV	AGVPGEAEQP	APELVEVEVG	STALLKCGLS	QSQGNLSHVD	60
	WFSVHKERT	LIFRVQGGG	QSEPEYEQR	LSLQDRGATL	ALTQVTPQDE	RIFLCQGRKP	120
	RSQERYQLR	VYKAPEEPNI	QVNPLGIPVN	SKEPEEATC	VGRNGYPIQ	VIWYKNGRPL	180
50	KEENRNVHIQ	SSQTVESSGL	YTLQSLKAQ	LVKEDKDAQF	YCELNYRLPS	GNHMKESREV	240
	TVPVFYFTEK	VWLEVEPVGM	LKEGDRVEIR	CLADGNPPPH	FSISKQNPST	REABEETND	300
	NGVLVLEPAR	KEHSGRYECQ	AWNLDTMISL	LSEPQELLVN	YVSDVRVSPA	APERQEGSSL	360
	TLTCEAESSQ	DLEFQWLREE	TDQVLERGPV	LQLHDLKREA	GGGYRCVASV	PSIPGLNRTQ	420
	LVKLAIFGPP	WMAFKERKVV	VKENMVLNLS	CEASGHPRPT	ISWNVNGTAS	EQDQDPQRLV	480
55	STLMNVLTPE	LLETGVBECTA	SNDLGKNTSI	LFLLELVNLT	LTPDSNTTGT	LSTSTASPH	540
	RANSTSTERK	LPEPESRGVV	IVAVIVCILT	LAVLGAVLYF	LYKKGKLPKR	RSQGKEITLP	600
	PSRKTSLVVE	VKSDKLPEEM	GLLQSSGDK	RAPGDQGERY	IDLRH		

Seq ID NO: 554 DNA sequence
Nucleic Acid Accession #: NM_003183.3
Coding sequence: 165..2639

65	1	11	21	31	41	51	
	TCGAGCCTGG	CGGTAGAATC	TTCCCACTAG	GCGGCGCGGG	AGGGAAAAAG	GGATTGAGGG	60
	GCTAGGCGCG	GCGGATCCCG	TCCTCCCCCG	ATGTGAGCAG	TTTTCCGAAA	CCCCGTGAGG	120
	CGAAGGCTGC	CCAGAGAGGT	GGAGTCGGTA	GCGGGGCGGG	GAACATGAGG	CAGTCTCTCC	180
	TATTCCTGAC	CAGCGTGGTT	CCTTTCGTGC	TGGCGCGCGG	ACCTCCGGAT	GACCCGGGCT	240
	TCGGCCCCCA	CCAGAGACTC	GAGAAGCTTG	ATTCTTTGCT	CTCAGACTAC	GATATTCTCT	300
70	CTTTATCTAA	TATCCAGCAG	CATTTCGGTAA	GAAAAAGAGA	TCTACAGACT	TCAACACATG	360
	TAGAAACACT	ACTAACTTTT	TCAGCTTTGA	AAAGGCATTT	TAAATTATAC	CTGACATCAA	420
	GTACTGAACG	TTTTTCACAA	AATTTCAAGG	TCGTGGTGGT	GGATGGTAAA	AACGAAAGCG	480
	AGTACACTGC	AAATGGCAG	GACTTCTTCA	CTGGACACGT	GGTTGGTGAG	CCTGACTCTA	540
	GGGTTCTAGC	CCACATAAGA	GATGATGATG	TTATAATCAG	AATCAACACA	GATGGGGCCG	600
75	AATATAACAT	AGAGCCACTT	TGGAGATTGG	TTAATGATAC	CAAGACAAA	AGAATGTTAG	660
	TTTATAAATG	TGAAGATATC	AAGAATGTTT	CACGTTTGCA	GTCTCCAAA	GTGTGTGGTT	720
	ATTTAAAGT	GGATAATGAA	GAGTTGCTCC	CAAAAGGGTT	AGTAGACAGA	GAACCACTG	780
	AAGAGCTTGT	TCATCGAGTG	AAAAGAAGAG	CTGACCCAGA	TCCCATGAAG	AACACGTGTA	840
80	AATTATTGGT	GGTAGCAGAT	CATCGCTTCT	ACAGATACAT	GGGCGAGGGG	GAAGAGAGTA	900
	CAACTACAAA	TTACTTAATA	GAGCTAATTG	ACAGAGTTGA	TGACATCTAT	CGGAACACTT	960
	CATGGGATAA	TGCAGGTTTT	AAAGGCTATG	GAATACAGAT	AGAGCAGATT	CGCATTCTCA	1020
	AGTCTCCACA	AGAGGTAAAA	CCTGGTGAAA	AGCACTACAA	CATGGCAAAA	AGTTACCCAA	1080
	ATGAAGAAAA	GGATGCTTGG	GATGTGAAGA	TGTTGCTAGA	GCAATTTAGC	TTTGATATAG	1140
	CTGAGGAAGC	ATCTAAAGTT	TGCTTGGCAC	ACCTTTTCAC	ATACCAAGAT	TTTGATATGG	1200
85	GAACTCTTGG	ATTAGCTTAT	GTTGGCTCTC	CCAGAGCAAA	CAGCCATGGA	GGTGTGTC	1260
	CAAAGGCTTA	TTATAGCCCA	GTTGGGAAGA	AAAATATCTA	TTTGAATAGT	GGTTTGACGA	1320
	GCACAAAGAA	TTATGGTAAA	ACCATCCTTA	CAAAGGAAGC	TGACCTGGTT	ACAACCTCATG	1380

	AATTGGGACA	TAATTTTGGG	GCAGAACATG	ATCCGGATGG	TCTAGCAGAA	TGTGCCCGGA	1440
	ATGAGGACCA	GGGAGGGAAA	TATGTCATGT	ATCCCATAGC	TGTGAGTGGC	GATCACGAGA	1500
	ACAAATAGAT	GTTTTCAAAC	TGCAGTAAAC	AATCAATCTA	TAAGACCATT	GAAGTAAGG	1560
5	CCGAGGAGTG	TTTTCAAGAA	CGCAGCAATA	AAGTTTGTGG	GAACCTCGAGG	GTGGATGAAG	1620
	GAGAAGAGTG	TGATCCTGGC	ATCATGTATC	TGAACAAACG	CACCTGCTGC	AACAGCGACT	1680
	GCACGTTGAA	GGAAAGGTGC	CAGTGCAGTG	ACAGGAACAG	TCCTTGCTGT	AAAAACTGTC	1740
	AGTTTGAGAC	TGCCAGTAAG	AAGTGCCAGG	AGGCGATTAA	TGCTACTTGC	AAAGGCGTGT	1800
	CCTACTGCAC	AGGTAATAGC	AGTGAGTGCC	CGCCTCCAGG	AAATGCTGAA	AATGACACTG	1860
10	TTTGTCTGGA	TCTTGCCAAG	TGTAAGGATG	GGAAATGCAT	CCCTTTCTGC	GAGAGGGAAC	1920
	AGCAGCTGGA	GTCTCTGTGA	TGTAATGAAA	CTGACAACTC	CTGCAAGGTG	TGCTGCAGGG	1980
	ACCTTTCTGG	CGCTGTGTG	CCCTATGTCG	ATGCTGAACA	AAAGAACTTA	TTTTTGAGGA	2040
	AAGGAAAGCC	CTGTACAGTA	GGATTTTGTG	ACATGAATGG	CAATATGTAG	AAACGAGTAC	2100
	AGGATGTAAT	TGAACGATT	TGGGATTTCA	TTGACAGCT	GAGCATCAAT	ACTTTTGGA	2160
15	AGTTTGTAGC	AGACAACATC	GTTGGGTCTG	TCCTGGTTTT	CTCCTTGATA	TTTTGGATTG	2220
	CTTTGAGCAT	TCTTGTCAT	TGTGTGGATA	AGAAATTGGA	TAAACAGTAT	GAATCTCTGT	2280
	CTCTGTTTCA	CCCCAGTAAC	GTCGAAATGC	TGAGCAGCAT	GGATTCTGCA	TCGGTTGCGA	2340
	TTATCAAACC	CTTCTCTGCG	CCCCAGACTC	CAGGCGCGCT	GCAGCCTGCC	CCTGTGATCC	2400
	CTTCGGCGCC	AGCAGCTCCA	AACTGGAGCC	ACCAGAGAAT	GGACACCATC	CAGGAAGACC	2460
20	CCAGCACAGA	CTCCCATATG	GACGAGGATG	GGTTTGAGAA	GGACCCCTTC	CCAAATAGCA	2520
	GCACAGCTGC	CAAGTCAATT	GAGGATCTCA	CGGACCATCC	GGTGGCCAGA	AGTGAAAAGG	2580
	CTGCCTCCTT	TAACTGTCAG	CGTCAGAAATC	GTGTTAACAG	CAAAGAAACA	GAGTGTCTAT	2640
	TTAGTTCTCA	GCTCTTCTGA	CTTAAGTGTG	CAAAATATTT	TTATAGATT	GACCTACAAA	2700
	TCATACACAG	TTGTATTTT	TGGAAGACTG	GGAAAGTACT	TAGCAGATGC	TGGTCATGTG	2760
	TTTGAATCTC	CTGCAGGTAA	ACAGTTCTTG	TGTGGTTTGG	CCCTTCTCCT	TTTGAAAAGG	2820
25	TAAGGTGAAA	GTGAATCTAC	TTATTTTGAG	GCTTTCAGGT	TTTAGTTTTT	AAAAATCTTT	2880
	TTGACCTGTG	GTGCAAAAGC	AGAAAATACA	GCTGGATTGG	GTTATGAATA	TTTACGTTTT	2940
	TGTAAATTA	TCCTTTATAT	TGATAACAGC	ACTGACTAGG	GAAATGATCA	GTTTTTTTTT	3000
	ATACACTGTA	ATGAACCGCT	GAATATGAAG	CATTTGGCAT	TTATTTGTGA	GAAAAGTGGG	3060
30	ATAGTTTTTT	TTTTTTTTTG	CTTCAACTAA	AAACAAAGGA	GATAAAATTA		3120
	GTATACATTG	TATCTAAAT	GTGGGTCTAT	TTCTAGTTAT	TACCCAGAGT	TTTTATGTAG	3180
	CAGGGAAT	ATATATCTAA	ATTTAGAAAT	CATTTGGGTT	AATATGGCTC	TTCATAAATC	3240
	TAAAGCTAAT	CTGCAGAAC	TAACCACTAC	CTTACAGTGA	GGGCTATACA	TGGTAGCCAG	3300
	TTGAATTTAT	GGAATCTACC	AACTGTTTAG	GGCCCTGATT	TGCTGGGCAG	TTTTCTGTGA	3360
	TTTTATAAGT	ATCTTCATGT	ATCCCTGTTA	CTGATAGGGA	TACATGTCTT	AGAAAATCTA	3420
35	CTATTGGCTG	GGAGTGGTGG	CTCATGCCCTG	TAATCCAGC	ACTTGGAGAG	GCTGAGGTTG	3480
	CGCCACTACA	CTCCAGCCTG	GGTGACAGAG	TGAGATCTGC	CTC		

Seq ID NO: 555 Protein sequence
Protein Accession #: NP_003174.2

	1	11	21	31	41	51	
	MRQSLFLTS	VVPFVLAPRP	PDDPGFGPHQ	RLEKLDLSS	DYDILSLSNI	QHSVRKRDL	60
	QTSTHVELL	TFSALKRHPK	LYLTSSTERF	SQNFKVVVD	GKNESEYTA	WQDFPTGHV	120
45	GEPSRVLAH	IRDDVVIIR	NTDGAENIE	PLWRFVNDK	DKRMLVYKSE	DIKNVSRILQ	180
	PKVGYLQVD	NEELLPKGLV	DREPPELVH	RVKRRADPD	MKNCTKLLV	ADHRFPYRMG	240
	RGEESTTNY	LIELIDRVDD	IYRNTSWDNA	GFKGYGIQIE	QIRILKSPQE	VKPEKHYNM	300
	AKSYPNEEKD	AWDVKMLLEQ	FSPDIAEEAS	KVCLAHLPTY	QDFDMGLGL	AYVGSPPRNS	360
	HGGVCPKAY	SPVGKKNIL	NSGLTSTKNY	GKTLTKEAD	LVTTHLGHN	FGAEHDPDGL	420
50	AECAPNEDQG	GKVMYPIAV	SGDHNNKMF	SNCSSQSIYK	TIESKAQECF	QERSNKVCGN	480
	SRVDEGEED	PGIMYLNNDT	CCNSDCTLKE	GVQCSDRNSP	CKKNCQFETA	QKKCQEAINA	540
	TKGVSYSYCT	NSSECPPPGN	AENDTVCLDL	GKCKDGKIP	FCEREQQLES	CACNETDNNS	600
	KVCCRDLSGR	CVFVYDAEQK	NLFRLKGPCC	TVGFCDMNGK	CEKRVQDVIE	RPWDFIDQLS	660
	INTFGKFLAD	NIVGSVLVFS	LIFWIPFSIL	VHCVDKLLDK	QYESLSLFHP	SNVEMLSMD	720
55	SASVRIIKPF	PAPQTPGRILQ	PAPVIPSAPA	APKLDHQRM	TIQEDPSTDS	HMEDGFEEKD	780
	PFNSNSTAAK	SPFDLTDHPV	ARSEKAASEK	LQRQNRVNSK	ETEC		

Seq ID NO: 556 DNA sequence
Nucleic Acid Accession #: NM_021832.1
Coding sequence: 164..2248

	1	11	21	31	41	51	
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65	CTAGGCCGGG	CGGATCCCGT	CCTCCCCCGA	TGTGAGCAGT	TTTCCGAAAC	CCCGTCAGGC	120
	GAAGGCTGCC	CAGAGAGGTG	GAGTCGGTAG	CGGGGCCGGG	AACATGAGGC	AGTCTCTCCT	180
	ATTCTGTACC	AGCGTGGTGT	CTTCTGTGCT	GGCGCCGCGA	CCTCCGGATG	ACCCGGGCTT	240
	CGGCCCCAC	CAGAGACTCG	AGAAGCTTGA	TTCTTTGCTC	TCAGACTACG	ATATTCTCTC	300
70	TTTATCTAAT	ATCCAGCAGC	ATTCCGTAAG	AAAAAGAGAT	CTACAGACTT	CAACACATGT	360
	AGAAACACTA	CTAATTTTT	CAGCTTTGAA	AAGGCATTTT	AAATTATACC	TGACATCAAG	420
	TACTGAACGT	TTTTACAAA	ATTTCAAGGT	CGTGGTGGTG	GATGGTAAAA	ACGAAAGCGA	480
	GTACACTGTA	AAATGGCAGG	ACTTCTTCAC	TGGACACGTG	GTTGGTGAGC	CTGACTCTAG	540
	GGTTCTAGCC	CACATAAGAG	ATGATGATGT	TATAATCAGA	ATCAACACAG	ATGGGGCCGA	600
	ATATAACATA	GAGCCACTTT	GGAGATTTGT	TAATGATACC	AAAGACAAAA	GAATGTTAGT	660
75	TTATAAATCT	GAAGATATCA	AGAATGTTTC	ACGTTTGCG	TCTCCAAAAG	TGTGTGGTTA	720
	TTTAAAGATG	GATAATGAAG	AGTTGCTCCC	AAAAGGGTTA	GTAGACAGAG	AACCACCTGA	780
	AGAGCTTGTT	CATCGAGTGA	AAAGAAGAGC	TGACCCAGAT	CCCATGAAGA	ACACGTGTAA	840
	ATTATTGGTG	GTAGCAGATC	ATCGCTTCTA	CAGATACATG	GGCAGAGGGG	AAGAGAGTAC	900
80	AACTACAAAT	TACTTAATAG	AGCTAATTTG	CAGAGTTGAT	GACATCTATC	GGAACACTTC	960
	ATGGGATAAT	GCAGGTTTAA	AAGGCTATGG	AATACAGATA	GAGCAGATTC	GCATTCTCAA	1020
	GTCTCCACAA	GAGGTAAAC	CTGGTGAAAA	GCACTACAA	ATGGCAAAAA	GTTACCCAAA	1080
	TGAAGAAAAG	GATGCTTGGG	ATGTGAAGAT	GTTGCTAGAG	CAATTTAGCT	TTGATATAGC	1140
	TGAGGAAGCA	TCTAAAGTTT	GCTTGGCACA	CCTTTTCA	TACCAAGATT	TTGATATGGG	1200
85	AACTCTTGGA	TTAGCTTATG	TTGGCTCTCC	CAGAGCAAA	AGCCATGGAG	GTGTTTGTCC	1260
	AAAGGCTTAT	TATAGCCAG	TTGGGAAGAA	AAATATCTAT	TTGAATAGTG	GTTTGAAGAG	1320
	CACAAAGAA	TATGGTAAAT	CCATCTTAC	AAAGGAAGCT	GACCTGGTTA	CAACTCATGA	1380
	ATTGGGACAT	AAATTTGGAG	CAGAACATGA	TCCGATGGT	CTAGCAGAA	GTGCCCCGAA	1440

Seq ID NO: 557 Protein sequence
Protein Accession #: NP_068604.1

Seq ID NO: 558 DNA sequence
Nucleic Acid Accession #: NM_004994.1
Coding sequence: 20..2143

397

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 GGTGCTGGGC CCGAGGCGTC TGGACAAGCT GGGCCTGGGA GCGGACGTGG CCCAGGTGAC 1860
 CGGGGCGCTC CGAGTGGCA GGGGAAGAT GCTGCTGTTC AGCGGGCGGC GCCTCTGGAG 1920
 GTTCGACGTG AAGGCGCAGA TGGTGGATCC CCGGAGCGCC AGCGAGGTGG ACCGGATGTT 1980
 CCCCAGGCTG CCTTTGGACA CGCACGACGT CTTCAGTAC CGAGAGAAAG CCTATTTCTG 2040
 CCAGGACGCG TTCTACTGGC GCGTGAGTTC CCGGAGTGAG TTGAACCAAG TGGACCAAGT 2100
 GGGTACGTG ACCTATGACA TCCTGCAATG CCCTGAGGAC TAGGGCTCCC GTCTGCTTT 2160
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 CAAACTGGTA TTCTGTTCTG GAGGAAAGG AGGAGTGGAG GTGGGCTGGG CCCTCTCTTC 2280
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Seq ID NO: 559 Protein sequence
 Protein Accession #: NP_004985.1

1 11 21 31 41 51
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 ITYWIQNYSE DLPRAVIDDA FARAPALWSA VTPLTFTRVY SRDADIVIQF GVAEHGDGYP 180
 FDGKDLGLAH AFPPGPGIQG DAHFDDELWL SLGKGVVVPF RFGNADGAAC HPPFIFEGRS 240
 YSACTTDGRS DGLPWCSTTA NYDTDDRFGF CPSERLYTRD GNADGKPCQF PFIFQGSYS 300
 ACTTDGRSDG YRWCAATANY DRDKLFGFCP TRADSTVMGG NSAGELCVFP FTFLGKEYST 360
 CTSEGRGDGR LWCAATSNPD SDKKWGFCDP QGYSFLVAA HEFGHALGLD HSSVPEALMY 420
 PMYRFTGEPG LHKDDVNGIR HLYGPRPEPE PRPPTTTTPQ PTAPPTVCPT GPPTVHPSER 480
 PTAGPTGPPS AGPTGPPTAG PSTATTVPLS PVDDACNVNI FDAIAEIGNQ LYLFKDGKYW 540
 RFSEGRGSRP QGFPLIADKW PALPRKLDV FEEPLSKLFP FFSGRQVWVY TGASVLGPRR 600
 LDKLGLGADV AQVTGALRSR RGMKLLFSGR RLWRFDVKAQ MVDPRSASEV DRMFPGVPLD 660
 THDFQYREK AYFCQDRFYW RVSSRSSELNQ VDQVGVVYTD ILQCPED

Seq ID NO: 560 DNA sequence
 Nucleic Acid Accession #: NM_000213.1
 Coding sequence: 127..5385

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 AAGAGGATGG CAGGGCCACG CCCAGCCCCA TGGGCCAGGC TGCTCCTGGC AGCCTTGATC 180
 AGCGTCAGCC TCTCTGGGAC CTGGGCAAAAC CGCTGCAAGA AGGCCCCAGT GAAGAGCTGC 240
 ACGAGTGTG TCCGTGTGGA TAAGGACTGC GCCTACTGCA CAGACGAGAT GTTCAGGGAC 300
 CGGCGCTGCA ACACCCAGGC GGAGCTGCTG GCCGCGGGCT GCCAGCGGGA GAGCATCGTG 360
 GTCATGGAGA GCAGCTTCCA AATCAGAGAG GAGACCCAGA TTGACACCAC CCTGCGGCGC 420
 AGCCAGATGT CCCCACAGG CCGTGGGGTC CGGTGAGGA GCGGCATTTT 480
 GAGCTGGAGG TGTGTGAGCC ACTGGAGAGC CCCGTGGACC TGTACATCCT CATGGACTTC 540
 TCCAACATCA GTGCCGATGA TCTGGACAAC CTCAAGAAGA TGGGGCAGAA CCTGGCTCGG 600
 GTCTCTAGCC AGCTCACACG CGACTACACT ATTGGATTGT GCAAGTTTGT GGACAAAGT 660
 AGCGTCCCGC AGACGGACAT GAGGCCTGAG AAGCTGAAGG AGCCCTGGCC CAACAGTGAC 720
 CCCCCTTCTT CCTTCAAGAA CGTCATCAGC CTGACAGAAG ATGTGGATGA GTTCCGGAAT 780
 AAATCTGACG GAGAGCGGAT CTCAGGCAAC CTGGATGCTC CTGAGGGCGG GTTCGATGCC 840
 ATCTGACAGA CAGCTGTGTG CACGAGGGAC ATGGCTGGC GCCCGGACAG CACCCACCTG 900
 TCGGTCTTCT CCACCGAGTC AGCCTTCCAC TATGAGGCTG ATGGCGCCAA CGTGCTGGTG 960
 GGCATCATGA CCGGCAACGA TGAACGGTGC CACCTGGACA CCAAGGGCAC CTACACCCAG 1020
 TACAGGACAC AGGACTACCC GTCCGTGCCC ACCCTGGTGC GCCTGCTCGC CAAGCACAAC 1080
 ATCATCCCCA TCTTGTCTGT CACCAACTAC TCCTATAGCT ACTACGAGAA GCTTCACACC 1140
 TATTTCCTGT TCTCCTACTG GGGGGTGTCT CAGGAGGACT CGTCCAACAT CGTGGAGCTG 1200
 CTGGAGGAGG CTTTCAATCG GATCCGCTCC AACCTGGACA TCCGGGCCCT AGACAGCCCC 1260
 CGAGGCTTTC GGACGAGAGT CACCTCCAAG ATGTTCCAGA AGACGAGGAC TGGGTCTCTT 1320
 CACATCCGGC GGGGGGAAGT GGGTATATAC CAGGTGCAGC TGCGGGCCCT TGACACGCTG 1380
 GATGGGACGC ACGTGTGCCA GCTGCCGGAG GACCAGAAGG GCAACATCCA TCTGAAACCT 1440
 TCCTTCTCCG ACGGCTCAA GATGGACGCG GGCATCATCT GTGATGTGTG CACCTGCGAG 1500
 CTGCAAAAAG AGGTGCGGTG AGCTCGCTGC AGCTTCAACG GAGACTTCTG GTGCGGACAG 1560
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 GACATTACGC CTGCTCTGCG GGAGGGCGAG GACAAGCCGT GCTCCGGCCG TGGGGAGTGC 1680
 CAGTCCGGGC ACTGTGTGTG CTACGGCGAA GCGCGCTACG AGGGTCAGTT CTGCGAGTAT 1740
 GACAACCTCC AGTGTCCCGC CACTTCCGGG TTCCTCTGCA ATGACCGAGG ACGCTGCTCC 1800
 ATGGGCCAGT GTGTGTGTGA GCCTGGTTGG ACAGGCCCAA GCTGTGACTG TCCCTCAGC 1860
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 GGCGCTGCC ACTGCCACCA GCAGTCGCTC TACACGGACA CCATCTGCGA GATCAACTAC 1980
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 CTCTCTCTCC TGCCGCTCCT GGCCTGCTA CTGCTGCTAT GCTGGAAGTA CTGTGCTGCT 2340
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 CTGCGCAGCG GGAACCTCAA GGGCCGTGAC GTGGTCCGCT GGAAGGTCAC CAACAACATG 2520
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 GGGCTGTCTT TGCGCTTGGC CCGCCTTTCG ACCGAGAACC TGCTGAAGCC TGACACTCGG 2640
 GAGTGCAGCC AGCTGCGCCA GGAGGTGGAG GAGAACCTGA ACGAGGTCTA CAGGCAGATC 2700
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 GGCTACTACA CCTTCACTGC AGACCAAGAC GCCCGGGGCA TGGTGGAGTT CCAGGAGGGC 2940
 GTGGAGCTCG TGGAGCTACG GGTGCCCTTC TTTATCCGGC CTGAGGATGA CGACGAGAAG 3000
 CAGCTGCTGG TGGAGGCCAT CGACGTGCCC GCAGGCACTG CCACCTCTCG CCGCGCCTG 3060

	GTAAACATCA	CCATCATCAA	GGAGCAAGCC	AGAGACGTGG	TGTCCTTTGA	GCAGCCTGAG	3120
	TTCTCGGTCA	GCCGCGGGGA	CCAGGTGGCC	CGCATCCCTG	TCATCCGGCG	TGTCTTGGAC	3180
	GGCGGGAAAT	CCCAGGTCTC	CTACCGCACA	CAGGATGGCA	CCGCGCAGGG	CAACCGGGAC	3240
5	TACATCCCGG	TGGAGGGTGA	GCTGCTGTTC	CAGCCTGGGG	AGGCCTGGAA	AGAGCTGCAG	3300
	GTGAAGCTCC	TGGAGCTGCA	AGAAGTTGAC	TCCCTCTGTC	GGGCGCGCCA	GGTCCGCCGT	3360
	TTCCAGCTCC	AGCTCAGCAA	CCCTAAGTTT	GGGCCCCACC	TGGGCCAGCC	CCACTCCACC	3420
	ACCATCATCA	TCAGGGACCC	AGATGAACTG	GACCGGAGCT	TCACGAGTCA	GATGTTGTCA	3480
	TCACAGCCAC	CCCCTACGGG	CGACCTGGGC	GCCCCGCGAG	ACCCCAATGC	TAAGGCCGCT	3540
10	GGGTCCAGGA	AGATCCATT	CAACTGGCTG	CCCCCTTCTG	GCAAGCCAAT	GGGGTACAGG	3600
	GTAAAGTACT	GGATTGAGG	TGACTCCGAA	TCCGAAGCCC	ACCTGCTCGA	CAGCAAGGTG	3660
	CCCTCAGTGG	AGCTCACCAG	CCTGTACCCG	TATTGCGACT	ATGAGATGAA	GGTGTGCGCC	3720
	TACGGGGCTC	AGGGCGAGGG	ACCCTACAGC	TCCCTGTGTG	CCTGCCGCAC	CCACCAAGGA	3780
	GTGCCACCG	AGCCAGGGCG	TCTGGCCTTC	AATGTGCTCT	CCTCCACGGT	GACCCAGCTG	3840
15	AGCTGGGCTG	AGCCGGCTGA	GACCAACGGT	GAGATCACAG	CCTACGAGGT	CTGCTATGGC	3900
	CTGGTCAACG	ATGACAACCG	ACCTATTGGG	CCCATGAAGA	AAGTGCTGGT	TGACAACCTT	3960
	AAGAACCAGA	TGCTGCTTAT	TGAGAACCTT	CGGGAGTCCC	AGCCCTACCG	CTACACGGTG	4020
	AAGGCGCGCA	ACGGGGCGCG	CTGGGGGCGT	GAGCGGGAGG	CCATCATCAA	CCTGGCCACC	4080
	CAGCCCAAGA	GGCCCATGTC	CATCCCCATC	ATCCTTGACA	TCCCTATCGT	GGACGCCACG	4140
20	AGCGGGGAGG	ACTACGACAG	CTTCCTTATG	TACAGCGATG	ACGTTCTACG	CTCTCCATCG	4200
	GGCAGCCAGA	GGCCCGAGCT	CTCCGATGAC	ACTGAGCACC	TGGTGAATGG	CCGGATGGAC	4260
	TTTGCCCTCC	CGGGCAGCAC	CAACTCCCTG	CACAGGATGA	CCACGACCAG	TGCTGCTGCC	4320
	TATGGCACCC	ACCTGAGCCC	ACACGTGCCC	CACCGCGTGC	TAAGCACATC	CTCCACCCTC	4380
	ACACGGGACT	ACAAGTCACT	GACCCGCTCA	GAACACTCAC	ACTCGACCAC	ACTGCCGAGG	4440
25	GACTACTCCA	CCCTCACCTC	CGTCTCCTCC	CACGACTCTC	GCCTGACTGC	TGGTGTGCCC	4500
	GACACGCCCA	CCCGCCTGGT	GTTCTCTGCC	CTGGGGCCCA	CATCTCTCAG	AGTGAGCTGG	4560
	CAGGAGCGCG	GCTGCGAGCG	GCCTGCTGAG	GGCTACAGTG	TGGAGTACCA	GCTGCTGAAC	4620
	GGCGGTGAGC	TGCATCGGCT	CAACATCCCC	AACCTGCCCC	AGACCTCGGT	GGTGGTGGAA	4680
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30	GGCCGAGAGC	GTGAGGGTGT	CATCACCATT	GAATCCGAGG	TGCACCCGCA	GAGCCCACTG	4800
	TGTCCTCTGC	CAGGCTCCGC	CTTCACTTTG	AGCACTCCCA	GTGCCCCAGG	CCGCTGGTGG	4860
	TTCACTGCCC	TGAGCCCACT	CTCGCTGCAG	CTGAGCTGGG	AGCGGCCACG	GAGGCCCAAT	4920
	GGGGATATCG	TCGGCTCAGA	GGTGACCTGT	GAGATGGCCC	AAGGAGGAGG	GCCAGCCACC	4980
	GCATTCCGGG	TGGATGGAGA	CAGCCCGGAG	AGCCGGCTGA	CCGTGCCGGG	CCTCAGCGAG	5040
35	AACGTGCCCT	ACAAGTTCAA	GGTGCAGGCC	AGGACCACTG	AGGGCTTCGG	GCCAGAGCGC	5100
	GAGGGCATCA	GTCACATAGA	GTCCAGGATG	GGAGGACCTT	TCCCGCAGCT	GGGCGCCGCT	5160
	GCCGGGCTCT	TCCAGCACCC	GCTGCAAGGC	GAGTACAGCA	GCATCACCAC	CACCCACACC	5220
	AGCGCCACCG	AGCCCTTCTC	AGTGGATGGG	CCGACCTTGG	GGGCCAGCA	CCTGGAGGCA	5280
	GGCGGCTCCC	CSFRDEDDDC	TGTGACCCAG	GAGTTTGTGA	GCCGGCACT	GACCAACGAG	5340
40	GGAACCTTA	GCACCCACAT	GGACCAACAG	TTCTTCCAAA	CTTGACCGCA	CCCTGCCCCA	5400
	CCCCCGCCAT	GTCCCACTAG	GGCTCCTCCC	GACTCCTCTC	CCGGAGCCTC	CTCAGCTACT	5460
	CCATCCTTGC	ACCCCTGAGG	GCCAGGCCCA	CCCGCATGCA	CAGAGCAGGG	GCTAGGTGTC	5520
	TCCTGGGAGG	CATGAAGGGG	GCAAGGTCGG	TCCTCTGTGG	GCCCAAACCT	ATTGTGTAAC	5580
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45	TACTG						

Seq ID NO: 561 Protein sequence
Protein Accession #: NP_000204.1

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	EVEFPLESPV	DLYILMDFSN	SMSDDLNLK	KMGQNLARVL	SQLTSDYTIG	FGKFVDKVS	180
55	PQTDMPREKL	KEPWNSDPP	FSFKNVISLT	EDVDEFNRKL	QGERISGNLD	APEGGFDAIL	240
	QTAVCTRDIG	WRPDSHTLLV	FSTESAFHYE	ADGANVLAGI	MSRNDERCHL	DTTGTYTQYR	300
	TQDYPSPVPTL	VRLLAKHNII	PIFAVTNYSY	SYYEKLHTYF	PVSSLGLVLE	DSSNIVELLE	360
	EAFNRIRSNL	DIRALDSPRG	LRTEVTSKMF	QKTRTGSFHI	RRGEVGIYQV	QLRALEHVDG	420
	THVCQLPEDQ	KGNILHKPSF	SDGLKMDAGI	ICDVCTCELQ	KEVRSARCSF	NGDFVCGQCV	480
60	CSEGSQGTCC	CSFRDEDDDC	QPCLRREGEDK	PCSGRGEQCQ	GHCVCYGEGR	YEGQFCEYDN	540
	FQCFRTSGFL	CNDRGRCSMG	QCVCEFGWTG	PSCDCPLSNA	TCIDSNGGIC	NGRGHCCEGR	600
	CHCHQQLSYT	DTICEINYSA	IHPGLCEDLR	SCVQCQANGT	GEKKGRTCCE	CNFKVKMVDL	660
	LKRAEEVVVR	CSFRDEDDDC	TYSYTMEDDG	APGPNSTVLV	HKKKDCPPGS	FWWLIPLLLL	720
	LLPLLALLLL	LCWKYCACK	ACLALLPCCN	RGHMVGFKED	HYMLRENLMA	SDHLDTPLMR	780
65	SGNLKGRDVG	RWKVTNNMQR	PGFATHAASI	NPTELVPYGL	SLRLARLCTE	NLLKPDTRC	840
	AQLRQVEVEN	LNEVYRQISG	VHKLQQTQKFR	QOPNAGKKQD	HTIVDTVLMA	PRSAKPALLK	900
	LTEKQVEQRA	FHDLKVAPGY	YTLTADQDAR	GMVEFQEGVE	LVDVRVPLFI	RPEDDEKQL	960
	LVEAIDVPAG	TATLGRRLVN	ITIIKEQARD	VVSFEQPEFS	VSRGDQVARI	PVIRRVLDGG	1020
	KSQVSYRTQD	GTAQGNRDYI	PVEGELLFQP	GEANKELQVK	LLELQEVDSL	LRGRQVRRFH	1080
70	VQLSNPKFGA	HLGQPHSTTI	IIRDPDELDR	SFTSQMLSSQ	PPPHGDLGAP	QNPNAKAAGS	1140
	RKIHFNWLP	SGKPMGYRVK	YWIQGDSESE	AHLSDSKVPS	VELTNLYPYC	DYEMKVCAYG	1200
	AQGEQPYSSL	VSCRTHQEPV	SEPGRILAFNV	VSSVTQLSW	AEPAETNGEI	TAYEVCYGLV	1260
	NDDNRPIGPM	KKVLVDNPKN	RMLLIENLRE	SQPYRYTVKA	RNGAGWGP	EAIINLATQP	1320
	KRPMSPPIIP	DIPVDAQSG	EDYDSFLMYS	DDVLRSPSGS	QRPSVSDDTE	HLVNGRMDFA	1380
75	PPGSTNSLHR	MTTIPVAAHYG	THLSPHVPHR	VLSTSTLTLR	DYNSLTRSEH	SHSTTLPRDY	1440
	STLTSVSSH	SRLTAGVPDT	PTLTVFSALG	PTSLRVSWQE	PRCERPLQGY	SVEYQLLNGG	1500
	ELHRLNIPNP	AQTSVVVEDL	LPNHSYVFRV	RAQSQEGWGR	EREGVITIES	QVHPQSPLCP	1560
	LPGSAFTLST	PSAQPPLVFT	ALSPDSLQLS	WERPRRPNGD	IVGYLVTCEN	AQGGGPATAP	1620
	RVDGDSPEER	LTVPLGSENV	PYKFKVQART	TEGFGPEREG	IITIESQDGG	PPQLGSRAG	1680
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	LSTHMDQQPF	QT					

Seq ID NO: 562 DNA sequence
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Coding sequence: 1..63

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 CGGTGTCTCC CCCGAGGGGT CCAGAGGCCT TTCAGAAGGA GAAGGCAGCT CTGTTTCTCT 180
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 GGTACTGACC CTACTCTCCA TCTTGGTTAG AGTGATGGAG TCCCTAGAAG GCTTACTAGA 300
 GAGCCCATCG CCTGGGACCT CCTGGACCAC CAGAAGCCAA CTAGCCAACA CAGAGCCCAC 360
 CAAGGCGCTT CCAGACCATC CATCCAGAAG CATGTGATAA GACCTCCTTC CATACTGGCC 420
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 10 CTCAATTGCTT GGGCAAGGCC TGTTTAGGCC GGTGCGGTG GCTCATGCCT GTAATCCTAG 600
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 GGCCTGTAAT CCCAGTTCCT TGGGAGGCTG AGGCGGGAGA ATTGCTTGAA CCGGGGACG 780
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 15 CATCTCAAAA AAAAAAAGAA AAGAAAAAGC CTGTTTAATG CACAGGTGTG AGTGGATTGC 900
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 20 CAGTTGAAGA GGTGTGTGG GTGGGCTGTT GGGAGTGAGG ATGGAGTGT CAGTGGCCAT 1200
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 GGTGGGATGC CAAAGCCTGC TCAAGTTATG GACATTGTGG CCACCATGTG GCTTAAATGA 1320
 TTTTCTTAA GGAATAAAGT GGAATATATA TTTCAAAAAA AAAAAAAAAA AA

25 Seq ID NO: 563 Protein sequence
 Protein Accession #: NP_037464.1

30 1 11 21 31 41 51
 MKHVLNLYLL GVVLTLLSIF VRVMESLEGL LESPSPGTSM TTRSQLANTE PTKGLPDHPS 60
 RSM

35 Seq ID NO: 564 DNA sequence
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 Coding sequence: 250..1326

40 1 11 21 31 41 51
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 AACTGAAGAA TGGGGTTCAA CTGACGCTT GCAAAATTAC CAAATAACGA GCTGCACGGC 300
 45 CAAGAGAGTC ACAATTCAAG CAACAGGAGC GACGGGCCAG GAAAGAACAC CACCCTTCAC 360
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 TTCTATCTCA AAAACATAGT GGTTCAGAC CTCATAATGA CGCTGACATT TCCATTTCGA 540
 ATAGTCCATG ATGCAGGATT TGGACCTTGG TACTTCAAGT TTATTCTCTG CAGATACACT 600
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 GTGGCTGTGT TTTTACCTG CTTTCTACCA TATCACTTGT GCAGAAATCC TTTTACTTTT 1080
 AGTCACCTAG ACAGGCTTTT AGATGAATCT GCACAAAAAA TCCTATATTA CTGCAAAGAA 1140
 ATTACACTTT TCTTGTCTGC GTGTAATGTT TGCCTGGATC CAATAATTTA CTTTTCATG 1200
 60 TGTAGGTCAT TTTCAAGAAG GCTGTTCAAA AAATCAATA TCAGAACCAAG GAGTGAAGC 1260
 ATCAGATCAC TGCAAGTGT GAGAAGATCG GAAAGTCGCA TATATTATGA TTACACTGAT 1320
 GTGTAGGCCT TTTATTGTTT GTTGAATCG ATATGTACAA AGTGTAATAA AATGTTTCTT 1380
 TTCATTATCC TAAAAAAA AA

65 Seq ID NO: 565 Protein sequence
 Protein Accession #: NP_076404

70 1 11 21 31 41 51
 MGFNLTAKL PNNELHGQES HNSGNRSDGP GKNTTLHNEF DTIVLPVLYL IIFVASILLN 60
 GLAVWIFFHI RNKTSIFIFL KNIVVADLIM TLTPFFRIVH DAGFGPWYFK FILCRYTSVL 120
 FYANMYTSIV FLGLISIDRY LKVVKPPGDS RMYSITFTKV LSVCVWVIMA VLSLPNIILT 180
 NGQPTEDNIH DCSKLKSPLG VKWHTAVTYV NSCLFVAVLV ILIGCYIAIS RYIHKSSRQF 240
 ISQSSRKRRH NQSIRVVAV FFTCFPLPHL CRIPFTFSLH DRLLDESAQK ILYYCKEITL 300
 75 PLSACNVCLD PIIFYPMCRS PSRRLPKRSN IRTRESIRS LQSVRRSEVR IYYDYTDV

80 Seq ID NO: 566 DNA sequence
 Nucleic Acid Accession #: NM_005365.1
 Coding sequence: 1..948

85 1 11 21 31 41 51
 ATGTCTCTCG AGCAGAGGAG TCCGCACTGC AAGCCTGATG AAGACCTTGA AGCCCAAGGA 60
 GAGGACTTGG GCCTGATGGG TGCACAGGAA CCCACAGGCG AGGAGGAGGA GACTACCTCC 120
 TCCTCTGACA GCAAGGAGGA GGAGGTGTCT GCTGCTGGGT CATCAAGTCC TCCCCAGAGT 180
 CCTCAGGGAG GCGCTTCCTC CTCCATTTCG GTCTACTACA CTTTATGGAG CCAATTGAT 240
 85 GAGGGCTCCA GCAGTCAAGA AGAGGAAGAG CCAAGCTCCT CGGTGACACC AGCTCAGCTG 300
 GAGTTATATG TCCAAGAAGC ACTGAAATTG AAGGTGGCTG AGTTGGTTCA TTTCTGCTC 360

CACAAATATC GAGTCAAGGA GCCGGTCACA AAGGCAGAAA TGCTGGAGAG CGTCATCAAA 420
 AATTACAAGC GCTACTTTCC TGTGATCTTC GGCAAAGCCT CCGAGTTCAT GCAGGTGATC 480
 TTTGGCACTG ATGTGAAGGA GGTGGACCCC GCCGGCCACT CCTACATCCT TGTCACGTCT 540
 CTTGGCCTCT CGTGGGATAG CATGCTGGGT GATGGTCATA GCATGCCCAA GGCGCCCTC 600
 CTGATCATTT TCCTGGGTGT GATCCTAACC AAAGACAAC TCGCCCCCTGA AGAGGTTATC 660
 TGGGAAGCGT TGAGTGTGAT GGGGGTGTAT GTTGGGAAGG AGCACATGTT CTACGGGGAG 720
 CCCAGGAAGC TGCTCACCCA AGATTGGGTG CAGGAAAAC TCCCTGGAGTA CCGGCAGGTG 780
 CCCGGCAGTG ATCCTGCACA CTACGAGTTC CTGTGGGGTT CCAAGGCCCA CGCTGAAACC 840
 AGCTATGAGA AGGTATATAA TTATTGGTTC ATGCTCAATG CAAGAGAGCC CATCTGCTAC 900
 CCATCCCTTT ATGAAGAGGT TTTGGGAGAG GAGCAAGAGG GAGTCTGA

Seq ID NO: 567 Protein sequence
 Protein Accession #: NP_005356.1

1 11 21 31 41 51
 MSLEQRSPHC KPDEDLEAQQ EDLGLMGAQE PTGEEEEETS SSDSKEEEVS AAGSSSPPPQS 60
 PQGGASSSIS VYITLWSQFD EGSSSQEEEE PSSSVDPQAL EFMFQEAALKL KVAELVHFL 120
 HKYRVKEPVT KAEMLESVIK NYKRYFPVIF GKASEFMQVI PGTDVKEVDP AGHSYILVTA 180
 LGLSCDSMLG DGHSMPKAAL LIIVLGVILT KDNCAPEEVI WEALSVMGVY VGKEHMFYGE 240
 PRKLLTQDWV QENYLEYRQV PGSDPAHYEF LWGSKAHAET SYEKVINYL VMLNAREFICY 300
 PSLYEEVLGE EQEGV

Seq ID NO: 568 DNA sequence
 Nucleic Acid Accession #: NM_014400
 Coding sequence: 86..1126

1 11 21 31 41 51
 GGTTACTCAT CTGGGCTCA GGTAAAGAGG CCGAGCTCG GAGGCGGCAC ACCCAGGGGG 60
 GACGCCAAGG GAGCAGGACG GAGCCATGGA CCCCAGCAGG AAAGCAGGTG CCCAGGCCAT 120
 GATCTGGACT GCAGGCTGGC TGCTGCTGCT GCTGCTTGC GGAGGAGCGC AGGCCCTGGA 180
 GTGCTACAGC TGCGTGACGA AAGCAGATGA CGGATGCTCC CCGAACAGA TGAAGACAGT 240
 GAAGTGCAGC CCGGGCGTGG ACGTCTGCAC CGAGGCCGTG GGGGCGGTGG AGACCATCCA 300
 CGGACAATTC TCGCTGGCAG TGCSGGGTTG CGGTTCCGGA CTCGCCGGA AGAATGACCG 360
 CGGCCTGGAT CTTACGGGCG TTCTGGCGTT CATCCAGCTG CAGCAATGCG CTCAGGATCG 420
 CTGCAACGCC AAGCTCAACC TCACCTCGCG GCGCTCGAC CCGGCAGGTA ATGAGAGTGC 480
 ATACCCGCCC AACCGCTGG AGTGCTACAG CTGTGTGGGC CTGAGCCGGG AGGCGTGCCA 540
 GGGTACATCG CCGCCGGTGG TGAGCTGCTA CAACGCCAGC GATCATGTCT ACAAGGGCTG 600
 CTTGACGGC AACGTCACCT TGACGGCAGC TAATGTGACT GTGTCTTTCG CTGTCCGGGG 660
 CTGTGTCCAG GATGAATTC GCACTCGGGA TGGAGTAACA GGCCAGGAGT TCACGCTCAG 720
 TGGCTCCTGT TGCCAGGGGT CCGCTGTAA CTCTGACCTC CGCAACAAGA CCTACTTCTC 780
 CCCTCGAATC CCACCCCTTA TCCGGCTGCG CCCTCCAGAG CCCACGACTG TGGCCTCAAC 840
 CACATCTGTC ACACCTTCTA CCTCGGCCCC AGTGAGACCC ACATCCACCA CCAAACCCAT 900
 GCCAGGCCCA ACCAGTCAGA CTCGAGACA GGGAGTAGAA CACGAGGCTC CCGGGATGA 960
 GGAGCCCAAG TTGACTGGAG GCGCCGCTGG CCACCAGGAC CGCAGCAATT CAGGGCAGTA 1020
 TCCTGCAAAA GGGGGGCCCC AGCAGCCCCA TAATAAAGGC TGTGTGGCTC CCACAGCTGG 1080
 ATTGGCAGCC CTTCTGTGG CCGTGGCTGC TGGTGTCTA CTGTGAGCTT CTCACCTGG 1140
 AAATTTCCCT CTCACCTACT TCTCTGGCCC TGGGTACCCC TCTTCTCATC ACTTCTGTT 1200
 CCCACCACTG GACTGGGCTG GCCAGCCCC TGTTTTCCA ACATTCCTCA GTATCCCCAG 1260
 CTTCTGCTGC GCTGTTTTC GGCCTTGGGA AATAAAATAC CGTTGTATAT ATTCTGGCAG 1320
 GGGTGTCTA GCTTTTGTAG GACAGCTCCT GTATCCTTCT CATCCTTGTC TCTCCGCTTG 1380
 TCCTCTTGTG ATGTGTAGAG AGAGTGAGAG AAGTCAGCTG TCACGGGGAA GGTGAGAGAG 1440
 AGGATGCTAA GCTTCTACT CACTTCTCC TAGCCAGCCT GGACTTTGGA GCGTGGGGTG 1500
 GTGGGGACAA TGGCTCCCCA CTCTAAGCAC TGCCTCCCT ACTCCCGCA TCTTTGGGGA 1560
 ATCGGTTCCC CATGTCTCTT CCTTACTAGA CTGTGAGCTC CTCGAGGGCA GGGACCGTGC 1620
 CTTATGTCTG TGTGTGATCA GTTCTGGCA CATAAATGCC TCAATAAAGA TTTAATTACT 1680
 TTGTATAGTG AAAAAAA

Seq ID NO: 569 Protein sequence
 Protein Accession #: NP_055215

1 11 21 31 41 51
 MDPARKAGAQ AMIWTAGWLL LLLLRGGAQA LECYSCVQKA DDGCSFNKMK TVKCAPGV 60
 CTEAVGAVET IHQFSLAVX GCGSGLPGKN DRGLDLHGLL AFIQLQCAQ DRCNAKLNLT 120
 SRALDPAGNE SAYPPNGVEC YSCVGLSREA CQGTSPPVVS CYNASDHVYK GCPDGNVLT 180
 AANVTVSLPV RGVQDEPCT RDGVTGPGFT LSGSCCGSR CNSDLRNKTY FSPRIPLVR 240
 LPPPEPTTVA STTSVTTST APVRPTSTK PMPAPTSQTP RQGVHEASR DEEPRLTGGA 300
 AGHQDRSNSG QYPAKGPPQ PHNKGCVAPT AGLAALLLAV AAGVLL

Seq ID NO: 570 DNA sequence
 Nucleic Acid Accession #: NM_005329.1
 Coding sequence: 1..1662

1 11 21 31 41 51
 ATGCCCGTGC AGCTGACGAC AGCCCTGCGT GTGGTGGGCA CCAGCCTGTT TGCCCTGGCA 60
 GTGCTGGGTG GCATCCTGGC AGCCTATGTG ACGGGCTACC AGTTTCATCA CACGGAAAAG 120
 CACTACCTGT CCTTCGGCCT GTACGGCGCC ATCCTGGGCC TGCACTGCT CATTCAGAGC 180
 CTTTTCGCTT TCCTGGAGCA CCGGCGCATG CGACGTGCGG GCCAGGCCCT GAAGCTGCCC 240
 TCCCGCGGCG GGGGCTCGGT GGCATGTGCT ATTGCGCGCT ACCAGGAGGA CCCTGACTAC 300
 TTGCGCAAGT CCGTGGCTCT GGCCAGCGC ATCTCCTTCC CTGACCTCAA GGTGGTCATG 360
 GTGGTGGATG GCAACGCCCA GGAGGACGCC TACATGCTGG ACATCTTCCA CGAGGTGCTG 420
 GCGGGCAGCG AGCAGGCCCG CTTCTTTGTG TGGCGCAGCA ACTTCCATGA GGCAGGCGAG 480
 GGTGAGACGG AGGCCAGCCT GCAGGAGGGC ATGGACCGTG TGCGGGATGT GGTGCGGGCC 540
 AGCACCTTCT CGTGATCAT GCAGAAAGTG GGAGGCAAGC CGAGGTCAT GTACACGGCC 600

	TTCAAGGCC	TCGGCGATTC	GGTGGACTAC	ATCCAGGTGT	GCGACTCTGA	CACGTGTCTG	660
	GATCCAGCCT	GCACCATCGA	GATGCTTCGA	GTCCTGGAGG	AGGATCCCCA	AGTAGGGGGA	720
	GTGCGGGGAG	ATGTCCAGAT	CCTCAACAAG	TACGACTCAT	GGATTTCTCT	CCTGAGCAGC	780
5	GTGCGGTACT	GGATGGCCTT	CAACGTGGAG	CGGGCTGCGC	AGTCCTACTT	TGGCTGTGTG	840
	CAGTGTATTA	GTGGGCCCTT	GGGCATGTAC	CGCAACAGCC	TCCTCCAGCA	GTTCCTGGAG	900
	GACTGGTACC	ATCAGAAGTT	CCTAGGCAGC	AAGTGCAGCT	TCGGGGATGA	CCGGCAGCTC	960
	ACCAACCCGAG	TGGTCAACGG	TGGTCAACGG	ACTAAGTATA	CCGCGCGCTC	CAAGTGCCTC	1020
	ACAGAGACCC	CCACTAAGTA	CCTCCGGTGG	CTCAACCAGC	AAACCCGCTG	GAGCAAGTCT	1080
10	TACTTCCGGG	AGTGGCTCTA	CAACTCTCTG	TGGTTCCATA	AGCACCACCT	CTGGATGACC	1140
	TACGAGTCAG	TGGTCAACGG	TTTCTTCCCC	TTCTTCTCTA	TTGCCACGGT	TATACAGCTT	1200
	TTCTACCGGG	GCCGCATCTG	GAACATTCTC	CTCTTCTCTG	TGACGGTGCA	GCTGGTGGGC	1260
	ATTATCAAGG	CCACCTACGC	CTGCTTCCTT	CGGGGCAATG	CAGAGATGAT	CTTCATGTCC	1320
	CTCTACTCCC	TCCTCTATAT	GTCCAGCCTT	CTGCCGGCCA	AGATCTTTGC	CATTGCTACC	1380
15	ATCAACAAT	CTGGCTGGGG	CACCTCTGGC	CGAAAAACCA	TTGTGGTGAA	CTTCATTGGC	1440
	CTCATTCCTG	TGTCCATCTG	GGTGGCAGTT	CTCCTGGGAG	GGCTGGCCTA	CACAGCTTAT	1500
	TGCCAGGACC	TGTTCACTGA	GACAGAGCTA	GCCTTCTCTG	TCTCTGGGGC	TATACTGTAT	1560
	GGCTGCTACT	GGGTGGCCCT	CCTCATGCTA	TATCTGGCCA	TCATCGCCCG	GCGATGTGGG	1620
	AAGAAGCCGG	AGCAGTACAG	CTTGGCTTTT	GCTGAGGTGT	GA		

20 Seq ID NO: 571 Protein sequence
Protein Accession #: NP_005320.1

	1	11	21	31	41	51	
25	MPVQLTTALR	VVGTSLSFALA	VLGGILAAYV	TGYQFIHTEK	HYLSFGLYGA	ILGLHLIIQS	60
	LPAPLEHRRM	RRAGQALKLP	SPRRGSVALC	IAAYQEDPDY	LRKCLRSAQR	ISFPDLKVVM	120
	VVDGNRQEDA	YMLDIFHEVL	GGTEQAGFFV	WRSNFHEAGE	GETEASLQEG	MDRVRDVVRA	180
	STFSICIMQKW	GGKREVMYTA	FKALGDSVDY	IQVCDSDTVL	PDACTIEMLR	VLEEDPQVGG	240
30	VGGDVQILNK	YDWSISFLSS	VRYWMAFNVE	RACQSYFGCV	QCISGPLGMY	RNSLLQGFLE	300
	DWYHQKFLGS	KCSFGDDRHL	TNRVLSLGYR	TKYTARSKCL	TETPTKYLRW	LNQQTWRSKS	360
	YFREWLYNSL	WFHKKHLNMT	YESVVTGFPF	FFLIATVIQL	FYRGRIWNIL	LFLLLTVQLVG	420
	IKATYACFL	RGNABEMISF	LYSLLYMSSL	LPAKIFAIAT	INKSGWGTSG	RKTIIVNFIG	480
	LIPVSIWVAV	LLGLLAYTAY	QDLEFSETEL	APLVSGAILY	GCVWVALLML	YLAIIRRCG	540
35	KKPEQYSLAP	AEV					

Seq ID NO: 572 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 148-7095

40	1	11	21	31	41	51	
	CACACATACG	CACGCACGAT	CTCACTTCGA	TCTATACACT	GGAGGATTAA	AACAAACAAA	60
	CAAAAAAACA	ATTTCTCTCG	CTCCCCCTCC	CTCTCCACTC	TGAGAAGCAG	AGGAGCCGCA	120
45	CGGCGAGGGG	CCGAGAGCCG	TCTGGAAATG	CGAATCCTAA	AGCGTTTCCT	CGCTTGCAAT	180
	CAGCTCCTCT	GTGTTTGGCG	CCTGGATTGG	GCTAATGGAT	ACTACAGACA	ACAGAGAAAA	240
	CTTGTGTAAG	AGATTGGCTG	GTCCTATACA	GGAGCACTGA	ATCAAAAAAA	TTGGGGAAAG	300
	AAATATCCAA	AGTGTTCATG	CCCAAAACAA	TCTCCTATCA	ATATTGATGA	AGATCTTACA	360
	CAAGTAAATG	TGAATCTTAA	GAAACTTAAA	TTTCAGGGTT	GGGATAAAAC	ATCATTGGAA	420
50	AACACATTCA	TTCATAACAC	TGGGAAAACA	GTGGAAATTA	ATCTCACTAA	TGACTACCGT	480
	GTGACGCGAG	AATGGTTCAGA	AATGGTGTTC	AAAGCAAGCA	AGATAACTTT	TCACTGGGGA	540
	AAATGCAATA	TGTCACTCTG	TGGATCAGAG	CATAGTTTAG	AAGGACAAAA	ATTTCCACTT	600
	GAGATGCAAA	TCTACTGCTT	TGATGCGGAC	CGATTTTCAA	GTTTTGAGGA	AGCAGTCAAA	660
	GGAAAAGGGA	AGTTAAGCTT	TTTATCCATT	TTGTTTGAGG	TTGGGACAGA	AGAAAATTTG	720
55	GATTTCAAAG	CGATTATTGA	TGGAGTCGAA	AGTGTTAGTC	GTTTTGGGAA	GCAGGCTGCT	780
	TTAGATCCAT	TCATACCTGT	GAACCTTCTG	CCAAACTCAA	CTGACAAGTA	TTACATTTAC	840
	AATGGCTCAT	TGCATCTCTC	TCCCTGCACA	GACACAGTTG	ACTGGATTGT	TTTTAAAGAT	900
	ACAGTTAGCA	TCTCTGAAAG	CCAGTTGGCT	GTTTTTGTG	AAGTTCTTAC	AATGCAACAA	960
60	TCTGGTTATG	TGATGCTGAT	GGACTACTTA	CAAAACAATT	TTGAGAGACA	ACAGTACAAG	1020
	TTCTCTAGAC	ACGTTTCTTC	CTCATACACT	GGAAAGGAAG	AGATTCTAGA	AGCAGTTTGT	1080
	AGTTCAGAAC	CAGAAAATGT	TCAGGCTGAC	CCAGAGAAAT	ATACCAGCCT	TCTTGTTACA	1140
	TGGGAAAGAC	CTCGAGTCGT	TTATGATACC	ATGATTGAGA	AGTTTGCAAT	TTTGTACCAG	1200
	CAGTTGGATG	TGATGGACAT	AACCAAGCAT	GAATTTTGA	CAGATGGCTA	TCAAGACTTG	1260
	GGTGTATTTC	TCAATAATTT	GCTACCCAAT	ATGAGTTATG	TTCTTCAGAT	AGTAGCCATA	1320
65	TGCACTAATG	GCTTATATGG	AAAATACAGC	GACCAACTGA	TTGTCGACAT	GCCTACTGAT	1380
	AATCCTGAAC	TTGATCTTTT	CCCTGAATTA	ATTGGAAGTC	AAGAAATAAT	CAAGGAGGAG	1440
	GAAGAGGGAA	AAGACATTGA	AGAAGGCGCT	ATTGTGAATC	CTGGTAGAGA	CAGTGCTACA	1500
	AACCAATCA	GGAAAAAGGA	ACCCAGAGAT	TCTACCACAA	CACACTACAA	TGCATAGGGG	1560
	ACGAAATACA	ATGAAGCCAA	GACTAACCGA	TCCCCAACAA	GAGGAAGTGA	ATTCTCTGGA	1620
70	AAGGGTGATG	TTCCCAATAC	ATCTTTAAAT	TCCACTTCCC	AACCAAGTAC	TAAATTAGCC	1680
	ACAGAAAAAG	ATATTTCTCT	GACTTCTCAG	ACTGTGACTG	AACTGCCACC	TCACACTGTG	1740
	GAAGGTACTT	CAGCCTCTTT	AAATGATGGC	TCTAAAAGTC	TTCTTAGATC	TCCACATATG	1800
	AACTTGTGCG	GGACTGCAGA	ATCCTTAAAT	ACAGTTTCTA	TAACAGAAAT	TGAGGAGGAG	1860
	AGTTTATTGA	CCAGTTTCAA	GCTTGATACT	GGAGCTGAAG	ATTCTTCAGG	CTCCAGTCCC	1920
75	GCAACTTCTG	CTATGCCATT	CATCTCTGAG	AACATATCCC	AAGGGTATAT	ATTTTCTCTC	1980
	GAAACCCAG	AGACAATTAAC	ATATGATGTC	CTTATACCAG	AATCTGCTAG	AAATGCTTCC	2040
	GAAGATTCAA	CTTCATCAGG	TTTCAAGAA	TCACTAAAGG	ATCCTTCTAT	GGAGGGAAAT	2100
	GTGTGGTTTC	TAGCTCTTAC	AGACATAACA	GCACAGCCCG	ATGTTGGATC	AGGCAGAGAG	2160
	AGCTTCTTCC	AGACTAATTA	CACGTGAGATA	CGTGTGATG	AATCTGAGAA	GACAACCAAG	2220
80	TCCTTTTCTG	CAGGCCAGT	GATGTCACAG	GGTCCCTCAG	TTACAGATCT	GGAAATGCCA	2280
	CATTATTCTA	CCTTTCTCTT	CTTCCCAACT	GAGGTAACAC	CTCATGCTTT	TACCCCATCC	2340
	TCCAGACAAC	AGGATTTGGT	CTCCACGGTC	AACGTGGTAT	ACTCGCAGAC	AACCCAACCG	2400
	GTATACAATG	GTGAGACACC	TCTTCAACCT	TCCTACAGTA	GTGAAGTCTT	TCCTCTAGTC	2460
	ACCCCTTTGT	TGCTTGACAA	TACAGATCCT	AACACTACCC	CTGCTGCTTC	AAGTAGTGAT	2520
	TCGGCCTTGC	ATGCTAGGCC	TGTATTTCCT	AGTGTGATG	TGTCATTGTA	ATCCATCTCT	2580
85	TCTTCTCTAT	ATGGTGACCT	TTTGCTTCCA	TTTCTCTCTG	CTTCTTTCAG	TAGTGAATTG	2640
	TTTCCCATC	TGATCAATAT	TTTCCCAATC	CTTCCCAAG	TTACTTCAGC	TACCGAGAGT	2700
	GATAAGGTGC	CCTTGCAATG	TTCTCTGCCA	GTGGCTGGGG	GTGATTGTCT	ATTAGAGCCC	2760

	AGCCTTGCTC	AGTATTCTGA	TGTGCTGTCC	ACTACTCATG	CTGCTTCAGA	GACGCTGGAA	2820
	TTTGGTAGTG	AATCTGGTGT	TCCTTTATAA	ACGCTTATGT	TTTCTCAAGT	TGAACCACCC	2880
	AGCAGTGATG	CCATGATGCA	TGCACGTTCT	TCAGGGCCTG	AACCTTCTTA	TGCCTTGTCT	2940
5	GATAATGAGG	GCTCCCAACA	CATCTTCACT	GTTTCTTACA	GTTCTGCAAT	ACCTGTGCAT	3000
	GATTCTGTGG	GTGTAACCTA	TCAGGGTTCC	TTATTTAGCG	GCCCTAGCCA	TATACCAATA	3060
	CCTAAGTCTT	CGTTAAATAAC	CCCAACTGCA	TCATTACTGC	AGCCTACTCA	TGCCCTCTCT	3120
	GGTGATGGGG	AATGGTCTGG	AGCCTCTTCT	GATAGTGAAT	TTCTTTTACC	TGACACAGAT	3180
	GGGCTGACAG	CCCTTAAACT	TTCTTCACCT	GTTTCTGTAG	CTGAATTTAC	ATATACAACA	3240
10	TCTGTGTTTG	GTGATGATAA	TAAGGCGCTT	TCTAAAAGTG	AAATAATATA	TGGAAATGAG	3300
	ACTGAACTGC	AAATTCCTTC	TTTCAATGAG	ATGGTTTACC	CTTCTGAAAG	CACAGTCATG	3360
	CCCAACATGT	ATGATAATGT	AAATAAGTTG	AATGCGTCTT	TACAAGAAAC	CTCTGTTTCC	3420
	ATTTCCTAGCA	CCAGGGGCAT	GTTTCCAGGG	TCCCTTGCTC	ATACCACCAC	TAAGGTTTTT	3480
	GATCATGAGA	TTAGTCAAGT	TCCAGAAAAT	AACTTTTCAG	TTCAACCTAC	ACATACTGTC	3540
15	TCTCAAGCAT	CTGGTGACAC	TTCGCTTAAA	CCTGTGCTTA	GTGCAAACTC	AGAGCCAGCA	3600
	TCCTCTGACC	CTGCTTCTAG	TGAAATGTTA	TCTCCTTCAA	CTCAGCTCTT	ATTTTATGAG	3660
	ACCTCAGCTT	CTTTTAGTAG	TGAAGTATTG	CTACAACCTT	CCTTTCAGGC	TTCTGATGTT	3720
	GACACCTTGC	TTAAAACTGT	TCTTCCAGCT	GTGCCAGTG	ATCCAATATT	GGTTGAAACC	3780
	CCCAAGTTTG	ATAAAATTAG	TTCTACAATG	TTGCATCTCA	TTGTATCAAA	TTCTGCTTCA	3840
20	AGTGAAAAA	TGCTGCACTC	TACATCTGTA	CCAGTTTTTG	ATGTGTCGCC	TACTTCTCAT	3900
	ATGCACCTCG	CTGCTCACTC	AGGTTTGACC	ATTTCTTATG	CAAGTGAGAA	ATATGAACCA	3960
	GTTTGTGTTA	AAAGTGAAAG	TTCCCAACAA	GTGGTACCTT	CTTTGTACAG	TAATGATGAG	4020
	TTGTTCCAAA	CGGCCAATTT	GGAGATTAAC	CAGGCCCATC	CCCCAAAAGG	AAGGCATGTA	4080
	TTTGCTACAC	CTGTTTATAT	AAATTGATGAA	CCATTAAATA	CACATAATAA	TAAGCTTATA	4140
25	CATTCCGATG	AAATTTTAAAC	CTCCACCAAA	AGTTCTGTGA	CTGGTAAGGT	ATTTGCTGGT	4200
	ATTCCAACAG	TTGCTTCTGA	TACATTGTGA	TCTACTGATC	ATTCTGTTCC	TATAGGAAAT	4260
	GGGCATGTTG	CCATTACAGC	TGTTTCTCCC	CACAGAGATG	GTTCTGTAAC	CTCAACAAGG	4320
	TTGCTGTTTC	CTTCTAAGGC	AACCTTCTGAG	CTGAGTCATA	GTGCCAAATC	TGATGCCGGT	4380
	TTAGTGGGTG	GTGGTGGAAG	TGGTGACACT	GATGATGATG	GTGATGATGA	TGATGATGAC	4440
30	AGAGGTAGTG	ATGGCTTATC	CATTATAAG	TGTATGTCAT	GCTCATCCTA	TAGAGAATCA	4500
	CAGGAAAAGG	TAATGAATGA	TTCAGACACC	CACGAAAACA	GTCTTATGGA	TCAGAATAAT	4560
	CCAATCTCAT	ACTCATCTAT	TGAGAATTCT	GAAGAAGATA	ATAGAGTCAC	AAGTGATATC	4620
	TCAGACAGTC	AAACTGTGAT	GGACAGAAGT	CCTGGTAAAT	CACCATCAGC	AAATGGGCTA	4680
	TCCCAAAAGC	ACAATGATGG	AAAAGAGGAA	AATGACATTC	AGACTGGTAG	TGCTCTGCTT	4740
35	CCTCTCAGCC	CTGATCTTAA	AGCATGGGCA	GTTCTGACAA	GTGATGAAGA	AAGTGGATCA	4800
	GGGCAAGGTA	CCTCAGATAG	CCTTAATGAG	AATGAGACTT	CCACAGATTT	CAGTTTGTGA	4860
	GACACTAATG	AAAAAGATGC	TGATGGGATC	CTGGCAGCAG	GTGACTCAGA	AATAACTCCT	4920
	GGATTCCAC	AGTCCCAAC	ATCATCTGTT	ACTAGCGAGA	ACTCAGAAGT	GTTCCACGTT	4980
	TCAGAGGAG	AGGCCGATTA	TAGTAGCCAT	GAGTCTCGTA	TTGGTCTAGC	TGAGGGGTTG	5040
40	GAATCCGAGA	AGAAGGCAGT	TATACCCCTT	GTGATCGTGT	CAGCCCTGAC	TTTTATCTGT	5100
	CTAGTGGTTC	TTGTGGGTAT	TCTCATCTAC	TGGAGGAAAT	GCTTCCAGAC	TGCACACTTT	5160
	TACTTAGAGG	ACAGTACATC	CCCTAGAGTT	ATATCCACAC	CTCCAACACC	TATCTTTCCA	5220
	ATTTCAGATG	ATGTCGGAGC	AATTCCAATA	AAGCACTTTC	CAAAGCATGT	TGCAGATTTA	5280
	CATGCAAGTA	CTGGGTTTAC	TGAAGAAATTT	GAGACACTGA	AAGAGTTTTA	CCAGGAAAGT	5340
45	CAGAGCTGTA	CTGTTGACTT	AGGTATTACA	GCAGACAGCT	CCAACCAACC	AGACACAAG	5400
	CACAAGAATC	GATACATAAA	TATCGTTGCC	TATGATCATA	GCAGGGTTAA	GCTAGCACAG	5460
	CTTGCTGAAA	AGGATGGCAA	ACTGACTGAT	TATATCAATG	CCAATTATGT	TGATGGCTAC	5520
	AACAGACCAA	AAGCTTATAT	TGCTGCCCAA	GGCCCACTGA	AATCCACAGC	TGAAGATTTT	5580
	TGGAGAATGA	TATGGGAACA	TAATGTGGAA	GTTATTGTCA	TGATAACAAA	CCTCGTGGAG	5640
50	AAAGGAAGGA	GAAATATGTA	TCAGTACTGG	CCTGCCGATG	GGAGTGAGGA	GTACGGGAAC	5700
	TTTCTGGTCA	CTCAGAAGAG	TGTGCAAGTG	CTTGCCCTATT	ATACTGTGAG	GAATTTTACT	5760
	CTAAGAAACA	CAAAAATAAA	AAAGGGCTCC	CAGAAAGGAA	GACCCAGTGG	ACGTGTGGTC	5820
	ACACAGTATC	ACTACACGCA	GTGGCCGTGAC	ATGGGAGTAC	CAGAGTACTC	CCTGCCAGTG	5880
	CTGACCTTTG	TGAGAAAAGG	AGCCTATGCC	AAGCGCCATG	CAGTGGGGCC	TGTTGTCTGT	5940
55	CACCTGCAGT	CTGGAGTTGG	AAGAACAGGC	ACATATATTG	TGCTAGACAG	TATGTTGCAG	6000
	CAGATTCAAC	ACGAAGGAAC	TGTCAACATA	TTTGGCTTCT	TAAACACAT	CCGTTCCAAA	6060
	AGAAATATT	TGTTACAAAC	TGAGGAGCAA	TATGTCTTCA	TTTATGATAC	ACTGGTTGAG	6120
	GCCATACTTA	GTAAGAAAC	TGAGGTGCTG	GACAGTCATA	TTTATGCCCTA	TGTTAATGCA	6180
	CTCCTCATTC	CTGGACACAG	AGGCAAAACA	AAGCTAGAGA	AACAATTCCA	GCTCCTGAGC	6240
60	CAGTCAAAATA	TACAGCAGAG	TGACTATTCT	GCAGCCCTAA	AGCAATGCAA	CAGGGAAGAG	6300
	AATCGAATCT	CTTCTATCAT	CCCTGTGGAA	AGATCAAGGG	TTGGCATTTC	ATCCCTGAGT	6360
	GGAGAAGGCA	CAGACTACAT	CAATGCCCTCC	TATATCATGG	GCTATTACCA	GAGCAATGAA	6420
	TTTCATCATTA	CCAGCACCCC	TCTCCTTCAT	ACCATCAAGG	ATTTCTGGAG	GATGATATGG	6480
	GACCATAATG	CCCAACTGGT	GGTTATGATT	CCTGATGGCC	AAAACATGGC	AGAAGATGAA	6540
65	TTTGTTTACT	GGCCAAATAA	AGATGAGCCT	ATAAATGTG	AGAGCTTTAA	GGTCACTCTT	6600
	ATGGCTGAAG	AACACAATAG	TCTATCTAAT	GAGGAAAAAC	TTATAATTCA	GGACTTTATC	6660
	TTAGAAGCTA	CACAGGATGA	TTATGTACTT	GAAGTGAGGC	ACTTTCAGTG	TCCTAAATGG	6720
	CCAAATCCAG	ATAGCCCCAT	TAGTAAAACT	TTTGAACTTA	TAAGTGTTAT	AAAAGAAGAA	6780
	GCTGCCAATA	GGGATGGGCC	TATGATTGTT	CATGATGAGC	ATGGAGGAGT	GACGGCAGGA	6840
70	ACTTTCGTG	CTCTGACAAC	CCTTATGCAC	CAACTAGAAA	AAGAAAATTC	CGTGGATGTT	6900
	TACCAGGTAG	CCAAGATGAT	CAATCTGATG	AGGCCAGGAG	TCCTTGCTGA	CATTGAGCAG	6960
	TATCAGTTTC	TCTACAAAGT	GATCCTCAGC	CTTGTGAGCA	CAAGGCAGGA	AGAGAATCCA	7020
	TCCACCTCTC	TGGACAGTAA	TGGTGCAGCA	TTGCCTGATG	GAAATATAGC	TGAGAGCTTA	7080
	GAGTCTTTAG	TTTAAACAG	AAAGGGGTGG	GGGGACTCAC	ATCTGAGCAT	TGTTTTCTCT	7140
75	TTCTTAAAT	TAGGCAAGAA	AAACAGTCTA	GTTCTGTTAT	CTGTGATTTT	CCCATCACCT	7200
	GACAGTAAT	TTTATGACAT	AGGATTCTGC	CGCCAAATTT	ATATCATTAA	CAATGTGTGC	7260
	CTTTTTCGAA	GACTTGTAAAT	TACTTATTA	TGTTTGAAT	AAAATGATTG	AATTTTACAG	7320
	TATTTCTAAG	AATGGAATTT	TGTTATTTT	TTCTGTATTG	ATTTTAAACG	AAAATTTCAA	7380
	TTTATAGAGG	TTAGGAATTC	CAAACTACAG	AAAATGTTTG	TTTTTAGTGT	CAAATTTTAA	7440
80	GCTGTATTTG	TAGCAATTAT	CAGGTTTGCT	AGAAAATATA	CTTTTAATAC	AGTAGCCGTG	7500
	AAATAAAACA	CTCTTCCATA	TGATATTCAA	CATTTTACAA	CTGCAGTATT	CACCTAAAGT	7560
	AGAAATAATC	TGTTACTTAT	TGTAAATACT	GCCCTAGTGT	CTCCATGGAC	CAAATTTATA	7620
	TTTATAATTG	TAGATTTTTA	TATTTTACTA	CTGAGTCAAG	TTTTCTAGTT	CTGTGTAATT	7680
	GTTTAGTTTA	TAGACGTAGT	TCAATTAGCTG	GTCTTACTCT	ACCAAGTTTC	TGACATTGTA	7740
	TTGTGTTACC	TAAGTCATTA	ACTTTGTTTC	AGCATGTAAT	TTTAACTTTT	GTGGAATAA	7800
85	GAAATACCTT	CATTTTGAAG	GAAGTTTFTA	TGAGAATAAC	ACCTTACCAA	ACATTTGTCA	7860
	AATGGTTTTT	ATCCAAGGAA	TTGCAAAAT	AAATATAAAT	ATTGCCATTA	AAAAAATAA	7920
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Seq ID NO: 573 Protein sequence:
Protein Accession #: Eos sequence

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	QSPINIDEDL	TQVNVNLLKKL	KFQGWDKTSL	ENTFIHNTGK	TVEINLTNDY	RVSGGVSEMV	120
10	FKASKITFWH	GKCNMSSDGS	EHSLEGQKFP	LEMQIYCFDA	DRFSSPEEAV	KGKGLRLALS	180
	ILFEVGTEN	LDFKAIIDGV	ESVSRFGKQA	ALDPPILLNL	LPNSTDKYVI	YNGSLTSPPC	240
	TDTVDWIVFK	DTVSISSSQL	AVFCEVLTMO	QSGYVLMMDY	LQNNFREQQY	KFSRQVFSSY	300
	TGKEIEHEAV	CSSEFENVQA	DPENYTSLLV	TWERPRVVDY	TMIEKFAVLY	QQLDGEDQTK	360
	HEFLTGDYQD	LGAILNNLLP	NMSYVLQIVA	ICTNGLYGKY	SDQLIVDMPT	DNPELDLPFE	420
	LIGTEEIIKE	EEEGKDIIEG	AIVNPGRDSA	TNQIRKKEPQ	ISTTTHYNRI	GTKYNEAKTN	480
15	RSPTRGSEFS	GKGDPVNTSL	NSTSQPVTKL	ATEKDISLTS	QTVTELPPhT	VEGTASASLND	540
	GSKTVLRSPH	MNLSGTAESL	NTVSITEYEE	ESLLTSFKLD	TGAEDSSGSS	PATSAIPFIS	600
	ENISQGYIFS	ENSPETTYD	VLIPESARNA	SEDSTSSGSE	ESLKDPSMEG	NVWFPSSTDI	660
	TAQPDVSGGR	ESFLQTNYTE	IRVDESEKTT	KSPSAGPVMS	QGPSVTDLEM	PHYSTFAYFP	720
	TEVTPhAFTP	SSRQDLVST	VNVVYSQTTQ	PVYNGETPLQ	PSYSSEVFPL	VTPLLLDNQI	780
20	LNTTPAASSS	DSALHATPVF	PSVDVSFESI	LSSYDGAPLL	PFSSASFSSS	LFRHLHTVSO	840
	ILPQVTSATE	SDKVPLHASL	PVAGGDLLE	PSLAQYSDVL	STTHAASETL	EFSGESGVLY	900
	KTLMPSQVEP	PKSDAMHAR	SSGPEPSYAL	SDNEGSQHIF	TVSYSSAIPV	HDSVGVTTYQG	960
	SLFSFGSHIP	ISSSLITPT	ASLLQPTHAL	SGDGEWSGAS	SDSEFLLPDT	DGLTALNISS	1020
	PVSVAEFTYT	TSVFGDDNKA	LSKSEIIYGN	ETELQIPSPN	EMVYPSESTV	MPNMYDNVVK	1080
25	LNASLQETSV	SISSTKGMFP	GSLAHTTTKV	FDHEISQVPE	NNFSVQPTH	VSQASGDTSL	1140
	KPVLANSSEP	ASSDPASSEM	LSPSTQLLFY	ETSASFSTEV	LLQPSFQASD	VDTLKTVLP	1200
	AVPSDPIIVE	TPKVDKISST	MLHLIVNSA	SSENMLHSTS	VPVFDVSPTS	HMSASLQGL	1260
	TISYASEKYE	PVLLKSESSH	QVVPISLYSD	ELFQTANLEI	NQAHPPKGRH	VFATPVLSID	1320
	EPLNTLINKL	IHSDEILTST	KSSVTGKVFA	GIPTVASDTP	VSTDHSPVIG	NGHVAITAVS	1380
30	PHRDGSVTST	KLLFPKSKATS	ELSHSAKSDA	GLVGGGEDGD	TDDGDGDDDD	DRGSDGLSIH	1440
	KCMSCSSYRE	SQEKVMNDS	THENSIMDQN	NPISYSLSEN	SEEDNRVTSV	SSDSQTMMDR	1500
	SPGKSPSANG	LSQKHNDGKE	ENDIQTSAL	LPLSPESKAW	AVLTSDEESG	SGQGTSDSLN	1560
	ENETSTDFSF	ADTNEKDADG	ILAAGDSEIT	PGFPQSPTSS	VTSENSEVFH	VSEAEASNSS	1620
	HESRIGLAEG	LESEKKAVIP	LVIVSALTFI	CLVVLVGILI	YWRKCFQTAH	FYLEDSTSPR	1680
35	VISTPPTPIF	PISDDVGAIP	IKHFPKHVAD	LHASSGFTEE	FETLKEFYQE	VQSCITVDLGI	1740
	TADSSNHDPN	KHKRYNINIV	AYDHSRVKLA	QLAEKDGKLT	DYINANYVDG	YNRPKAYIAA	1800
	QGPKLSTAED	FLRWIWEHNV	EVIVMITNLV	EKGRRKCDQY	WPADGSEEEY	NFLVTQKSVQ	1860
	VLAYTYVRNF	TLRNTKIKKG	SQGRPSGRV	VTQYHYTQWP	DMGVPEYSLP	VLTFVRKAAY	1920
40	AKRHAVGPVV	VHCASAGVRT	GTIVVLDSML	QQIQHEGTVN	IFGFLKHIRS	QRNYLVQTEE	1980
	QYVFIHDTLV	EAILSKETEV	LDSHIHAYVN	ALLIPGPAGK	TKLEKQFQLL	SQSNIQQSDY	2040
	SAALKQCNRE	KNRTSSIIIPV	ERSRVGISSL	SGEGTDYINA	SYIMGYQSN	EFIITQHPLL	2100
	HTIKDFWRMI	WDHNAQLVVM	IPDQGNMAED	EFVYVWPNKDE	PINCESFKVT	LMAEEHKCLS	2160
	NEEKLIQDPF	ILEATQDDYV	LEVRHFQCPK	WPNPDSPIK	TFELISVIKE	EAANRDGPMI	2220
45	VHDEHGGVTA	GTFCALITLM	HQLEKENSVD	VYQVAKMINL	MRPGVFADIE	QYQFLYKVL	2280
	SLVSTRQEN	PSTSLDSNGA	ALPDGNIAES	LESVL			

Seq ID NO: 574 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 148-4518

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55	CGGCGAGGGG	CGGCAGACCG	TCTGGAAATG	CGAATCCTAA	AGCGTTTCCT	CGCTTGCAAT	180
	CAGCTCCTCT	TGTGTTGCCG	CCTGGATTGG	GCTAATGGAT	ACTACAGACA	ACAGAGAAAA	240
	CTTGTTGAAG	AGATTGGCTG	GTCCTATACA	GGAGCACTGA	ATCAAAAAAA	TTGGGGAAAG	300
	AAATATCCAA	CATGTAATAG	CCCAAAACAA	TCTCCTATCA	ATATTGATGA	AGATCTTACA	360
60	CAAGTAAATG	TGAATCTTAA	GAAACTTAAA	TTTCAGGGTT	GGGATAAAAC	ATCATTTGAA	420
	AACACATTCA	TTCATAACAC	TGGGAAAACA	GTGGAAATTA	ATCTCACTAA	TGACTACCGT	480
	GTCAGCGGAG	GAGTTTCAGA	AATGGTGTTC	AAAGCAAGCA	AGATAACTTT	TCACTGGGGA	540
	AAATGCAATA	TGTCATCTGA	TGGATCAGAG	CATAGTTTAG	AAGGACAAAA	ATTTCCACTT	600
	GAGATGCAAA	TCTACTGCTT	TGATCGCGAC	CGATTTTCAA	GTTTGTAGGA	AGCAGTCAAA	660
	GGAAAAGGGA	AGTTAAGAGC	TTTATCCATT	TTGTTTGAGG	TTGGGACAGA	AGAAAATTGT	720
65	GATTTCAAAG	CGATTATTGA	TGGAGTCGAA	AGTGTTAGTC	GTTTGGGAA	GCAGGCTGCT	780
	TTAGATCCAT	TCATAGCTTT	GAACCTTCTG	CCAACTCAA	CTGACAAGTA	TTACATTTAC	840
	AATGGCTCAT	TGACATCTCC	TCCTTGACCA	GACACAGTTG	ACTGGATTGT	TTTTAAAGAT	900
	ACAGTTAGCA	TCTCTGAAAG	CCAGTTGGCT	GTTTTTGTG	AAGTTCCTAC	AATGCAACAA	960
70	TCTGGTTATG	TCATGCTGAT	GGACTACTTA	CAAAACAATT	TTGAGAGCA	ACAGTACAAG	1020
	TTCTCTAGAG	AGGTGTTTTT	CTCATACACT	GGAAAGGAAG	AGATTCTATG	AGCAGTTTGT	1080
	AGTTCTAGAAC	CAGAAAATGT	TCAGGCTGAC	CCAGAGAATT	ATACCAGCCT	TCTTGTATCA	1140
	TGGGAAAGAC	CTCGAGTCGT	TTATGATACC	ATGATTGAGA	AGTTTGCACT	TTGTACCAG	1200
	CAGTTGGATG	GAGAGGACCA	AACCAAGCAT	GAATTTTTGA	CAGATGGCTA	TCAAGACTTG	1260
75	GGTGCTATTCT	TCAATAATTT	GACTACCAAT	ATGAGTTATG	TTCTTCAGAT	AGTAGCCATA	1320
	TGCACTAATG	GCTTATATGG	AAAATACAGC	GACCAACTGA	TTGTCGACAT	GCCTACTGAT	1380
	AATCCTGAAC	TTGATCTTTT	CCCTGAATTA	ATTGGAAGTG	AAGAAATAAT	CAAGGAGGAG	1440
	GAAGAGGGAA	AAGACATTTA	AGAAGGCCTG	ATTGTGAATC	CTGGTAGAGA	CAGTGCTACA	1500
	AACCAATCA	GGAAGGAGGA	ACCCAGATT	TCTACCACAA	CACACTACAA	TCGCATAGGG	1560
	ACGAAATACA	ATGAGAGCAA	GACTAACCAG	TCCCCAACAA	GAGGAAGTGA	ATTCTCTGGA	1620
80	AAGGTGATG	TTCCCAATTA	ATCTTTAAAT	TCCACTTCCC	AACCACTCAC	TAAATTAGCC	1680
	ACAGAAAAG	ATATTTCTCT	GACTTCTCAG	ACTGTGACTG	AACTGCCACC	TCACACTGTG	1740
	GAAGGTACTT	CAGCCTCTTT	AAATGATGGC	TCTAAAACCT	TTCTTAGATC	TCCACATATG	1800
	AACTTGTGCG	GGACTGACGA	ATCTTTAAAT	ACAGTTTCTA	TAACAGAAAT	TGAGGAGGAG	1860
	AGTTTATTGA	CCAGTTTCAA	GCTTGATACT	GGAGCTGAAG	ATTCTTCAGG	CTCCAGTCCC	1920
85	GCACTTCTCT	CTATCCCATC	CATCTCTGAG	AACATATCCC	AAGGGTATAT	ATTTTCTCTC	1980
	GAAAACCCAG	AGACAATATG	ATATGATGTC	CTTATACCA	AATCTGCTAG	AAATGCTTCC	2040
	GAAGATTCAA	CTTCATCAGG	TTCAGAAGAA	TACTAAAGG	ATCCTTCTAT	GGAGGGAAAT	2100

	GTGTGGTTTC	CTAGCTCTAC	AGACATAACA	GCACAGCCCG	ATGTTGGATC	AGGCAGAGAG	2160
	AGCTTTCTCC	AGACTAATTA	CACTGAGATA	CGTGTGATG	AATCTGAGAA	GACAACCAAG	2220
	TCCTTTCTCG	CAGGCCCACT	GATGTACAG	GGTCCCTCAG	TTACAGATCT	GGAAATGCCA	2280
5	CATTATTCTA	CCTTTGCCTA	CTTCCCAACT	GAGGTAACAC	CTCATGCTTT	TACCCCATCC	2340
	TCCAGACAAAC	AGGATTGGT	CTCCACGGTC	AACGTGGTAT	ACTCGCAGAC	AACCCAACCG	2400
	GTATACAATG	CAGAGGCCAG	TAATAGTAGC	CATGAGTCTC	GTATTGGTCT	AGCTGAGGGG	2460
	TTGGAATCCG	AGAAGAAGGC	AGTTATACCC	CTTGTGATCG	TGTCAGCCCT	GACTTTTATC	2520
	TGCTCTAGTGG	TTCTTGTGGG	TATTTCTATC	TACTGGAGGA	AATGCTTCCA	GACTGCACAC	2580
10	TTTTACTTAG	AGGACAGTAC	ATCCCCCTAGA	GTATATATCCA	CACCTCCAAC	ACCTATCTTT	2640
	CCAATTTTCA	ATGATGTCCG	AGCAATTCCA	ATAAAGCACT	TTCCAAAGCA	TGTTGCAGAT	2700
	TTACATGCAA	GTAGTGGGTT	TACTGAAGAA	TTTGAGACAC	TGAAAGAGTT	TTACCAGGAA	2760
	GTGCAGAGCT	GTACTGTTGA	CTTAGGTATT	ACAGCAGACA	GCTCCAACCA	CCCAGACAAC	2820
	AAGCACAAGA	ATCGATACAT	AAATATCGTT	GCCTATGATC	ATAGCAGGTT	TAAGCTAGCA	2880
15	CAGCTTGTCTG	AAAAGGATGG	CAAACTGACT	GATTATATCA	ATGCCAATTA	TGTTGATGGC	2940
	TACACAGAC	CAAAAGCTTA	TATTGCTGCC	CAAGGCCAC	TGAAATCCAC	AGCTGAAGAT	3000
	TTCTGGAGAA	TGATATGGGA	ACATAATGTG	GAAGTTATTG	TCATGATAAC	AAACCTCGTG	3060
	GAGAAAGGAA	GGAGAAATAG	TGATCAGTAC	TGGCCTGCCG	ATGGGAGTGA	GGAGTACGGG	3120
	AACTTTCTGG	TCACCTCAGAA	GAGTGTGCAA	GTGCTTGCCCT	ATTATACTGT	GAGGAATTTT	3180
20	ACTCTAAGAA	ACACAAAAAT	AAAAAAGGGC	TCCCAGAAAG	GAAGACCCAG	TGGACGTGTG	3240
	GTACACAGAT	ATCATTACAC	GCAGTGGCCT	GACATGGGAG	TACCAGAGTA	CTCCCTGCCA	3300
	GTGCTGACCT	TTGTGAGAAA	GGCAGCCTAT	GCCAAGCGCC	ATGCAGTGGG	GCCTGTTGTC	3360
	GTCCACTGCA	GTGCTGGAGT	TGGAAGAAC	GGCACATATA	TTGTGCTAGA	CAGTATGTTG	3420
	CAGCAGATTG	AACACGAGG	AACGTGCAAC	ATATTTGGCT	TCTTAAACCA	CATCCGTTCA	3480
25	CAAAGAAATT	ATTTGGTACA	AACGTAGGAG	CAATATGTCT	TCATTATGA	TACACTGGTT	3540
	GAGGCCATAC	TTAGTAAAGA	AACGTAGGAG	CTGGACAGTC	ATATTCATGC	CTATGTTAAT	3600
	GCATCTCTCA	TTCTTGGACC	AGCAGGCAAA	ACAAAGCTAG	AGAAACAATT	CCAGCTCCTG	3660
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	AAGAATCGAA	CTTCTTCTAT	CATCCCTGTG	GAAAGATCAA	GGGTTGGCAT	TTTATCCCTG	3780
30	AGTGGAGAAG	CTTCTTCTAT	CATCAATGCC	TCTTATATCA	TGGGCTAATTA	CCAGAGCAAT	3840
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	CTTATGGCTG	AAGAACACAA	ATGCTATCT	AATGAGGAAA	AACCTTAAT	TCAGGACTTT	4080
35	ATCTTAGAAG	CATACACAGG	TGATTATGTA	CTTGAAGTGA	GGCACTTTCA	GTGCTCTAAA	4140
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	GGAACTTTCT	GTGCTCTGAC	AACCTTATG	CACCAACTAG	AAAAAGAAAA	TTCCGTGGAT	4320
	GTTTACCAGG	TAGCCAAAGT	GATCAATCTG	ATGAGGCCAG	GAGTCTTTGC	TGACATTGAG	4380
40	CAGTATCAGT	TTCTCTACAA	AGTGATCCTC	AGCCTTGCTG	GCACAAGGCA	GGAAGAGAAT	4440
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	CCTGACAGTA	ACTTTTATGA	CATAGGATTC	TGCCGCCAAA	TTTATATCAT	TAACAATGTG	4680
45	TGCTTTTGTG	CAAGTACTGT	AATTACTTAA	TTATGTTTGA	ACTAAAATGA	TGGAATTTTA	4740
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50	AGTAGAAATA	ATCTGTACTT	TATGTAAAT	ACTGCCCTAG	TGCTCTCATG	GACCAAAATTT	5040
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	GTATTTGTGT	ACCTAAGTGA	TTAATTTTGT	TTTCTCATGT	AATTTTAACT	TTTGTGGAAA	5220
	ATAGAAATAC	CTTCATTTTG	AAAGAAGTTT	TTATGAGAAT	AACACCTTAC	CAACATTGT	5280
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Seq ID NO: 575 Protein sequence:
Protein Accession #: Eos sequence

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	FKASKITFHW	GKCNMSSDGS	EHSLEGQKFP	LEMQIYCFDA	DRFSFEEAV	KGKGLRLALS	180
	ILFEVGTEN	LDFKAIIDGV	ESVSRFGKQA	ALDPFILLNL	LPNSTDKYI	YNGSLTSPPC	240
	TDTVDWIVFK	DTVSISESQL	AVFCEVLTMQ	QSGYVMLMDY	LQNNFREQQY	KFSRQVFSY	300
	TGKEEIHFAV	CSSEPENVQA	DPENYTSLLV	TWERPRVVDY	TMIEKFAVLV	QQLDGEDQTK	360
70	HEFLTDGYQD	LGAILNNLLP	NMSYVLQIVA	ICTNGLYGKY	SDQLIVDMPT	DNPELDLPPE	420
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	RSPTRGSEFS	GKGDVPNTSL	NSTSQPVTKL	ATEKDLSLTS	QVTTELPFHT	VEGTSASLND	540
	GSKTVLRSFH	MNLSGTAEAL	NTVSITEYEE	ESLLTSFKLD	TGAEDSSGSS	PATSAIPFIS	600
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	TEVTPHAFPT	SSRQQLVST	VNVVYSQTTQ	PVYNAEASNS	SHESTRIGLAE	GLESEKKAVI	780
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	PIKHPFKHVA	DLHASSGTFE	EPETLKEFYQ	EVQSCTVDLG	ITADSSNHDP	NKHQRYINI	900
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80	VEVIVMITNL	VEKGRRKCDQ	YWPADGSEFY	GNFLVTQKSV	QVLAAYTVRN	FTLRNTKIKK	1020
	GSQGRPSGR	VVTQYHYTQW	PDGMVPEYSL	PULTFVRKAA	YAKRHAVGPV	VVHCSAGVGR	1080
	TGTYIVLDSM	LQQIQHEGTV	NIFGFLKHIR	SQRNYLVQTE	EQYVFIHDTL	VEAILSKETE	1140
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85	VERSRVGISS	LSGEGTDYIN	ASYIMGYYSQ	NEFIITQHPL	LHTIKDFWRM	IWDHNAQLVV	1260
	MIPDQGNMAE	DEFVYWPNDK	EPINCESFKV	TLMAEEHKCL	SNEKLIQD	FILEATQDDY	1320
	VLEVRHFCQP	KWNPDPSPIS	KTFELISVIK	EEAANRDGPM	IVHDEHGGVT	AGTFALCTL	1380
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Seq ID NO: 576 DNA sequence
Nucleic Acid Accession #: EOS sequence
Coding sequence: 148-4494

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	CAGCTCCTCT	GTGTTTGCCG	CCTGGATTGG	GCTAATGGAT	ACTACAGACA	ACAGAGAAAA	240
	CTTGTTGAAG	AGATTGGCTG	GTCCTATACA	GGAGCACTGA	ATCAAAAAAA	TTGGGGAAAG	300
	AAATATCCAA	CATGTAATAG	CCCCAAACAA	TCTCCTATCA	ATATTGATGA	AGATCTTACA	360
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	AACACATTCA	TTCATAACAC	TGGGAAACAA	GTGGAAATTA	ATCTCACTAA	TGACTACCGT	480
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	AAATGCAATA	TGTCACTTGA	TGGATCAGAG	CATAGTTTAG	AAGGACAAAA	ATTTCCACTT	600
	GAGATGCAAA	TCTACTGCTT	TGATGCAGAC	CGATTTTCAA	GTTTGTAGGA	AGCAGTCAAA	660
20	GGAAAAGGGA	AGTTAAGAGC	TTTATCCATT	TTGTTTGAGG	TTGGGACAGA	AGAAAAATTG	720
	GATTTCAAAG	CGATTATTGA	TGGAGTCGAA	AGTGTTAGTC	GTTTGGGAA	CGAGGCTGCT	780
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 Protein Accession #: EOS sequence

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Seq ID NO: 578 DNA sequence
 Nucleic Acid Accession #: EOS sequence
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Protein Accession #: EOS .sequence

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Seq ID NO: 580 DNA sequence
Nucleic Acid Accession #: EOS sequence
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Seq ID NO: 581 Protein sequence:
 Protein Accession #: EOS sequence

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Seq ID NO: 583 Protein sequence
 Protein Accession #: NP_002842.1

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Protein Accession #: NP_005679.1

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Seq ID NO: 586 DNA sequence
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 GCTGAATGGA TGCTGCAGAT GCGGGGCCAG GGGGCCGGAG AGCCGCCTGC TTGAGTTCTA 360
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 GGATGCCCCA CCGCTTCCCG TGCCAGGGGT GCTTCTGAAG GAGTTCAGT TGTCCGGCAA 480
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 CTGTCTCCAG CAGCTTTCCT TGTGTATGTG GATCACGCAG TGCTTCTGCG CCGTGTTTT 600
 GGCTCAGCCT CCCTCAGGGC AGAGGCGCTA AGCCAGCCT GCGCGCCCTT CCTAGGTCAT 660
 GCCTCTCTCC TCGGGAATG GTCCAGCAC GAGTGGCCAG TGCATTGTGG GGGCCTGATT 720
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Seq ID NO: 587 Protein sequence
 Protein Accession #: NP_001318.1

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Seq ID NO: 588 DNA sequence
 Nucleic Acid Accession #: Eos sequence
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 TAGGTCATGC CTCCTCCCTC AGGGAATGGT CCCAGCACGA GTGGCCAGTT CATTGTGGGG 540
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 CTGAGCTA

Seq ID NO: 589 Protein sequence
 Protein Accession #: Eos sequence

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 FLPLVLAQAP SQRR

Seq ID NO: 590 DNA sequence
 Nucleic Acid Accession #: NM_005562.1
 Coding sequence: 90..3671

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 GCTTCTCGCT CCTCTGCCCC GCAGCCCGGG CCACCTCCAG GAGGGAAGTC TGTGATTGCA 180
 ATGGGAAGTC CAGGCAGTGT ATCTTTGATC GGGAACTTCA CAGACAACT GGTAAATGGAT 240
 TCCGCTGCCT CAACTGCAAT GACAACTAG ATGGCATTCA CTGCGAGAAG TGCAAGAATG 300
 GCTTTTACCG GCACAGAGAA AGGGACCGCT GTTTGCCCTG CAATTGTAACT TCCAAGGTT 360
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 CCAGATGCGA CCGATGCTGC CCAGGCTTCC ACATGCTCAC GGATGCGGGG TGCACCCAAG 480
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 TTCAACAAGA TGCTGAGTGC TGGAAAGGCTG TCCAACGAAA TGGGTCTCCT GCAAAGCTCC 780
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	GTGCTGGTCT	ACGGATCACA	GCTCCCTTGA	TGCCACTTGG	CAAGACACTG	CCTTGTGGGC	1020
5	TCACCAAGAC	TTACACATTC	AGGTTAAATG	AGCATCCAAG	CAATAATTGG	AGCCCCAGC	1080
	TGAGTTACTT	TGAGTATCGA	AGGTTACTGC	GGAATCTCAC	AGCCCTCCGC	ATCCGAGCTA	1140
	CATATGGAGA	ATACAGTACT	GGGTACATTG	ACAATGTGAC	CCTGATTTC	GCCCGCCCTG	1200
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10	GCACCTGTAT	TCCTTGTAA	TGTCAAGGGG	GAGGGGCTTG	TGATCCAGAC	ACAGGAGATT	1380
	GTTATTTCAGG	GGATGAGAA	CCTGACATTG	AGTGATGTGA	CTGCCCAATT	GGTTTCTACA	1440
	ACGATCCGCA	CGACCCCGCG	AGCTGCAAGC	CATGTCCCTG	TCATAACGGG	TTGAGCTGCT	1500
	CAGTGATGCC	GGAGACGGAG	GAGGTGGTGT	GCAATAACTG	CCCTCCCGGG	GTACCCGGTG	1560
	CCCGCTGTGA	GCTCTGTGCT	GATGGCTACT	TTGGGGACCC	CTTGTGGTGA	CATGGCCAG	1620
	TGAGGCCCTTG	TGAGCCCTGT	CAATGCAACA	ACAATGTGGA	CCCCAGTGCC	TCTGGGAATT	1680
15	GTGACCGGCT	GACAGGCAGG	TGTTTGAAGT	GTATCCACAA	CACAGCCGGC	ATCTACTGCG	1740
	ACCACTGCAA	AGCAGGCTAT	TTGGGGGACC	CATTGGCTCC	CAACCCAGCA	GACAAGTGTG	1800
	GAGCTTGCAA	CTGTAAACCC	ATGGGCTCAG	AGCCTGTAGG	ATGTGGAAGT	GATGGCACCT	1860
	GTGTTTGCAA	GCCAGGATT	GGTGGCCCCA	ACTGTGAGCA	TGGAGCATTG	AGCTGTCCAG	1920
	CTTGCTATAA	TCAAGTGAAG	ATTGAGATGG	ATCAGTTTAT	GCAGCAGCTT	CAGAGAATGG	1980
20	AGGCCCTGAT	TTCAAAGGCT	CAGGGTGGTG	ATGGAGTAGT	ACCTGATACA	GAGCTGGAAG	2040
	GCAGGATGCA	GCAGGCTGAG	CAGGCCCTTC	AGGACATTCT	GAGAGATGCC	CAGATTTCAG	2100
	AAGGTGCTAG	CAGATCCCTT	GGTCTCCAGT	TGGCCAAGGT	GAGGAGCCAA	GAGAACAGCT	2160
	ACCAGAGCCG	CCTGATGATG	CTCAAGATGA	CTGTGGAAG	AGTTCCGGGT	CTGGGAAGTC	2220
25	AGTACCAGAA	CCGAGTTCGG	GATACTCACA	GGCTCATCAC	TCAGATGCAG	CTGAGCCTGG	2280
	CAGAAAGTGA	AGCTTCCCTG	GGAAACACTA	ACATTCTCTG	CTCAGACCAC	TACGTGGGGC	2340
	CAAAATGGCTT	TAAAAGTCTG	GCTCAGGAGG	CCACAAGATT	AGCAGAAAGC	CACGTTGAGT	2400
	CAGCCAGTAA	CATGGAGCAA	CTGACAAGGG	AAACTGAGGA	CTATTCCAAA	CAAGCCCTCT	2460
	CACCTGGTGG	CAAGGCCCTG	CATGAAGGAG	TGGGAAGCGG	AAGCGGTAGC	CCGGAAGGTTG	2520
30	CTGTGGTGCA	AGGGCTTGTG	GAAAAATTGG	AGAAAAACCA	GTCCTGGGCC	CAGCAGTTGA	2580
	CAAGGGAGGC	CAGTCAAGCG	GAAATTGAAG	CAGATAGGTC	TTATCAGCAC	AGTCTCCGCC	2640
	TCCTGGATTG	AGTGTCTCGG	CTTCAGGGAG	TCAGTGATCA	GTCTTTCAG	GTGGAAGAAG	2700
	CAAAGAGGAT	CAAAACAAAA	CGGATTTCAC	TCTCAACGCT	GGTAACCAAG	CATATGGATG	2760
	AGTTCAAGCG	TACACAAAAG	AATCTGGGAA	ACTGGAAAGA	AGAAGCACAG	CAGCTCTTAC	2820
	AGAAATGAAA	AAGTGGGAGA	GAGAAATCAG	ATCAGCTGCT	TTCCCGTGCC	AATCTTGCTA	2880
35	AAAGCAGAGC	ACAAGAAGCA	CTGAGTATGG	GCAATGCCAC	TTTTTATGAA	GTGAGAGCA	2940
	TCCTTAAAAA	CCTCAGAGAG	TTTGACCTGC	AGGTGGACAA	CAGAAAAGCA	GAAGCTGAAG	3000
	AAGCCATGAA	GAGACTCTCC	TACATCAGCC	AGAAGGTTTC	AGATGCCAGT	GACAAGACCC	3060
	AGCAAGCAGA	AAGAGCCCTG	GGGAGCGCTG	CTGCTGATGC	ACAGAGGGCA	AAGAATGGGG	3120
40	CCGGGGAGGC	CCTGGAAATC	TCCAGTAGAG	TTGAACAGGA	GATTGGGAGT	CTGAACCTGG	3180
	AAGCCCAATG	GACAGCAGAT	GGAGCCTTGG	CCATGGAAAA	GGGACTGGCC	TCTCTGAAAG	3240
	GTGAGATGAG	GGAAGTGGAA	GGAGAGCTGG	AAAGGAAGGA	GCTGGAGTTT	GACACGAATA	3300
	TGGATGCAGT	ACAGATGGTG	ATTACAGAAG	CCCAGAAGGT	TGATACCAGA	GCCAAGAAGC	3360
	CTGGGGTTAC	AATCCAAGAC	ACACTCAACA	CATTAGACGG	CCTCTGCAAT	CTGATGGACC	3420
45	AGCCTCTCAG	TGTAGATGAA	GAGGGGCTGG	TCTTACTGGA	GCAGAACTT	TCCCGAGCCA	3480
	AGACCCAGAT	CAACAGCCAA	CTGCGGCCCA	TGATGTGAGA	GCTGGAAGAG	AGGGCACGTC	3540
	AGCAGAGGGG	CCACCTCCAT	TTGCTGGAGA	CAAGCATAGA	TGGGATTCTG	GCTGATGTGA	3600
	AGAAGCTGGA	GAACATTAGG	GACAACCTGC	CCCCAGGCTG	CTACAATACC	CAGGCTCTTG	3660
	AGCAACAGTG	AAGCTGCCAT	AAATATTTCT	CAACTGAGGT	CTTTGGGATA	CAGATCTCAG	3720
	GGCTCGGGAG	CCATGTCTATG	TGAGTGGGTG	GGATGGGGAC	ATTTGAACAT	GTTTAATGGG	3780
50	TATGCTCAGG	TCAACTGACC	TGACCCCAT	CCTGATCCCA	TGGCCAGGTG	GTTGTCTTAT	3840
	TGCACCATAC	TCTTGTCTTC	CTGATGCTGG	GCAATGAGGC	AGATAGCACT	GGGTGTGAGA	3900
	ATGATCAAGG	ATCTGGACCC	CAAAGAATAG	ACTGGATGGA	AAGACAAACT	GCACAGGCAG	3960
	ATGTTTGCC	CATAATAGTC	GTAAGTGGAG	TCTTGGAAAT	TGGACAAGTG	CTGTTGGGAT	4020
55	ATAGTCAACT	TATTCTTTGA	GTAATGTGAC	TAAAGGAAAA	AACTTTGACT	TTGCCCAGGC	4080
	ATGAAATCT	TCTAATGTG	AGAACAGAGT	GCAACCCAGT	CACACTGTGG	CCAGTAAAT	4140
	ACTATTGCC	CATATTGTCC	TCTGCAAGCT	TCTTGCTGAT	CAGAGTTCCT	CCTACTTACA	4200
	ACCCAGGGTG	TGAAGCTGTT	CTCCATTTTC	AAGCTGGAAG	AAGTGAGCAG	TGTTGGAGTG	4260
	AGGACCTGTA	AGGCAGGCC	ATTGAGAGCT	ATGGTGCTTG	CTGGTGCCCTG	CCACCTTCAA	4320
60	GTCTTGAGC	TGGGCATGAC	ATCCTTTCTT	TTAATGATGC	CATGGCAACT	TAGAGATTGC	4380
	ATTTTATTA	AAGCTTTTCC	TACCAGCAAA	GCAATGTGTT	GGAAAGTATT	TACTTTTTCG	4440
	GTTTCAAAGT	GATAGAAAAG	TGTGGCTTGG	GCAATTGAAAG	AGGTAAATTT	CTCTAGATT	4500
	ATTAGTCTTA	ATTCAATCCT	ACTTTTCGAA	CACCAAAAT	GATGCGCATC	AATGTATTTT	4560
	ATCTTATTTT	TCTCAATCTC	TCTCTCTTTC	CTCCACCCAT	AATAAGAGAA	TGTTCTTACT	4620
	CACACTTCAG	CTGGGTCA	TCCATCCCTC	CATTATCCTT	TCCATCCATC	TTTCCATCCA	4680
65	TTACCTCCAT	CCATCCTTCC	AACATATATT	TATTGAGTAC	CTACTGTGTG	CCAGGGGCTG	4740
	GTGGACAGT	GGTGACATAG	TCTCTGCCCT	CATAGAGTTG	ATTGTCTAGT	GAGGAAGACA	4800
	AGCATTTT	AAAAATAAT	TAAACTTAC	AACTTTGTT	TGTCAAGT	GGTGTATT	4860
	GCAATAACCG	CTTGGTTTGC	AACCTCTTTG	CTCAACAGAA	CATATGTTGC	AAGACCTTCC	4920
	CATGGGGGCA	CTTGAATTTT	GGCAAGGCTG	ACAGAGCTCT	GGGTGTGCA	CATTTCTTTG	4980
70	CATTCCAGCT	GTCACTCTGT	GCCTTTCTAC	AACTGATTGC	AACAGACTGT	TGAGTTATGA	5040
	TAACACCAGT	GGGAATTGCT	GGAGGAACCA	GAGGCATTTC	CACCTTGGCT	GGGAAGACTA	5100
	TGCTCTGCC	TGCTCTCTGT	ATTTCTTGG	ATTTCTCTGA	AAGTGTTTT	AAATAAGAA	5160
	CAATTGTTAG	ATGCC					

Seq ID NO: 591 Protein sequence
Protein Accession #: NP_005553.1

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	DGHEKCKKN	GFYRHRERDR	CLPCNCSKG	SLSARCDNSG	RCSCPKPGVTG	ARCDRLPGF	120
	HMLTDAGCTQ	DQRLDLSKCD	CDPAGIAGPC	DAGRCVCKPA	VTGERCDRCR	SGYYNLDGGN	180
	PBGCTQCFY	GHSASCRSSA	EYSVHKITST	FHQDVGWKA	VQRNGSPAKL	QWSQRHQDVF	240
	SSAQRLDPVY	FVAPAKFLGN	QQVSYGQSL	FDYRVDGRGR	HPSAHDVILE	GAGLRITAPL	300
85	MPLGKTLPCG	LTKTYTFLN	EHPSNNWSQ	LSYFEYRLL	RNLTLRLIRA	TYGEYSTGYI	360
	DNVTILISAR	VSGAPAPWVE	QCICPVGYKG	QFCQDCASGY	KRDSARLPGF	GTICPCNCQG	420
	GGACDPDTGD	CYSGDENPDI	ECADCPIGFY	NDPDPDRSCK	PCPCHNGFSC	SVMPEEEV	480

CNNCPGVTG	ARCELADGY	FGDPFGEHGP	VRPCQPCQCN	NNVDPASGN	CDRLTGRCLK	540
CIHNTAGIYC	DQCKAGYFGD	PLAPNPADKC	RACNCNPMGS	EPVGCSDGT	CVCKPGFPGP	600
NCEHGAFSCP	ACYNQVKIQM	DQFMQQLQRM	EALISKAQGG	DGVVPDTELE	GRMQQAQAL	660
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RLITQMQLSL	AESEASLGNT	NIPASDHYVG	PNGFKSLAQE	ATRLAESHVE	SASNMEQLTR	780
ETEDYSKQAL	SLVRKALHEG	VGSGSGSPDG	AVVQGLVEKL	EKTKSLAQQL	TREATQAEIE	840
ADRSYQHSRL	LLDSVSRLQG	VSDQSFQVEE	AKRIKQKADS	LSTLVTRHMD	EFKRTQKNLG	900
NWKEEAQQLL	QNGKSGREKS	DQLLSRANLA	KSRAQEALSM	GNATFYEVES	ILKNLREFDL	960
QVDNRKAEAE	EA MKRLSYIS	QKVSADSDKT	QQAERALGSA	AADAQRAKNG	AGEALEISSE	1020
IEQEIGSLNL	EANVTADGAL	AMEKGLASLK	SEMRVEVEGEL	ERKELEFDTN	MDAVQMVITE	1080
AQKVDTRAKN	AGVTIQDTLN	TLDGLLHLM	QPLSVDEEGL	VLEQKLSRA	KTQINSQLRP	1140
MMSELEERAR	QQRGHLHLE	TSIDGILADV	KNLENIRDNL	PPGCYNTQAL	EQQ	

Seq ID NO: 592 DNA sequence
Nucleic Acid Accession #: AF101051.1
Coding sequence: 221.856

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CGGGGGCCCC	GCCACCTTCG	GGAGTCCGGG	TTGCCACCTC	GCAAACTCTC	CGCCTTCTGC	180
ACCTGCCACC	CCTGAGCCAG	CGCGGCGGCC	CGAGCGAGTC	ATGGCCAACG	CGGGGCTGCA	240
GCTGTTGGGC	TTCTTCTCG	CCTTCTGGG	ATGGATCGGC	GCCATCGTCA	GCACTGCCTT	300
GCCCCAGTGG	AGGATTTACT	CCTATGCCGG	CGACAACATC	GTGACCGCCC	AGGCCATGTA	360
CGAGGGGCTG	TGGATGTCCT	GGGTGTCGCA	GAGCACCGGG	CAGATCCAGT	GCAAGTCTT	420
TGACTCCTTG	CTGAATCTGA	GCAGCACATT	GCAAGCAACC	CGTGCCTTGA	TGGTGGTTGG	480
CATCCTCCTG	GGAGTGATAG	CAATCTTTGT	GGCCACCGTT	GGCATGAAGT	GTATGAAGTG	540
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TCTTGCAAGT	CTGGCTATTT	TAGTTGCCAC	AGCATGGTAT	GGCAATAGAA	TCGTTCAAGA	660
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GAAAGACTAC	GTGTGACACA	GAGGCAAAAG	GAGAAATCA	TGTTGAAACA	AACCGAAAT	900
GGACATTGAG	ATGACTTCAT	TAACATTAGG	ACCTTAGAAT	TTTGGGTATT	GTAATCTGAA	960
GTATGGTATT	ACAAAACAAA	CAAAACAAACA	AAAAACCCAT	GTGTTAAAT	ACTCAGTGCT	1020
AAACATGGCT	TAATCTTATT	TTATCTTCTT	TCCTCAATAT	AGGAGGGAAG	ATTTTACCAT	1080
TTGTATTACT	GCTTCCCAT	GAGTAATCAT	ACTCAAATGG	GGGAAGGGGT	GCTCCTTAAA	1140
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CTCATATTGT	TGATACTAGC	ATACITAAAA	TATCTCTAAA	ATAGGTAAAT	GTATTTAATT	1260
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CAGTCAAATA	TCATTTACTC	TTCTTCATTA	GCTTTGGGTG	CCTTTGCCAC	AAGACCTAGC	1380
CTAATTTACC	AAGGATGAAT	TCITTTCAAT	CTTCATGCGT	GCCCTTTTCA	TATACTTATT	1440
TTATTTTFTA	CCATAATCTT	ATAGCACTTG	CATCGTTATT	AAGCCCTTAT	TTGTTTGTG	1500
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AATATTAATT	AGTTTATATT	ACTCTCATTC	TTTGAACATG	AACATAGCCT	ATGTAGTGTC	2100
TTTATTTGCT	CAGCTGGCTG	AGACACTGAA	GAAGTCACTG	AACAAAACCT	ACACACGTAC	2160
CTTCATGTGA	TTCACTGCTT	TCTCTCTCT	ACCACTCTAT	TCCAATGAA	CAAAAACCTAC	2220
ACACATACCT	TCATGTGGTT	CAGTGCCTTC	CTCTCTCTAC	CAGTCTATTT	CCACTGAACA	2280
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TGTTAGCTGG	CAGCTGACGC	TGCTAGGATA	GTTAGTTTGG	AAATGGTACT	TCATAATAAA	3060
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TTTGATCTTT	TTATATTCTT	CTACCACACC	TGGAACAGA	CCAATAGACA	TTTTGGGGTT	3360
TTATAATGGG	AATTTGTATA	AAGCATTACT	CTTTTCAAT	AAATGTGTTT	TTAATTTAAA	3420
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Seq ID NO: 593 Protein sequence
Protein Accession #: AAD16433.1

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LLCCSCPRKT	TSYPTPRPYP	KPAESGKDY	V			

Seq ID NO: 594 DNA sequence
Nucleic Acid Accession #: NM_006180.1
Coding sequence: 352..2820

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TGCCCGGCGC	GCCGGGCCAT	GCAGCGACGG	CCGCCGCGGA	GCTCCGAGCA	GCGGTAGCGC	120
CCCCCTGTAA	AGCGGTTCGC	TATGCGGGGA	CCACTGTGAA	CCCTGCCGCC	TGCCGGAACA	180
CTCTTCGCTC	CGGACCACTC	CAGCCTCTGA	TAAGCTGGAC	TGGCACGCC	CGCAACAAGC	240
ACCGAGGAGT	TAAGAGAGCC	GCAAGCGCAG	GGAAGGCCTC	CCCCGACGGG	TGGGGGAAAG	300
CGGCCGGTGC	AGCGCGGGGA	CAGGCACTCG	GGCTGGCACT	GGCTGCTAGG	GATGTCGTCC	360
TGGATAAGGT	GGCATGGACC	CGCCATGGCG	CGGCTTTGGG	GCTTCTGCTG	GCTGGTTGTG	420
GGCTTCGGGA	GGGCCGCTTT	CGCCTGTCCC	ACGTCTCTGA	AATGCAGTGC	CTCTCGGATC	480
TGGTGCAGCG	ACCCTTCTCC	TGGCATCGTG	GCATTTCCGA	GATTGGAGCC	TAACAGTGTA	540
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GAAGATGATG	TTGAAGCTTA	TGTGGGACTG	AGAAATCTGA	CAATTGTGGA	TTCTGGATTA	660
AAATTTGTGG	CTCATAAAGC	ATTTCTGAAA	AACAGCAACC	TGCAGCACAT	CAATTTTACC	720
CGAAACAAAC	TGACGAGTTT	GTCTAGGAAA	CATTTCCGTC	ACCTTGACTT	GCTGAACTG	780
ATCCTGGTGG	GCAATCCATT	TACATGCTCC	TGTGACATTA	TGTGGATCAA	GACTCTCCAA	840
GAGGCTAAAT	CCAGTCCAGA	CACCTCAGGAT	TTGTACTGCC	TGAATGAAAG	CAGCAAGAAT	900
ATTCCCTCGG	CAAACCTGCA	GATACCCAAT	TGTGGTTTGC	CATCTGCAAA	TCTGGCCGCA	960
CCTAACCTCA	CTGTGGAGGA	AGGAAAGTCT	ATCACATTAT	CCTGTAGTGT	GGCAGGTGAT	1020
CCGGTTCCTA	ATATGTATTG	GGATGTTGGT	AACCTGGTTT	CCAAACATAT	GAATGAAACA	1080
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ATCTCTTGTG	TGGCGGAAAA	TCTTGTAGGA	GAAGATCAAG	ATTCTGTCAA	CCTCACTGTG	1200
CATTTTGCAC	CAACTATCAC	ATTTCTCGAA	TCTCCAACCT	CAGACCACCA	CTGGTGCATT	1260
CCATTTCATC	TGAAAGGCAA	CGCCAAACCA	CGCCTTCAGT	GGTTCTATAA	CGGGGCAATA	1320
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CGGAATGACA	TGCGGGACAC	CACGAACAGA	AGTAATGAAA	TCCCTTCCAC	AGACGTCAT	1620
GATAAAACCG	GTCCGGGAACA	TCTCTCGGTC	TATGCTGTGG	TGGTGATTGC	GCTCGTGGTG	1680
GGATTTTGCC	TTTTGGTAAT	GCTGTTTCTG	CTTAAGTTGG	CAAGACATC	CAAGTTTGGC	1740
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ATCTCCAAAT	GGAGTAACAC	TCCATCTTCT	TGCGAAGGTG	GCCGAGATGC	TGTCATTATT	1860
GGAATGACCA	AGATCCCTGT	CATTGAAAAT	CCCCAGTACT	TTGGCATCAC	CAACAGTCAG	1920
CTCAAGCCAG	ACACATTGTT	TACGACATC	AAGCGACATA	ACATTGTTCT	GAAAAGGGAG	1980
CTAGGCGAAG	GAGCCTTTGG	AAAAGTGTTC	CTAGCTGAAT	GCTATAACCT	GCTGCTCGAG	2040
CAGGACAAGA	TCTTGGTGGC	AGTGAAGACC	CTGAAGGATG	CCAGTGACAA	TGCACGCAAG	2100
GACTTCCACC	TGGAGGCCGA	GCTCTGACC	AACCTCCAGC	ATGAGCACAT	CGTCAAGTTC	2160
TATGGCTGCT	GGCTGGAGGG	CGACCCCTC	ATCATGGTCT	TTGAGTACAT	GAAGCATGGG	2220
GACCTCAACA	AGTTCCTCAG	GGCACACGGC	CCTGATGCCG	TGCTGATGGC	TGAGGGCAAC	2280
CCGCCCAACG	AACCTGACGA	GTCCGAGATG	CTGCATATAG	CCCAGCAGAT	CGCCGCGGGC	2340
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AGCATCATGT	ACAGGAAATT	CACGACGGAA	AGCGACGTCT	GGAGCCTGGG	GGTGTGTTG	2580
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CATCTTTTAA	CTGCCGCTGG	AGGCCACCAA	GCTGCTCTCC	TTCACTCTGA	CAGTATTAAC	2940
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GTATTGACTT	CTTTTGGGCA	TTATCTCTTT	CTCTCTTTCC	ATCTCCCTTG	GTTGTTCCCT	3060
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ACCCTTTTCT	TTGAATCAAT	CTGGCTTCTG	CATTACTATT	AACTCTGCAT	AGACAAAGGC	3180
CTTAACAAAC	GTAATTTGTT	ATATCAGCAG	ACACTCCAGT	TTGCCACCA	CAACTAACAA	3240
TGCCCTTGTG	TATTCTGTGA	TTTGATGTGG	ATGAAAAAAA	GGGAAAAACA	ATATTTCACT	3300
TAAACTTTGT	CACCTCTGCT	GTACAGATAT	CGAGAGTTTC	TATGGATTCA	CTTCTATTTA	3360
TTTATTATTA	TTACTGTTCT	TATTGTTTTT	GGATGGCTTA	AGCCTGTGTA	TAAAAAGAG	3420
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CCTGAGGACC	TTTCTGAGGA	GTAAAAAGAC	TACTGGCCTC	TGTGCCATGG	ATGATTCTTT	3660
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Seq ID NO: 595 Protein sequence
Protein Accession #: NP_006171.1

75
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85

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NFTRNKLTSL	SRKHFRHL	SELILVGNPF	TCSCDIMWIK	TLQEAQSSPD	TQDLYCLNES	180
SKNPLANLQ	IPNCGLPAN	LAAPNLTVEE	GKSITLSCSV	AGDPVPMYV	DVGNLVSXHM	240
NETSHQGS	RITNISDD	GKQISCAEN	LVGEDQSVN	LTVHFAPTIT	FLESPTSDDH	300
WCIPFTVKGN	PKPALQWFYN	GAILNESKYI	CTKIHVTNHT	EYHGCLQLDN	PTHMNGDYT	360
LIAKNEYGKD	EKQISAFHMG	WPGIDDGANP	NYPDVIYEDY	GTAANDIGDT	TNRSENPST	420
DVTDKRGREH	LSVYAVVVIA	SVVGFCLLVM	LFLLLKLARHS	KFGMKGPASV	ISNDDDSASP	480
LHHISNGSNT	PSSSEGGPDA	VIIGMTKIPV	IENPQYFGIT	NSQLKPDFTV	QHIKRHNIVL	540
KRELGEAGFG	KVFLAECYNL	CPEQDKILVA	VKTLKDAASN	ARKDFHREAE	LLTNLQHEHI	600
VKPYGVCEVG	DPLIMVFEYM	KHGDNLKFLR	AHGPDAVLMA	EGNPPELTQ	SQMLHIAQOI	660
AAGMVYLASQ	HFVHRDLATR	NCLVGENLLV	KIGDFGMSRD	VYSTDYRVG	GHTMLPIRWM	720

PPESIMYRKF TTESDVWSLG VVLWEIFTYG KQPWYQLSNN EVIECITQGR VLQRPRTPCQ 780
 EVYELMLGCW QREPHMRKNI KGIHTLLQNL AKASPVYLDI LG

Seq ID NO: 596 DNA sequence
 Nucleic Acid Accession #: AF410899
 Coding sequence: 483..2999

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    CCGCCGGTCC GTGCCCGGCG CGCCGGGCCA TGCAGCGACG GCGCCGCGCG AGCTCCGAGC 240
15  AGCGGTAGCG CCCCTCTGTA AAGCGGTTCT CTATGCCGGG ACCACTGTGA ACCCTGCGCG 300
    CTGCCGGAAC ACTCTTCGCT CCGGACCAGC TCAGCCTCTG ATAAGCTGGA CTCCGACACG 360
    CCGCAACAAG CACCGAGGAG TTAAGAGAGC CGCAAGCGCA GGAAGGCCTT CCCCGCACGG 420
    GTGGGGGAAA GCGGCGGGTG CAGCGCGGGG ACAGGCATCT GGGCTGGCAC TGGCTGCTAG 480
    GGATGTCGTC CTGGATAAAG TGGCATGGAC CCGCCATGGC GCGGCTCTGG GGCTTCTGCT 540
20  GGCTGGTTGT GGGCTTCTGG AGGGCCGCTT TCGCCTGTCC CACGTCTGTC AAATGCAGTG 600
    CCTCTCGGAT CTGGTTCAGC GACCCCTTCT CTGGCATCGT GGCATTTCCG AGATTGGAGC 660
    CTAACAGTGT AGATCTCTAG AACATCACCG AAATTTTCAT CGCAAACAG AAAAGGTTAG 720
    AAATCATCAA CGAAGATGAT GTTGAAGCTT ATGTGGGACT GAGAAATCTG ACAATTGTGG 780
    ATTCTGGATT AAAATTGTGT GCTCATAAAG CATTCTGAA AAAACAGCAAC CTGCAGCACA 840
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    GCAGCAAGAA TATTCCTCCTG GCAAACTGTC AGATACCCAA TTGTGGTTTG CCATCTGCAA 1080
    ATCTGGCCCG ACCTAACCTC ACTGTGGAGG AAGGAAAGTC TATCACATTA TCCTGTAGTG 1140
    TGGCAGGTGA TCGGTTTCTT AATATGTATT GGGATGTTGG TAACTCTGTT TCCAAACATA 1200
30  TGAATGAAAC AAGCCACACA CAGGGCTCCT TAAGGATAAC TAACATTTC A TCCGATGACA 1260
    GTGGGAAGCA GATCTCTTGT GTGGCGGAAA ATCTTGTAGG AGAAGATCAA GATTCTGTCA 1320
    ACCTCACTGT GCATTTGCA CCAACTATCA CATTCTCGA ATCTCCAACC TCAGACCAAC 1380
    ACTGGTGCAT TCCATTCACT GTGAAAGGCA ACCCCAAACC AGCGCTTCAG TGGTTCATATA 1440
    ACGGGGCAAT ATTGAATGAG TCCAAATACA TCTGTACTAA AATACATGTT ACCAATCACA 1500
35  CGAGTACCA CCGTCCCTC CAGCTGGATA ATCCCACTCA CATGAACAAT GGGGACTACA 1560
    CTCTAATAGC CAAGAATGAG TATGGGAAGG ATGAGAAACA GATTCTGCT CACTTCATGG 1620
    GCTGGCTCGG AATTGACGAT GGTGCAAAAC CAAATTATCC TGATGTAATT TATGAAGATT 1680
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40  CGTCTGTGGT GGGATTTTGC CTTTGTGTAA TGCTGTTTCT GCTTAAGTTG GCAAGACACT 1860
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    ATACCTCTCT TCAGAACTTG GCCAAGGCAT CTCGGTCTA CCTGGACATT CTAGGCTAGG 3000
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70  TTATTATTAT TACTGTTCTT ATTGTTTTTG GATGGCTTAA GCCTGTGTAT AAAAAGAAA 3600
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75  ATGGCGCATA GTGTGCTCGG ACACAGTTT GTCTCTGCTG GTTGTGATGA TAGCACTGGT 3960
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Seq ID NO: 597 Protein sequence
 Protein Accession #: AAL67965.1

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    NPTRNKLTSL SRKHFRHLDL SELILVGNPF TSCSDIMWIK TLQBAKSSPD TDQLYCLNES 180
    SKNIPLANLQ IPNCGLPAN LAAPNLTVEE GKSIITLSCSV AGDPVPNNYW DVGNLVSKHM 240
  
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NETSHTQSSL RITNISSDDS GKQISCVAEN LVGEDQDSVN LTVHFAPTIT FLESPTSDHH 300
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 LIAKNEYGKD EQQISAHFMG WPGIDDGANP NYPDVIYEDY GTAANDIGDT TNRSEIPST 420
 DVTDKTKGREH LSVYAVVVIA SVVGFCLLVM LFLKLARHS KFGMKDFSWF GFGVKSRQG 480
 VGPASVISND DDSASPLHHI SNGSNTPPSS EGGPDVAVIG MTKIPVIENP QYFGITNSQL 540
 KPDTFVQHIK RHNIVLKRKL GSGAFGKVPFL AECYNLCPEQ DKILVAVKTL KDASDNARKD 600
 FHREAEELLTN LQHEHIVKFY GVCVEGDPLI MVFEYMKHGD LNKFLRAHGP DAVLMAEGNP 660
 PTELTSQSQL HIAQQIAAGM VYLASQHFVH RDLATRNCLV GENLLVKIGD FGMSRDVYST 720
 DYYRVGGHTM LPIRWMPPEP IMYRKFTTES DVWSLGVVLW EIFTYKQFPW YQLSNNEVIE 780
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 AGTGGGTACA GCGTGCCTTT CACTTCGCCA TCAGCGAGTA TAACAAGGCC ACCAAAGATG 240
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 ATTACTTCTT CGACGTAGAG GTGGGCCGCA CCATATGTAC CAAGTCCCAG CCCAACTTGG 360
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 GACAGACAGA GAAGGTGCA GGAGTCTTT GTTGCTCAGC AGGGCGCTCT GCCCTCCCTC 660
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Seq ID NO: 601 Protein sequence
 Protein Accession #: NP_001889.1

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Seq ID NO: 602 DNA sequence
 Nucleic Acid Accession #: NM_003976.2
 Coding sequence: 299..961

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 GGGTGGCAGG CCGGTCCCCC ACAAAAGATA ACTCATCTCT TAAATTGCAA GCTGCTCAA 240
 CAGGAGGGTG GGGGAACAGC TCAACAATGG CTGATGGGCG CTCCTGGTGT TGATAGAGAT 300
 GGAACCTGGA CTCTGGAGGCC TCTCCACGCT GTCCCACTGC CCCTGGCCTA GCGGCGAGCC 360
 TGCCCTGTGG CCTTCTCGGC CCGCTCTGGC TCTGCTGAGC AGCGTCGAG AGGCCTCCCT 420
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 CGACGAGCTG GTGCGTTTCC GCTTCTGAGC CGGCTCCTGC CGCGCGCGC GCTCTCCACA 780
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 CCTCCGCGAG AGTCCCACTA GCCACGGGCC TCAGCCAGGG ACGAAGGCCT CAAAGCTGAG 1080
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 GGAGCCCTTC GGACCCACTT CTCACAGACT CTGGCACTGG CCAGGCTCG AACCTGGGAC 1260
 CCCTCTCTG ATGAACACTA CAGTGGCTGA GGCATCAGCC CCGCGCCAGG CCCTGTAGGG 1320
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 CCTGTACTCA CTATGGGAG CTGGCCCC

Seq ID NO: 603 Protein sequence
 Protein Accession #: NP_003967.1

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 RGCLRLSQLV PVRALGLGHR SDELVRFRFC SGSCRRARSP HDLSLASLLG AGALRPPPGS 180
 RPVSQPCCRP TRYEAVSFMD VNSTWRTVDR LSATACGCLG

Seq ID NO: 604 DNA sequence
 Nucleic Acid Accession #: NM_057091.1
 Coding sequence: 783..1445

1 11 21 31 41 51
 | | | | |
 ACTGGCCGCT GAGAGAAGAA TCGGGTGGAG CAGAGAGCAG CTGCTGCAGG GCAGACAGCC 60
 GGACCCCAAA ATCTGCACGT ACCAGCAGTC AGCCGCCCCA CGCAGGGACC GGCTTACCCC 120
 TCGCTCCCCG CCTCTACTCA CTTTCTCCCG CCCTCGGCCG GGCCTCCAG CTCTACTT 180
 CGCGTGTCTA CAACTCAAC TCCCGGTTTC CGTGCCTCTC CACGCTCGA GTTCTCTACT 240
 CTCCATATCC GAGGGGCCCC TCCAGCATC TACCCCTCTC CCAACCTCGG GGGACCTAGC 300
 CAACTAGGG GGGACTGGAT CCGACGGGTG GAGCAGCCAG GTGAGCCCCG AAAGGTGGGG 360
 CGGGGCGAGG GCCTCCAG CCGCAGCCCG GGATCTGGTG ACGCTGGGGC TGGAAATTGA 420
 CACCGGACGG CTGCGCGGGC GGGCAGGAGG CTGCTGAGGG ATGGAGTTGG GCCCGGCCCC 480
 CAGACAAGGC CCGGGGGCTC CGCCAGCAGC AGGTCCCTCG GGGCCAGGCC CTGCTGCCA 540
 CCCGGGCTG GAGCCCCACA CCGAGGGGTG CAGACTGGCT GCCAAGGCCA CACTTTTGGC 600
 TAAAGAGGC ACTGCCAGGT GTACAGTCTT GGGCATGCGC TGTTTGAGCT TCGGGGAGA 660
 GCCCAGCACT GGTCCCCCGA AAGGTGCCCTA GAAGAACAAG GTGCAGGACC CCGTCTGCC 720
 TCAACAGGAG GGTGGGGGAA CAGCTCAACA ATGGCTGATG GGCCTCCTG GTGTTGATAG 780
 AGATGGAACT TGGACTTGA GGCCTCTCCA CGCTGTCCCA CTGCCCTTGG CCTAGGCGGC 840
 AGCTTGCCTT GTGGCCCACT CTGGCCGCTC TGGCTCTGCT GAGCAGCGTC GCAGAGGCT 900
 CCCTGGGCTC CGGCCCCGCG AGCCCTGCCC CCGCGGAAGG CCCCCCGCT GTCTTGGCT 960
 CCCCCGCGG CCACCTGCGG GGGGGACGCA CGGCCGCTG GTGAGTGA AGAGCCCGGC 1020
 GCGCGCGCGC GCAGCTTCTT CCGCCGCGCG CCGCGCGGCC TGCAACCCCA TCTGCTCTTC 1080
 CCGCGGGGG CCGCGCGGCG CCGGCTGGGG GCGCGGCGC CCGCTCGG GCAGCGGGG 1140
 CGCGGGGCTG CCGCTTGGC TCGCAGCTGG TGCCGGTGGC GCGCTCGG CTGGGCCACC 1200
 GCTCCGACGA GCTGGTGGCT TCCGCTTCT GCAGCGGCTC CTGCGCGCGC GCGGCTCTC 1260
 CACACGACCT CAGCTTGGCC AGCTACTGG GCGCGGGG CCGCGAGCG CCGCGGGCT 1320
 CCGCGCCCT CAGCCAGCCC TGCTGCCGAC CCACGCGCTA CGAAGCGGTC TCCTTCATGG 1380
 ACGTCAACAG CAGCTGGAGA ACCGTGGACC GCCTCTCCG CACCGCTGCG GGCTGCTGG 1440
 GCTGAGGGCT CGCTCAGGG CTTTGACAG TGGACCTTA CCGGTGGCTC TTCCTGCTG 1500
 GGACCCCTCC GCAGAGTCCC ACTAGCCAGC GGCCTCAGCC AGGGACGAAG GCCTCAAAGC 1560
 TGAGAGGCCC CTACCGGTGG GTGATGGATA TCATCCCCGA ACAGGTGAAG GGACAACCTGA 1620
 CTAGCAGCCC CAGAGCCCTC ACCCTGCGGA TCCAGCCTA AAAGACACCA GAGACCTCAG 1680
 CTATGGAGCC CTTCGAGCCC ACTTCTCACA GACTCTGGCA CTGGCCAGGC CTCGAACCTG 1740
 GGAACCCCTC TCTGATGAAC ACTACAGTGG CTGAGGCATC AGCCCCCGCC CAGGCCCTGT 1800
 AGGACAGCA TTTGAAGGAC ACATATTGCA GTTGCTTGGT TGAAGTGCC TGTGCTGGAA 1860
 CTGGCCTGTA CTCACTCATG GGAGCTGGCC CC

Seq ID NO: 605 Protein sequence
 Protein Accession #: NP_003967.1

1 11 21 31 41 51
 | | | | |
 MELGLGLST LSHCPWPRRQ PALWPTLAAL ALLSSVAEAS LGSAPRSPAP REGPPPVLAS 60
 PAGHLPGGRT ARWCSGRARR PPPQPSRPAP PPPAPPSALP RGGRAARAGG PGSRARAAGA 120
 RGCLRLSQLV PVRALGLGHR SDELVRFRFC SGSCRRARSP HDLSLASLLG AGALRPPPGS 180
 RPVSQPCCRP TRYEAVSFMD VNSTWRTVDR LSATACGCLG

Seq ID NO: 606 DNA sequence
 Nucleic Acid Accession #: NM_057160.1

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1      11      21      31      41      51
5      |      |      |      |      |      |
      ATGCCCGGCC TGATCTCAGC CCGAGGACAG CCCCTCCTTG AGGTCCTTCC TCCCCAAGCC 60
      CACCTGGGTG CCCTCTTTCT CCCTGAGGCT CCACTTGGTC TCTCCGCGCA GCCTGCCCTG 120
      TGGCCCAACC TGGCGCTCTT GGCTCTGCTG AGCAGCGTCG CAGAGGCCTC CCTGGGCTCC 180
      CGGCCCGGCA GCGCTGCCCC CGCGGAAGGC CCCCAGCTTG TCCTGGGCTC CCCCAGCGGC 240
      CACCTGCCCG GGGGACGCAC GGCCCGCTGG TGCAGTGGAA GAGCCCGCGG GCCGCCGCGG 300
10     |      |      |      |      |      |
      GAGCCTTTCT GGGCCGCGCC CCCGCGCGCT GCACCCCAT CTGCTCTTCC CCGCGGGGGC 360
      CGCGCGGCGC GGGCTGGGGG CCGGGGAGGC CGCGCTCGGG CAGCGGGGGC GCGGGGCTGC 420
      CGCTGCGCTC CCGAGCTGGT GCCGCTGCGC GCGCTCGGCC TGGGCCACCG CTCGACGAG 480
      CTGGTGGGTT TCCGCTTCTG CAGCGGCTCC TGCCGCGCGC CGCGCTCTCC ACACGACCTC 540
      AGCCTGGCCA GCTACTGTGG CCGCGGGGCC CTGCGACCGC CCGGGGCTC CCGGCCGCTC 600
15     |      |      |      |      |      |
      AGCCAGCCCT GCTGCCGACC CACGCGCTAC GAAGCGGTCT CCTTCATGGA CGTCAACAGC 660
      ACCTGGAGAA CCGTGGACCG CCTCTCCGCC ACCGCTGCG GCTGCCTGGG CTGAGGGCTC 720
      GCTCCAGGGC TTTGCAGACT GGACCTTAC CGGTGGCTCT TCCTGCGCTG GACCCCTCCG 780
      CAGAGTCCCA CTAGCCAGCG GCCTCAGCCA GGGACGAAGG CCTCAAAGCT GAGAGGCCCC 840
      TACCGTGGGG TGATGGATAT CATCCCGGAA CAGGTGAAGG GACAACTGAC TAGCAGCCCC 900
20     |      |      |      |      |      |
      AGAGCCCTCA CCGTGGGGAT CCCAGCCTAA AAGACACCAG AGACCTCAGC TATGGAGCCC 960
      TTGGGACCCA CTCTCAGAG ACTCTGGCAC TGGCCAGGCC TCGAACCTGG GACCCCTCCT 1020
      CTGATGAACA CTACAGTGGC TGAGGCATCA GCCCCCGCCC AGGCCCTGTA GGGACAGCAT 1080
      TTGAAGGACA CATATTGCGT TGGCTTGGTT GAAAGTGCTT GTGCTGGAAC TGGCCTGTAC 1140
25     |      |      |      |      |      |
      TCACTCATGG GAGCTGGCCC C

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Seq ID NO: 607 Protein sequence
Protein Accession #: NP_476501.1

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1      11      21      31      41      51
30     |      |      |      |      |      |
      MPGLISARGQ PLLEVLPPQA HLGALFLPEA PLGLSAQPAL WPTLAALALL SSVAEASLGS 60
      APRSPAPREG PPPVLASPAH HLPGGRTARW CSGRARRPPF QPSRPAPPPP APPSALPRGG 120
      RAARAGGPGS RARAAGARGC RLRSQLVFVR ALGLGHRSD LVRFRFCSGS CRRARSPHDL 180
35     |      |      |      |      |      |
      SLASLLGAGA LRPFGSRPV SQPCRPRTRY EAVSFMDVNS TWRTVDRLSA TACGCLG

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Seq ID NO: 608 DNA sequence
Nucleic Acid Accession #: NM_057090.1
Coding sequence: 29..715

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1      11      21      31      41      51
40     |      |      |      |      |      |
      CTGATGGGCG CTCCTGGTGT TGATAGAGAT GGAACCTGGA CTTGGAGGCC TCTCCACGCT 60
      GTCCCACTGC CCCTGGCCTA GCGCGCAGGC TCCACTTGGT CTCTCCGCGC AGCCTGCCCT 120
      TGGGCCACCC CTGGCCGCTC TGGCTCTGCT GAGCAGCGTC GCAGAGGCCT CCCTGGGCTC 180
45     |      |      |      |      |      |
      CGGCCCCGCG AGCCCTGCCC CCGCGGAAGG CCCCCCGCCT GTCTGGCGT CCCCCGCGG 240
      CCACCTGCCG GGGGACGCA CCGCCCGCTG GTGCACTGGA AGAGCCCGGC GCGCCGCGCC 300
      GCAGCCTTCT CCGCCCGCGC CCGCCCGGCC TGCACCCCA TCTGCTCTT CCGCGGGGG 360
      CCGCGCGGCG CCGGCTGGGG GCGCGGGCAG CCGCGCTCGG GCAGCGGGGG CCGGGGGCTG 420
      CCGCCTGCGC TGCAGCTGG TGCCGGTGCG CGCGCTCGGC CTGGGCCACC GCTCCGACGA 480
50     |      |      |      |      |      |
      GCTGGTGGGT TTCCGCTTCT GCGCGGCTC CTGCGCGCGC GCGCGCTCTC CACACGACCT 540
      CAGCCTGGCC AGCCTACTGG GCGCGGGGCG CCTGCGACCG CCGCGGGCT CCGGGCCCGT 600
      GAGCCAGCCC TGCTGCCGAC CCACGCGCTA CGAAGCGGTC TCCTTCATGG ACCTCAACAG 660
      CACCTGGAGA ACCGTGGACC GCCTCTCCGC CACCGCCTGC GGCTGCTTGG GCTGAGGGCT 720
      CGCTCCAGGG CTTTGCAGAC TGGACCCCTA CCGGTGGCTC TTCCTGCTTG GACCCCTCCC 780
55     |      |      |      |      |      |
      GCAGAGTCCC ACTAGCCAG GGCCTCAGCC AGGACGGAAG GCCTCAAAGC TGAGAGGCC 840
      CTACCGGTGG GTGATGGATA TCATCCCGA ACAGGTGAAG GGACAACTGA CTAGCAGCCC 900
      CAGAGCCCTC ACCCTGCGGA TCCCAGCCTA AAAGACACCA GAGACCTCAG CTATGGAGCC 960
      CTTGCGACCC ACTTCTCACA GACTCTGGCA CTGGCCAGGC CTCGAACCTG GACCCCTCC 1020
      TCTGATGAAC ATACAGTGG CTGAGGCATC AGCCCCCGCC CAGGCCCTGT AGGGACAGCA 1080
60     |      |      |      |      |      |
      TTTGAAGGAC ACATATTGCA GTTGCTTGGT TGAAAGTGCC TGTGCTGGAA CTGGCCTGTA 1140
      CTCACTCATG GGAGCTGGCC CC

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Seq ID NO: 609 Protein sequence
Protein Accession #: NP_476431.1

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1      11      21      31      41      51
65     |      |      |      |      |      |
      MELGLGLST LSHCPWPRRQ APLGLSAQPA LWPTLAALAL LSSVAEASLG SAPRSPAPRE 60
      GPPPVLASPA GHLPGGRTAR WCSGRARRPP PQPSRPAPPP PAPPSALPRG GRAARAGGPG 120
70     |      |      |      |      |      |
      SRARAAGARG CRLRSQLVFV RALGLGHRSD ELVRFRFCSG SCRARSFPHD LSLASLLGAG 180
      ALRPPGSRP VSQPCRPRTR YEAVSFMDVN STWRTVDRLS ATACGCLG

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Seq ID NO: 610 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..1746

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1      11      21      31      41      51
80     |      |      |      |      |      |
      ATGCCACTGA AGCATTATCT CCTTTGCTG GTGGGCTGCC AAGCCTGGGG TGCAGGGTTG 60
      GCTTACCATG GCTGCCCTAG CAGAGTGTACC TGCTCCAGGG CCTCCAGGT GGAGTGCACC 120
      GGGGCACGCA TTGTGGCGGT GCCCACCCTT CTGCCCTGGA ACGCCATGAG CCTGCAGATC 180
      CTCAAACAGC ACATCACTGA ACTCAATGAG TCCCCGTTC TCAATATCTC AGCCCTCATC 240
      GCCTGAGGAA TTGAGAAGAA TGAGCTGTGC GCATCACGC CTGGGGCCTT CCGAAACCTG 300
85     |      |      |      |      |      |
      GGCTCGTGC GCTATCTCAG CCTCGCCAAC AACAGCTGC AGGTTCTGCC CATCGGCTC 360
      TTCAGGGGCC TGGACAGCCT TGAGTCTCTC CTTCTGTCCA GTAACAGCT GTTGACAGATC 420
      CAGCCGGGCC ACTTCTCCA GTGCAGCAAC CTCAGGAGC TGCAGTTGCA CGGCAACCAT 480
      CTGGAATACA TCCCTGACGG AGCCTTCGAC CACCTGGTAG GACTCACGAA GCTCAATCTG 540

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	GGCAGAATA	GCCTCACCCA	CATCTCACCC	AGGGTCTTCC	AGCACCTGGG	CAATCTCCAG	600
	GTCTCTCGGC	TGTATGAGAA	CAGGCTCAGC	GATATCCCCA	TGGGCACTTT	TGATGGGCTT	660
	GTTAACCTGC	AGGAACCTGC	TCTACAGCAG	AACCAGATTG	GACTGCTCTC	CCCTGGTCTC	720
5	TTCCACAACA	ACCACAACCT	CCAGAGACTC	TACCTGTCCA	ACAACCCAT	CTCCCAGCTG	780
	CCACCCAGCA	TCTTCATGCA	GCTGCCCCAG	CTCAACCGTC	TTACTCTCTT	TGGGAATTCC	840
	CTGAAGGAGC	TCTCTCTGGG	GATCTTCGGG	CCCATGCCCA	ACCTGCGGGA	GCTTTGGCTC	900
	TATGACAACC	ACATCTCTTC	TCTACCCGAC	AATGTCTTCA	GCAACCTCCG	CCAGTTGCAG	960
	GTCTGTATTC	TTAGCCGCAA	TCAGATCAGC	TTTCTCTCCC	CGGGTGCCTT	CAACGGGCTA	1020
10	ACGGAGCTTC	GGGAGCTGTG	CCTCCACACC	AACGCACTGC	AGGACCTGGA	CGGGAATGTC	1080
	TTCCGCATGT	TGGCCAACCT	GCAGAACATC	TCCCTGCAGA	ACAATCGCCT	CAGACAGCTC	1140
	CCAGGGAATA	TCTTCGACCA	CGTCAATGGC	CTCATGGCCA	TCCAGCTGCA	GAACCAACCAG	1200
	CTGGAGAACT	TGCCCCCTCG	CATCTTCGAT	CACCTGGGGA	AACGTGTGTA	GCTGCGGCTG	1260
	TATGACAATC	CCTGGAGGTG	TGACTCAGAC	ATCCTTCCGC	TCCGCAACTG	GCTCCTGCTC	1320
15	AACCAGCCTA	TGAGCTGCTA	GGACACTGTA	CCTGTGTGTT	TCAGCCGAGC	CAATGTCCGA	1380
	GGCCAGTCCC	TCATTATCAT	CAATGTCAAC	GTGTCTGTTC	CAAGCGTCCA	TGTCCCTGAG	1440
	TGCTCTAGTT	ACCCAGAAAC	ACCATGGTAC	CCAGACACAC	CCAGTTACCC	TGACACCACA	1500
	TCCTGTCTTT	TTAGCCCTGA	GCTAACCCAGC	CCTGTGGAAG	ACTACACTGA	TCTGACTACC	1560
	ATTGAGGTCA	CTGATGACCG	CAGCGTTTGG	GGCATGACCC	AGGCCCCAGAG	CGGGCTGGCC	1620
20	ATTGCCGCCA	TTGTAATTGG	CATTGTGCGC	CTGGCCTGCT	CCCTGGCTGC	CTGCGTGGGC	1680
	TGTTGTCTGT	GCTTAGGGAG	GAGCCAAAGCT	GTCCCTGATG	AGATGAAGGC	ACCCAAATGAG	1740
	TGTTAAAGAG	GCAGGCTGGA	GCAGGGCTGG	GGAAATGATGG	GACTGGAGGA	CCTGGGAATT	1800
	TCATCTTTCT	GCCTCCACCC	CTGGGTCCAT	GGAGCTTTCC	CGTGATTGCT	CTTTCTGGCC	1860
	CTAGATAAAG	GTGTGCTCTA	CTTCTCTGTA	CTTCCCTGAT	TCTCCCGTAG	AGAAGCAGGT	1920
25	CGTGCCGGAC	CTTCTCTACA	TCAGGAAGAT	AGATCCAAC	GGCCATGGCA	AAAGCCCTGG	1980
	GGATTTCCGA	TTTCTACCCC	TGGGCTTCTT	TGAGAGGGGC	TCTTCTCTCA	AATCCTCCCC	2040
	ACCTGTCTCT	CAAGAACAGC	GTTCCTGCG	CCCAGGCCCC	CTCCGGGCTT	CTGTAGACTC	2100
	AGTTAGTCCA	CAGCCTGCTC	ACTTCGTGGG	AATAGTTCTC	CGCTGAGATA	GCCCTCTCTG	2160
	CCTAAGTATT	ATGTAAGTTG	ATTTCCCTTC	TTTTGTTTCT	CTTGTTTGTG	CTATGGCTTG	2220
30	ACCCAGCATG	TCCCCTCAAA	TGAAAGTTCT	CCCCTTGATT	TTCTGCTCCT	GAAGGCAAGG	2280
	TGAGTTCTCT	CCTCAAGAA	GACTTCAAAC	CATTTAACTG	GTTTCTTAAG	AGCCGTCAAT	2340
	CAGCCTGGTT	TTGGGGATGC	TATGAAAGAG	AGAAGGAAAA	TCATGCCGCT	CAGTTCTCTG	2400
	AGACAGAAAG	GCGGTCTACT	GTGTCTCACT	TGTGATTTT	ATCTGGAATA	GGAGAAACAA	2460
	CCCCAGCACA	GCAAGCTCAG	CCTTTTAGAG	AAGGATATTT	CCAACTGCA	AATTTGCTT	2520
35	TGAAAGGTTT	AGCCCTTTAA	GGAAATGAAAT	CATGTAGAAT	TTTGGACTTC	TAAAAACATT	2580
	AAATCAGCT	TATTAATACG	GGATAGAGAA	AGAAATCTGG	TGCCCTGGGG	TCCCTGTGTT	2640
	CACCCCTAGA	GTTTGTTTTA	AAATTTTAA	TTGAAGCATG	TGAAGGTAC	STGCAGAAAA	2700
	GTGGGAACAT	GATAGTGTAT	GGCTTGGTGG	ATTTTCACAA	ACTGAACATA	CCTGTGTAAT	2760
	CAGCATCTAG	ACCCAGACCC	AGAGCATCAC	AAATATCCCC	CATCCTGGGC	TTTTCCCGA	2820
40	GGAGATGGGG	GCTTCTGAAG	ATGGACTTAC	CTGGGACCTG	CCCCCATGA	GCCAGGACGG	2880
	TCCCCCCACA	GTGAGCTGT	GCAAGGCCCC	CGTGGCCAGG	GGTGGAGGAG	AATATGTGGG	2940
	TGTGGACAGG	ATGGGAGACT	GTGGCTGAA	CAGGAGATT	TATTATATCT	GGAGACCTCG	3000
	AGAGACCCTG	AGACCTGGGG	CACCATGGCT	GGCCAGGTCA	GAAGCATCCT	GACTGCAGAG	3060
	GTCCGTGCAG	CCACACCTCT	TTCCCTGCCA	GCAAGTTGTC	TGCGGCTCAT	CGGAGGCCCT	3120
45	TCCGCTGGA	GCCTTCTATG	GACGTGATAT	GCCTGTATCT	GTTTAAAT	TTTCTCTTC	3180
	ACTTAGGGGA	AGTGAATCG	CTCAGAGATG	AGATCCTTTA	ATTGAAAACG	AAGTGTAAAG	3240
	GAATCTAGTG	TCTTTCTAAT	GTGGTAAAT	TCTCCATCAA	CATCACAGTC	AGCTGGCAGC	3300
	TGAACTTCAG	AATCTCACTT	ACAGCAGGCG	ACACGGGGGT	ACACCGATGG	GTCACTGCTG	3360
	GTCTGGGGGC	TCCCTGGAGC	TCTCCTGCG	TGTGGTCTGG	TTAGGAGTTG	AGTTGTTTGC	3420
50	TCCAGGGTTA	TTCTCTCTCT	CGAGTCACAG	TCACACGAAT	ACCTGCCTTC	TCTGGCTTTC	3480
	CTGTATATCA	CATATTCACT	TGGCGCTCAA	GAAATTAGGC	TCATGGCAAC	GTTGTCTTTT	3540
	CTCTGGACAA	CTGGCCCACT	TTACAGTGAA	ATGGAGAATT	TCAGGTCTCC	ACGTCTGCCC	3600
	AGGAAAGAAC	TTCAGCTGAT	TTCCAGGGGA	TCTGGAAATC	CACGACCAAT	CCCGATCGGC	3660
	TCTTATTAGC	TCCCGCTGAC	ACAAGACACC	TGTGCTTTGG	AAATCCACCA	CCAATCCCGA	3720
55	TCCGCTCTTA	TTAGCTCCCC	GCTCCACAAG	ACACCTGTGA	TCTGGAAATC	TACCACCAAT	3780
	CCCGATCGGC	TCTTATTAGC	TCCCGCTCC	ACAAGACACC	TGTGACATCC	TCCAGGGCCA	3840
	CAGGAGCACG	TTTTCCCTTC	CAGTTCTCTG	ACAAAAAGTG	TCCAGAGGGC		3900
	TGTTTGCAAA	CACTAGTGCA	CTTTGTAGCT	TTTCACTCTC	TGTCCAGGG	AATCTAGGAG	3960
	AGATGAGGCC	CGTCAGAGTC	AAGAGATGTC	ATCCCCCAG	GGTCTCCAAG	GCATTTCCAC	4020
60	ACTATTGGTG	GACCTGTGAG	GACATGCACC	AAGGCTTGCC	AGAGCCAACA	GGAAAGTGAG	4080
	CCAGAGCATG	GCACATGAGC	ATCACCCGCT	GATGGTGGCC	TGCTGTGCTT	GGTGCCAACA	4140
	GGGGCATCCC	GGCCCGTACC	CCTCCAGACA	GGAAGCATGG	GTTTGCCAC	AGACCTGTCT	4200
	GGTGCTCTGT	TGAGTGGCTT	CAGATGTCT	TTGTGCATAG	GCACAAAGTG	GCCAGGGCTG	4260
	GAGGAGGGTG	GGAAACCTCA	TCATCCGGTG	GGCCCTGCCA	ATCTTAACCC	AGAACCCTTA	4320
65	GGTATTCTGT	GCAGTAGCCA	TGACATTGGA	GCACTTCTCT	CTCCAGCCAG	AGGCTGACCT	4380
	GAGGGCCACT	GTCTCAGAT	GACACCACCC	AGGAGCACCC	TAGGTGAGGG	GTGAGGGCCC	4440
	CCTTATGTGA	ACCTCTTGCC	TCTTCTTTTC	TCCCATCAGA	GTGGTTGGAT	GGAGCCATTG	4500
	GCCTCTCTTT	CTTCAGCGGG	CCCTTCAACC	TCTCTGCACC	ATGTTGTCTG	GCTGAGGAGC	4560
	TACTAGAAAA	GCTGAGTGGG	GTCTCTTTTC	CAACAGGATG	ATGCATTGTC	TCAATTCTCA	4620
70	GGGCTGGAAT	GAGCCGGCTG	GTCCCCCAGA	AAGCTGGAGT	GGGTACAGA	GTTTCACTTT	4680
	CCTCTCTGTT	TACAGCTCCT	TGACAGTCCC	ACGCCCATCT	GGAGTGGGAG	CTGGGAGTTA	4740
	GTGTTGGAGA	AGAAACAACA	AAAGCCAATT	AGAACCACCTA	TTTTTAAAAA	GTGCTTACTG	4800
	TGCACAGATA	CTCTTCAAGC	ACTGGACGTG	GATTCTCTCT	CTAGCCCTCA	GCACCCCTGC	4860
	GGTAGGAGTG	CCGCTCTTAC	CCACTTGTGA	TGGGGTACAG	AGGCACCTGC	TCTTCTGCAT	4920
75	GGTGTTCAT	AGGCTGGGAG	TTTTATTAT	CTCTTCAAAC	TTTGTACAAG	AGCTCATGGC	4980
	TTGTCTTGGG	CTTCTGTCAT	TAAACCAAAG	GAAATGGAAG	CCATTCCTCT	GTTGCTCTCC	5040
	TTAGTCTTGG	TCATCAGAAG	CTCACTTGGT	ACCATATAGA	TCAAAAGCTT	TGTAACCACA	5100
	GGAAAAAATA	AACCTCTCCA	TCCCTTAAAG	AATAGAAATG	TTTGTCCCTC	TCATGGGAAT	5160
	TGGGCTGTAT	GTATATTGTT	CTTCTCTCTT	AGAATTTAGA	GATACAAGAG	TTCTACTTAG	5220
80	AACCTTTTCA	GGACACAAAT	TCCACAACCT	TTCAGATGCT	GATGTAGAGC	TATTGGGAAA	5280
	GAACCTTCAA	ACTCAGGAGT	TTTGACAGAG	GCAGACAGCT	AGAGATAACT	CGGACCCAG	5340
	AGTTGGTCTG	CAGATGTTAG	ATGTATCCTA	GCTTTTAGCC	ATAAACCACT	CAAAGATTCA	5400
	GCCCCAGAT	CCCCAGTCA	GAATGAATC	TGCGTTGTTG	GGAGCCAGC	AGTGGCCCTG	5460
	GGAAAGGAGC	CATGGCTGTG	TTTCAGAGAG	GGTGGGCTGG	CAAGCCACTT	CCGGGAAAAA	5520
	CTCTTCTCGC	CCCAGGTTTC	TTCTTCTCTT	AAGGAGAGAT	TGTTCTCACC	AACCCGCTGC	5580
85	CTTCATGCTG	CTTCTCAAAGC	TAGATCATGT	TTGCCTTGTG	TAGAGAATTA	CTGCAATCA	5640
	GCCCCAGTGC	CTTCTCAAGT	ATTTACAGAT	TTCTAGGCC	TCAGGGTTT	GTAGAGTGTG	5700
	AGCCCTGGTG	GGCAGGGTTG	GGGGTCTGT	CTTCTGCTGG	ATGCTGCTTG	TAATCCATTT	5760

GGTGTACAGA ATCAACAATA AATAATATAC ATGTAT

Seq ID NO: 611 Protein sequence

Protein Accession #: BAB84587.1

5

1	11	21	31	41	51	
MPLKHYLLLL	VGCQAWGAGL	AYHGCPSECT	CSRASQVECT	GARIVAVPTP	LPWNAMSLQI	60
LNTHITELNE	SPFLNISALI	ALRIEKNELS	RITPGAFRNL	GSLRYLSLAN	NKLQVLPIGL	120
10	FQGLDSLES	LLSSNQLLQI	QPAHFSQCSN	LKELQLHGNH	LEYIPDGAFF	180
GKNSLTHISP	RVFQHLGNLQ	VLRLYENRLT	DIPMGTFDGL	VNLQELALQQ	NQIGLLSPGL	240
FHNHNLQRL	YLSNNHISQL	PPSIFMQLPQ	LNRLTLFGNS	LKELSLGIFG	PMPNLRELWL	300
YDNHISLPD	NVFSNLRQLQ	VLILSRNQIS	FISPGAFNGL	TELRELSLHT	NALQDLGDNV	360
15	FRMLANLQNI	SLQNNRLRQL	PGNIFANVNG	LMAIQLQNNQ	LENLPLGIFD	420
YDNPWRCDS	ILPLRNWLLL	NQPRLGTDVT	PVCFSPANVR	QQSLIIINVN	VAVPSVHVPE	480
VPSYPETPMY	PDTPSPYDPT	SVSSTTELTS	PVEDYTDLTT	IQVTDDRSVW	GMTQAQSGLA	540
IAAIVIGIVA	LACSLAACVG	CCCCKKRSQA	VLMQMKAPNE	C		

Seq ID NO: 612 DNA sequence

Nucleic Acid Accession #: XM_098151

Coding sequence: 1..447

20

1	11	21	31	41	51	
ATGATGCATT	TGCTCAATTC	TCAGGGCTGG	AATGAGCCGG	CTGGTCCCCC	AGAAAGCTGG	60
25	AGTGGGGTAC	AGAGTTTCAGT	TTTCTCTCT	CTTTACAGCT	CCTTGACAGT	120
TCTGGAGTGG	GAGCTGGGAG	TCAGTGTGG	AGAAGAAACA	ACAAAGCCA	ATTAGAACCA	180
CTATTTTAA	AAAGTGCTTA	CTGTGCACAG	ATACTCTTCA	AGCACTGGAC	GTGGATTCTC	240
30	TCCTAGCCC	TCAGCACCCC	TGCGGTAGGA	GTGCCGCCCTC	TACCCACTTG	300
CAGAGGCACT	TGCTCTTCTG	CATGGTGTCT	AATAGGCTGG	GAGTTTATT	TATCTCTTCA	360
AACTTTGTAC	AAGAGCTCAT	GGCTTGTCTT	GGGCTTTCGT	CATTAAACCA	AAGGAAATGG	420
AAGCCATTCC	CCGTGTGCTC	TCCTTAG				

Seq ID NO: 613 Protein sequence

Protein Accession #: XP_098151

35

1	11	21	31	41	51	
MMHLLNSQGW	NEPAGPPESW	SGVQSSVFLS	VYSSLTVPRP	SGVGAGSQCW	RRNNKSQLEP	60
40	LFLKSAYCAQ	ILFKHWTWIL	SLALSTPAVG	VPPLPTCDGV	QRHLDFCMVF	120
NFVQELMACL	GLSSLNQKRW	KPFPCCS				

Seq ID NO: 614 DNA sequence

Nucleic Acid Accession #: NM_002658.1

Coding sequence: 77..1372

45

1	11	21	31	41	51	
GTCCCCGCG	CGCCGTCGCG	CCCTCCTGCC	GCAGGCCACC	GAGGCGCGCG	CCGTCTAGCG	60
50	CCCCGACCTC	GCCACCATGA	GAGCCCTGCT	GGCGCGCCTG	CTTCTCTGCG	120
GAGCGACTCC	AAAGGCGACA	ATGAACCTCA	TCAAGTTCCA	TGGAAGCTGT	ACTGTCTAAA	180
TGGAGGAACA	TGTGTGTCCA	ACAAGTACTT	CTCCAACATT	CACTGGTGCA	ACTGCCCAAA	240
GAAATTCGGA	GGCGAGCACT	GTGAAATAGA	TAAGTCAAAA	ACCTGCTATG	AGGGGAATGG	300
60	TCACCTTTAC	CGAGGAAAGG	CCAGCACTGA	CACCATGGGC	CGGCCCTGCC	360
CTCTGCCACT	GTCTTTCAGC	AAACGTACCA	TGCCCCACAGA	TCTGATGCTC	TTCAGCTGGG	420
CCTGGGGAAA	CATAATTACT	GCAGGAACCC	AGACAACCGG	AGGCGACCCT	GGTGTATGTT	480
GCAGGTGGGC	CTAAAGCCGC	TTGTCCAAGA	GTGCATGGTG	CATGACTGCG	CAGATGGAAA	540
AAAGCCCTCC	TTCTCTCCAG	AAGAAATAAA	ATTTCACTGT	GGCCAAAAGA	CTCTGAGGCC	600
CCGCTTTAAG	ATTATTGGGG	GAGAAATCAC	CACCATCGAG	AACCAGCCCT	GGTTGCGGC	660
70	CATCTACAGG	AGGCACCGGG	GGGGCTCTGT	CACCTACGTG	TGTGGAGGCA	720
CCCTTGCTGG	GTGATCAGCG	CCACACACTG	CTTCATTGAT	TACCCAAAAGA	AGGAGGACTA	780
CATCGTCTAC	CTGGGTGCGT	CAAGGCTTAA	CTCCAACACG	CAAGGGGAGA	TGAAGTTTGA	840
GGTGGAAAAC	CTCATCTTAC	ACRAGGACTA	CAGCGCTGAC	ACGCTTGCTC	ACCACAACGA	900
CATTCGCTTG	CTGAAGATCT	GTTCACAGGA	GGGCAGGTGT	GCGCAGCCAT	CCCGGACTAT	960
65	ACAGACCATC	TGCTCGCCCT	CGATGTATAA	CGATCCCCAG	TTTGGCACA	1020
CACCTGGCTT	GGAAAAGAGA	ATTCTACCGA	CTATCTCTAT	CCGGAGCAGC	TGAAAATGAC	1080
TGTTGTGAAG	CTGATTTCCT	ACCGGGAGTG	TCAGCAGCCC	CACTACTACG	GCTCTGAAGT	1140
CACCACCAAA	ATGCTATGTG	CTGCTGACCC	CCAATGGAAA	ACAGATTCCCT	GCCAGGGAGA	1200
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70	CTGGGGCGGT	GGATGTGCCC	TGAAGGACAA	GCCAGGCGTC	TACACGAGAG	1320
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75	CACCAACAGG	GTGAACGACA	ATAGCTTTAC	CCTCACGGAT	AGGCCCTGGT	1560
CAGACCTCT	GGCCAGGATG	GAGGGGTGGT	CCTGACTCAA	CATGTTACTG	ACCAGCAACT	1620
TGCTTTTTTC	TGACTGAAG	CCTGCAGGAG	TAAAAAGGG	CAGGGCATCT	CCTGTGCATG	1680
GGCTCGAAGG	GAGAGCCAGC	TCCCCGACC	GGTGGGCATT	TGTGAGGCC	ATGGTTGAGA	1740
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80	AATGTGGGAG	CAGCGGTTTG	GGGAGCAGAG	ACACTAACGA	CTTCAGGGCA	1860
ATTCCATGAA	TGATCATGGA	AATATATATG	TGTGTGTATG	TTTGACACT	TGTTGTGTGG	1920
GCTGTGAGTG	TAAGTGTGAG	TAAGAGCTGG	TGTCTGATTG	TTAAGTCTAA	ATATTTCTCT	1980
AAACTGTGTG	GACTGTGATG	CCACACAGAG	TGGTCTTTCT	GGAGAGGTTA	TAGGTCACTC	2040
CTGGGGCTCT	TTGGGTCCCC	CACGTGACAG	TGCCTGGGAA	TGTACTTATT	CTGCAGCATG	2100
ACCTGTGACC	AGCACTGTCT	CAGTTTCACT	TTCACATAGA	TGTCCCTTTC	TTGGCCAGTT	2160
85	ATCCCTTCT	TTTAGCCTAG	TTCATCCAAT	CCTCACTGGG	TGGGGTGAGG	2220
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ATCAATAAAA	TGTGATTTTT	CTGA				

Seq ID NO: 615 Protein sequence
Protein Accession #: NP_002649.1

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10    GGEFTTIENQ PWFAAIYRRH RGGSVTVVCG GSLISPCWVI SATHCFIDYP KKEDYIVVYG 240
RSRLNSNTQGG EMKFEVENLI LHKDYSADTL AHNDIALLLK IRSKEGRCAQ PSRTIQTICL 300
PSMYNDPQFQG TSCBITGFGK ENSTDYLYPE QLKMTVVVKLI SHRECCQPHY YGSEVTTKML 360
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Seq ID NO: 616 DNA sequence
Nucleic Acid Accession #: NM_024422.1
Coding sequence: 202..2907

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25    GACCTGCCCC GAGCCTCTCT CATGGAGGCA GCCCGCCCTC CCGGCTCCTG GAACGGAGCC 240
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30    TTTACCATAT TACTTCCCAA CACTGAGAAC CAAGAAAAGA AGAAAATATT TGTCTTTTGT 540
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35    AACTTGTATT GTTCTCGTCC TGTAGATCGT GAGCAGTATG AATCTTTTGA GATAATTGCC 840
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40    CTATTTTCTA TGCATCCCAAC TACAGGCGTG ATCACCACAA CATCATCTCA GCTAGACAGA 1140
GAGTTAATTG ACAAGTACCA GTTGAAAATA AAAGTACAAG ACATGGATGG TCAGTATTTT 1200
GGTCTACAGA CAACTTCAAC TTGTATCATT AACATTGATG ATGTAAATGA CCACTTGCCA 1260
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CAAAATGGTG TAGTTAATGA AGCTCCATTT TCCAGAGAGG TAGTCCAAAG ATCAGCCATG 1560
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Seq ID NO: 617 Protein sequence
Protein Accession #: NP_077740.1

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 VTSVEENTVD VEILRVTVED KDLVNTANWR ANYTILKNE NGNFKIVTDA KTNEGVLCVV 420
 KPLNYEKKQ MLQIGVVNE APFSREASPR SAMSTATVTV NVEDQDEGPE CNPPIQTVRM 480
 KENAEGVGTTS NGYKAYDPET RSSSGIRYKK LTDPTGWVTI DENTGSIKVF RSLDREAETI 540
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 TSQPKVIPD DLAQNLIVS NTEAPGDDKV YSANGFTTQT VGASAGVCG TVGSGIKNGG 780
 QETIEMVKGQ HQTSSECRGA GHHTLDSCR GGHTVDNCR YTYSEWHSFT QPRLGEKVYL 840
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Seq ID NO: 618 DNA sequence
 Nucleic Acid Accession #: NM_004949.1
 Coding sequence: 202..2745

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Seq ID NO: 619 Protein sequence
 Protein Accession #: NP_004940.1

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 KENAEVGTTS NGYKAYDPET RSSSGIRYKK LTDPTGWTI DENTGSIKVF RSLDREASTI 540
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Seq ID NO: 620 DNA sequence
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Seq ID NO: 621 Protein sequence
 Protein Accession #: NP_115934.1

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 SECAGLEHGA WTLRACHLCR CIFGALHCLP LQTPDRCDPK DFLASHAHGP SAGGAPSLLL 180
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Seq ID NO: 622 DNA sequence
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 Coding sequence: 1..390

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Seq ID NO: 623 Protein sequence
 Protein Accession #: FGENESH predicted

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Seq ID NO: 624 DNA sequence
 Nucleic Acid Accession #: M18728.1
 Coding sequence: 51..1085

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 TGCCCAAGCC CTCATCTCC AGCAACAAC CCAACCCCGT GGAGGACAAG GATGCTGTGG 540
 CCTTCACTG TGAACCTGAG GTTCAGAAAC CAACCTACCT GTGGTGGGTA AATGTCAGA 600
 GCCTCCCGGT CAGTCCAGG CTGCAGCTGT CCAATGGCAA CATGACCTC ACTCTACTCA 660

	GCCTCAAAAG	GAACGATGCA	GGATCCTATG	AATGTGAAAT	ACAGAACCCA	GCGAGTGCCA	720
	ACCGCAGTGA	CCCAGTCACC	CTGAATGTCC	TCTATGGCCC	AGATGTCCCC	ACCATTTCCC	780
	CCTCAAAAGC	CAATTACCGT	CCAGGGGAAA	ATCTGAACCT	CTCCTGCCAC	GCAGCCTCTA	840
5	ACCCACCTGC	ACAGTACTCT	TGGTTTATCA	ATGGGACGTT	CCAGCAATCC	ACACAAGAGC	900
	TCTTTATCCC	CAACATCACT	GTGAATAATA	GCGGATCCTA	TATGTGCCAA	GCCCATAACT	960
	CAGCCACTGG	CCTCAATAGG	ACCAAGTCA	CGATGATCAC	AGTCTCTGGA	AGTGTCTCTG	1020
	TCCTCTCAGC	TGTGGCCACC	GTCGGCATCA	CGATTGGAGT	GCTGGCCAGG	GTGGCTCTGA	1080
	TATAGCAGCC	CTGGTGTATT	TTCGATATTT	CAGGAAGACT	GGCAGATTGG	ACCAGACCCCT	1140
10	GAATTCTTCT	AGCTCCTCCA	ATCCCATTTT	ATCCCATGGA	ACCACTAAAA	ACAAGGTCTG	1200
	CTCTGCTCCT	GAAGCCCTAT	ATGCTGGAGA	TGGACAATC	AATGAAAATT	TAAAGGGAAA	1260
	ACCTCAGGC	CTGAGGTGTG	TGCCACTCAG	AGACTTCACC	TAACTAGAGA	CAGTCAAACT	1320
	GCAAACCATG	GTGAGAAATT	GACGACTTCA	CACATATGGAC	AGCTTTTCCC	AAGATGTCAA	1380
	AACAAGACTC	CTCATCATGA	TAAGGCTCTT	ACCCCTTTT	AATTTGTCTT	TGCTTATGCC	1440
	TGCTCTTTT	CTGTGGCAGG	ATGATGCTGT	CATTAGTATT	TCACAAGAAG	TAGCTTCAGA	1500
15	GGGTAACTTA	ACAGAGTGTG	AGATCTATCT	TGTCAATCCC	AACGTTTAC	ATAAAATAAG	1560
	AGATCCTTTA	GTGCACCCAG	TGACTGACAT	TAGCAGCATC	TTTAACACAG	CCGTGTGTTC	1620
	AAATGTACAG	TGGTCTTTT	CAGAGTTGGA	CTTCTAGACT	CACCTGTCTT	CACTCCCTGT	1680
	TTTAATTCAA	CCCAGCCATG	CAATGCCAAA	TAATAGAATT	GCTCCCTACC	AGCTGAACAG	1740
	GGAGGAGTCT	GTGCAGTTTC	TGACACTTGT	TGTTGAACAT	GGCTAAATAC	AATGGGTATC	1800
20	GCTGAGACTA	AGTTGTAGAA	ATTAACAAAT	GTGCTGCTTG	GTTAAATAGG	CTACACTCAT	1860
	CTGACTCATT	CTTTATTCTA	TTTGTATGTT	TTTGTATCTT	GCCTAAGGTG	CGTAGTCCAA	1920
	CTCTTGGTAT	TACCTCCTTA	ATAGTCATAC	TAGTAGTCAT	ACTCCCTGGT	GTAGTGTATT	1980
	CTCTAAAAGC	TTTAAATGTC	TGCATGCAGC	CAGCCATCAA	ATAGTGAATG	GTCTCTCTTT	2040
25	GGCTGGAATT	ACAAAACCTCA	GAGAAATGTG	TCATCAGGAG	AACATCATAA	CCCATGAAGG	2100
	ATAAAAGCCC	CAATGTGTGG	TAAGTGATAA	TAGCACTAAT	GCTTTAAGAT	TTGGTCACAC	2160
	TCTCACCTAG	GTGAGCGCAT	TGAGCCAGTG	GTGCTAAATG	CTACATACTC	CAACTGAAAT	2220
	GTTAAGGAAG	AAGATAGATC	CAATTAAAAA	AAATTAATAA	CAATTTAAAA	AAAAAAAGA	2280
	ACACAGGAGA	TTCAGTCTA	CTTGAGTTAG	CATAATACAG	AAGTCCCTTC	TACTTTAACT	2340
30	TTTACAAAAA	AGTAACTGGA	ACTAATCTGA	TGTTAAACCA	TGTATTATT	TCTGTGGTTC	2400
	TGTTTCTCTG	TTCCAATTG	ACAAACCCA	CTGTTCTTGT	ATTGTATTGC	CCAGGGGGAG	2460
	CTATCACTGT	ACTGTAGAG	TGGTGCTGCT	TTAATTCATA	AATCACAAT	AAAAGCCAAT	2520
	TAGCTCTATA	ACT					

Seq ID NO: 625 Protein sequence
Protein Accession #: AAA59907.1

	1	11	21	31	41	51	
40	MGPPSAPPCR	LHVPWKEVLL	TASLLTFWNP	PTTAKLTIES	TPFNVAEGKE	VLLLAHNLPO	60
	NRIGVSWYK	ERVDGNSLIV	GYVIGTQAT	PGPAYSGRET	IYPNASLLIQ	NVTQNDTGFY	120
	TLQVIKSLV	NEEATGQFHV	YPELPKPSIS	SNNSNPVEDK	DAVAFTCEPE	VQNTTYLWHV	180
	NGQSLPVSPR	LQLSNGMNTL	TLLSVKRND	GSYECEIQNP	ASANRSDPVT	LNVLVGPDPV	240
	TIKSPSKANYR	PGENLNLSCH	AASNPPAQYS	WFINGTFQOS	TQELFIPNIT	VNNSGSSYMCQ	300
45	AHNSATGLNR	TTVTMITVSG	SAPVLSAVAT	VGITIGVLAR	VALI		

Seq ID NO: 626 DNA sequence
Nucleic Acid Accession #: M18728.1
Coding sequence: 1355..1657

50	1	11	21	31	41	51	
	GGAGCTCAAG	CTCCTCTACA	AAGAGGTGGA	CAGAGAAGAC	AGCAGAGACC	ATGGGACCCC	60
	CCTCAGCCCC	TCCCTGCAGA	TTGCATGTCC	CCTGGAAGGA	GGTCTGTCTC	ACAGCCTCAC	120
55	TTCTAACCTT	CTGGAACCCA	CCCACCACCTG	CCAAGCTCAC	TATTGAATCC	ACGCCATTCA	180
	ATGTCGCAGA	GGGGAAGGAG	GTTCTTCTAC	TCGCCCACAA	CCTGCCCCAG	AATCGTATTG	240
	GTTACAGCTG	GTACAAAGGC	GAAAGAGTGG	ATGGCAACAG	TCTAATTGTA	GGATATGTAA	300
	TAGGAACCTA	ACAAGCTACC	CCAGGGCCCG	CATACAGTGG	TCGAGAGACA	ATATACCCCA	360
	ATGCATCCCT	GCTGATCCAG	AACGTCACCC	AGAATGACAC	AGGATTCTAT	ACCCTACAG	420
60	TCATAAGTTC	AGATCTTGTG	AATGAAGAAG	CAACCGGACA	GTTCCATGTA	TACCCGGAGC	480
	TGCCCCAGCC	CTCCATCTCC	AGCAACAACCT	CCAACCCCGT	GGAGGACAAG	GATGCTGTGG	540
	CCTTCACCTG	TGAACCTGAG	GTTCAGAACA	CAACCTACCT	GTGGTGGGTA	AATGTCAGAA	600
	GCCTCCCGGT	CAGTCCAGG	CTGCAGCTGT	CCAATGGCAA	CATGACCCCTC	ACTCTACTCA	660
	GCGTCAAAAG	GAACGATGCA	GGATCCTATG	AATGTGAAAT	ACAGAACCCA	GCGAGTGCCA	720
65	ACCGCAGTGA	CCCAGTCACC	CTGAATGTCC	TCTATGGCCC	AGATGTCCCC	ACCATTTCCC	780
	CCTCAAAAGC	CAATTACCGT	CCAGGGGAAA	ATCTGAACCT	CTCCTGCCAC	GCAGCCTCTA	840
	ACCCACCTGC	ACAGTACTCT	TGGTTTATCA	ATGGGACGTT	CCAGCAATCC	ACACAAGAGC	900
	TCTTTATCCC	CAACATCACT	GTGAATAATA	GCGGATCCTA	TATGTGCCAA	GCCCATAACT	960
	CAGCCACTGG	CCTCAATAGT	ACCACAGTCA	CGATGATCAC	AGTCTCTGGA	AGTGTCTCTG	1020
70	TCCTCTCAGC	TGTGGCCACC	GTCGGCATCA	CGATTGGAGT	GCTGGCCAGG	GTGGCTCTGA	1080
	TATAGCAGCC	CTGGTGTATT	TTCGATATTT	CAGGAAGACT	GGCAGATTGG	ACCAGACCCCT	1140
	GAATTCTTCT	AGCTCCTCCA	ATCCCATTTT	ATCCCATGGA	ACCACTAAAA	ACAAGGTCTG	1200
	CTCTGCTCCT	GAAGCCCTAT	ATGCTGGAGA	TGGACAATC	AATGAAAATT	TAAAGGGAAA	1260
	ACCTCAGGC	CTGAGGTGTG	TGCCACTCAG	AGACTTCACC	TAACTAGAGA	CAGTCAAACT	1320
75	GCAAACCATG	GTGAGAAATT	GACGACTTCA	CACATATGGAC	AGCTTTTCCC	AAGATGTCAA	1380
	AACAAGACTC	CTCATCATGA	TAAGGCTCTT	ACCCCTTTT	AATTTGTCTT	TGCTTATGCC	1440
	TGCTCTTTT	GCTTGGCAGG	ATGATGCTGT	CATTAGTATT	TCACAAGAAG	TAGCTTCAGA	1500
	GGGTAACTTA	ACAGAGTGTG	AGATCTATCT	TGTCAATCCC	AACGTTTAC	ATAAAATAAG	1560
	AGATCCTTTA	GTGCACCCAG	TGACTGACAT	TAGCAGCATC	TTTAACACAG	CCGTGTGTTC	1620
80	AAATGTACAG	TGGTCTTTT	CAGAGTTGGA	CTTCTAGACT	CACCTGTCTT	CACTCCCTGT	1680
	TTTAATTCAA	CCCAGCCATG	CAATGCCAAA	TAATAGAATT	GCTCCCTACC	AGCTGAACAG	1740
	GGAGGAGTCT	GTGCAGTTTC	TGACACTTGT	TGTTGAACAT	GGCTAAATAC	AATGGGTATC	1800
	GCTGAGACTA	AGTTGTAGAA	ATTAACAAAT	GTGCTGCTTG	GTTAAATAGG	CTACACTCAT	1860
	CTGACTCATT	CTTTATTCTA	TTTGTATGTT	TTTGTATCTT	GCCTAAGGTG	CGTAGTCCAA	1920
85	CTCTTGGTAT	TACCTCCTTA	ATAGTCATAC	TAGTAGTCAT	ACTCCCTGGT	GTAGTGTATT	1980
	CTCTAAAAGC	TTTAAATGTC	TGCATGCAGC	CAGCCATCAA	ATAGTGAATG	GTCTCTCTTT	2040
	GGCTGGAATT	ACAAAACCTCA	GAGAAATGTG	TCATCAGGAG	AACATCATAA	CCCATGAAGG	2100
	ATAAAAGCCC	CAATGTGTGG	TAAGTGATAA	TAGCACTAAT	GCTTTAAGAT	TTGGTCACAC	2160

TCTCACCTAG GTGAGCGCAT TGAGCCAGTG GTGCTAAATG CTACATACTC CAACTGAAAT 2220
 GTTAAGGAAG AAGATAGATC CAATTAAAAA AAATTAAAAAC CAATTTAAAAA AAAAAAAGA 2280
 ACACAGGAGA TTCCAGTCTA CTTGAGTTAG CATAATACAG AAGTCCCTC TACTTTAACT 2340
 TTTACAAAAA AGTAACCTGA ACTAATCTGA TGTAAACCA TGTATTATT TCTGTGGTTC 2400
 TGTTCCTTG TTCCAATTG ACAAACCCA CTGTTCTGT ATTGTATTGC CCAGGGGAG 2460
 CTATCACTGT ACTGTAGAG TGGTGCTGCT TTAATTCATA AATCACAAT AAAAGCCAAT 2520
 TAGCTCTATA ACT

Seq ID NO: 627 Protein sequence
 Protein Accession #: AAA59908.1

1 11 21 31 41 51
 | | | | |
 MDSFSQDVKT RLLIMIRLLP PFNLSLLMPA SPAWQDDAVI SISQEVASEG NLTECQIYLV 60
 NPNVLHKIRD PLVHPVTDIS SIFNTAVCSN VQWSFSELDP

Seq ID NO: 628 DNA sequence
 Nucleic Acid Accession #: M18728.1
 Coding sequence: 2370..2501

1 11 21 31 41 51
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 GGAGCTCAAG CTCCTCTACA AAGAGGTGGA CAGAGAAGAC AGCAGAGACC ATGGGACCCC 60
 CCTCAGCCCC TCCCTGCAGA TTGCATGTCC CCTGGAAGGA GGTCTGTCTC ACAGCCTCAC 120
 TTCTAACCTT CTGGAACCCA CCCACCACTG CCAAGCTCAC TATTGAATCC ACGCCATTCA 180
 ATGTCGCGA GGGGAAGGAG GTTCTTCTAC TCGCCACAA CCTGCCCCAG AATCGTATTG 240
 GTTACAGCTG GTACAAGGC GAAAGAGTGG ATGGCAACAG TCTAATTGTA GGATATGTAA 300
 TAGGAACCTA ACAAGCTACC CCAGGGCCCG CATACTAGTG TCGAGAGACA ATATACCCCA 360
 ATGCATCCCT GTGATCCAG AACGTCACCC AGAATGACAC AGGATTCTAT ACCCTACAAG 420
 TCATAAAGTC AGATCTGTG AATGAAGAAG CAACCGGACA GTTCCATGTA TACCCGGAGC 480
 TGCCCAAGCC CTCCATCTCC AGCAACAAC CCAACCCCGT GGAGGACAAG GATGCTGTGG 540
 CCTTCACCTG TGAACCTCAG GTTCAGAACA CAACCTACCT GTGGTGGGTA AATGGTCAGA 600
 GCCTCCCGGT CAGTCCCAGG CTGCAGCTGT CCAATGGCAA CATGACCCCTC ACTCTACTCA 660
 GCGTCAAAAG GAACGATGCA GGATCCTATG AATGTGAAAT ACAGAACCCA GCGAGTGCCA 720
 ACCGCAGTGA CCCATCAGG CTGAATGTCC TCTATGGCCC AGATGTCCCC ACCATTTCCT 780
 CCTCAAGGCG CAATTACCGT CCAGGGGAAA ATCTGAACCT CTCCTGCCAC GCAGCCTCTA 840
 ACCCACTGCG ACAGTACTCT TGGTTTATCA ATGGGACGTT CCAGCAATCC ACACAAGAGC 900
 TCTTTATCCC CAACATCACT GTGAATAATA GCGGATCCTA TATGTGCCAA GCCCATAACT 960
 CAGCCACTGG CCTCAATAGG ACCACAGTCA CGATGATCAC AGTCTCTGGA AGTGTCTCTG 1020
 TCCTCTCAGC TGTGGCCACC GTCGGCATCA CGATTGGAGT GCTGGCCAGG GTGGCTCTGA 1080
 TATAGCAGCC TGGGTGTATT TTCGATATT CAGGAAGACT GGCAGATTGG ACCAGACCTT 1140
 GAATTCCTCT AGCTCCTCCA ATCCCATTTT ATCCCATGGA ACCACTAAAA ACAAGGTCTG 1200
 CTCTGTCTCT GAAGCCCTAT ATGCTGGAGA TGGACAATC AATGAAATTT TAAAGGGAAA 1260
 ACCCTCAGCG CTGAGGTGTG TGCCACTCAG AGACTTCACC TAACCTAGAGA CAGTCAAACT 1320
 GCAAAACCATG GTGAGAAATT GACGACTTCA CACTATGGAC AGCTTTTCCC AAGATGTCAA 1380
 AACAAGACTC CTCATCATGA TAAGGCTCTT ACCCCCTTTT AATTTGTCCT TGCTTATGCC 1440
 TGCTCTCTTC GCTTGGCAGG ATGATGCTGT CATTAGTATT TCACAAGAAG TAGCTTCAGA 1500
 GGGTAACCTA ACAGAGTGTG AGATCTATCT TGTCAATCCC AACGTTTAC ATAAAAAAG 1560
 AGATCCTTTA GTGCACCCAG TGACTGACAT TAGCAGCATC TTTAACACAG CCGTGTGTTT 1620
 AAATGTACAG TGGTCTTTT CAGAGTTGGA CTTCTAGACT CACTGTCTCT CACTCCCTGT 1680
 TTTAATTCAA CCCAGCCATG CAATGCCAAA TAATAGAATT GCTCCTTACC AGCTGAACAG 1740
 GGAGGAGTCT GTGCAGTTTC TGACACTTGT TGTGTAACAT GGCTAAATAC AATGGGTATC 1800
 GCTGAGACTA AGTTGTAGAA ATTAACAAAT GTGCTGCTTG GTTAAATGG CTACACTCAT 1860
 CTGACTCAT TTTTATTCTA TTTTAGTTGG TTTGTATCTT GCCTAAGGTG CGTAGTCCAA 1920
 CTCTTGGTAT TACCTCCTA ATAGTCATAC TAGTAGTCAT ACTCCCTGGT GTAGTGTATT 1980
 CTCATAAAGC TTTAAATGTC TGCATGCAGC CAGCCATCAA ATAGTGAATG GTCTCTCTTT 2040
 GGCTGGAATT ACAAACTCA GAGAAATGTG TCATCAGGAG AACATCATAA CCCATGAAGG 2100
 ATAAAAGCCC CAAATGGTGG TAACGTGATA TAGCACTAAT GCTTTAAGAT TTGGTCACAC 2160
 TCTCACCTAG GTGAGCGCAT CAATTAAAAA AAATTAAAAAC CAATTTAAAAA AAAAAAAGA 2280
 ACACAGGAGA TTCCAGTCTA CTTGAGTTAG CATAATACAG AAGTCCCTC TACTTTAACT 2340
 TTTACAAAAA AGTAACCTGA ACTAATCTGA TGTAAACCA TGTATTATT TCTGTGGTTC 2400
 TGTTCCTTG TTCCAATTG ACAAACCCA CTGTTCTGT ATTGTATTGC CCAGGGGAG 2460
 CTATCACTGT ACTGTAGAG TGGTGCTGCT TTAATTCATA AATCACAAT AAAAGCCAAT 2520
 TAGCTCTATA ACT

Seq ID NO: 629 Protein sequence
 Protein Accession #: AAA59909.1

1 11 21 31 41 51
 | | | | |
 MLTNVFIIVV LPPCSNLTKP TVLVLYCPGG AITVLVEWCC FNS

Seq ID NO: 630 DNA sequence
 Nucleic Acid Accession #: NM_016639.1
 Coding sequence: 40..429

1 11 21 31 41 51
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 CGGTTGCTGC GGCTCCTCGT GCTGGGGCTC TGGCTGGCGT TGTGCGCTC CGTGGCCGGG 120
 GAGCAAGCGC CAGGACCGCG CCCCTGCTCC CGCGGCGAGT CCTGGAGCGG GGACCTGGAC 180
 AAGTGCATGG ACTGCGGCTC TTGCAGGGCG CGACCGCACA GCGACTTCTG CCTGGGCTGC 240
 CTGTCAGCAG CTCCTGCCCT CTTCCGGCTG CTTTGGCCCA TCCTTGGGGG CGCTCTGAGC 300
 CTGACCTTGC TGCTGGGGCT GCTTCTGCGC TTTTGGTCTT GGAGACGATG CCGCAGGAGA 360
 GAGAAGTTCA CCACCCCAT AGAGGAGACC GCGGAGAGG GCTGCCAGC TGTGGGCTG 420

ATCCAGTGAC AATGTGCCCC CTGCCAGCCG GGGCTCGCCC ACTCATCATT CATTATCCCA 480
 TTCTAGAGCC AGTCTCTGCC TCCCAGACGC GCGGGGAGCC AAGCTCCTCC AACCAACAGG 540
 GGGGTGGGGG GCGGTGAATC ACCTCTGAGG CCTGGGCCCA GGGTTCAGGG GAACCTTCCA 600
 AGGTGTCTGG TTGCCCTGCC TCTGGCTCCA GAACAGAAAG GGAGCCTCAC GCTGGCTCAC 660
 ACAAACAGC TGACACTGAC TAAGGAACTG CAGCATTTGC ACAGGGGAGG GGGGTGCCCT 720
 CCTTCTTAG GACCTGGGGG CCAGGCTGAC TTGGGGGGCA GACTTGACAC TAGGCCCCAC 780
 TCACCTAGAT GTCTGAAAT TCCACCAGG GGGTCACCT GGGGGTTAG GGACCTATT 840
 TTAACACTAG GGGCTGGCCC ACTAGGAGGG CTGGCCCTAA GATACAGACC CCCCCAATC 900
 CCCAAGCGG GGAGGAGATA TTTATTTTGG GGAGAGTTTG GAGGGGAGGG AGAATTTATT 960
 AATAAAGAA TCTTTAATT TAAAAAATA AAAAAAATA

Seq ID NO: 631 Protein sequence
 Protein Accession #: NP_057723.1

1 11 21 31 41 51
 MARGSLRRLL RLLVLGLWLA LLRSVAGEQA PGTAPCSRGS SWSADLDKCM DCASCRARPH 60
 SDFCLGCAAA PPAPFRLWLP ILGGALSLTF VLGLLSGLFV WRRCRREKEF TPIETETGGE 120
 GCPAVALIQ

Seq ID NO: 632 DNA sequence
 Nucleic Acid Accession #: NM_003816.1
 Coding sequence: 79..2538

1 11 21 31 41 51
 CGGCAGGGTT GGAATATGAT GGAAGAGGCG GAGGTGGAGG CGACCGAGTG CTGAGAGGAA 60
 CCTGCGGAAT CGGCCGAGAT GGGGTCTGGC GCGCGCTTTC CCTCGGGGAC CCTTCGTGTC 120
 CGGTGGTTGC TGTGTCTTGG CCTGGTGGGC CCAGTCTCTG GTGCGGCGCG GCCAGGCTTT 180
 CAACAGACCT CACATCTTTC TTCTTATGAA ATTATACTC CTGAGGAGAT AACTAGAGAA 240
 AGAAGAGAAG CCCCTAGGCT CTATTCAAAA CAAGTATCTT ATGTTATTCA GGCTGAAGGA 300
 AAAGAGCATA TATTACTTCT GGAAAGGAAC AAAGACCTTT TGCTTGAAGA TTTTGTGGTT 360
 TATACTTACA ACAAGGAAGG GACTTTAATC ACTGACCATC CCAATATACA GAATCATTGT 420
 CATTATCGGG GCTATGTGGA GGGAGTTCAT AATTATCCCA TTGCTCTTAG CGACTGTTTT 480
 GGACTCAGAG GATTGCTGCA TTTAGAGAAT GCGAGTTATG GGATTGAACC CTGCAGAAC 540
 AGCTCTCATT TTGAGCACAT CATTATCGA ATGGATGATG TCTACAAAGA GCCTCTGAAA 600
 TGTGGAGTTT CCAACAAGGA TATAGAGAAA GAAACTGCAA AGGATGAAGA GGAAGAGCCT 660
 CCCAGCATGA CTCAGTACT TCGAAGAAGA AGAGCTGTCT TGCCACAGAC CCGTATGTG 720
 GAGCTGTTC TGTGCTAGA CAAGGAAAGG TATGACATGA TGGGAAGAAA TCAGACTGCT 780
 GTGAGAGAAG AGATGATTCT CCTGGCAAC TACTTGGATA GTATGTATAT TATGTTAAAT 840
 ATTGGAATTG TGCTAGTTGG ACTGGAGATT TGGACCAATG GAAACCTGAT CAACATAGTT 900
 GGGGTGCTG GTGATGTGCT GGGGAACCTC GTGCACTGGC GGGAAAAGTT TCTTATACA 960
 CGTGGGAGAC ATGACAGTGC ACAGCTAGTT CTAAGAAAG GTTTTGGTGG AACTGCAGGA 1020
 ATGGCATTG TGGAACAGC GTGTTCAAGG AGCCACGCGAG GCGGGATTAA TGTGTTTGA 1080
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 ATGAATCAGC ATGATGGGAG AGATTGTTCC TGTGGAGCAA AGAGCTGCAT CATGAATTCA 1200
 GGAGCATCGG GTTCCAGAAA CTTTAGCAGT TGCAGTGCAG AGGACTTTGA GAAGTTAACT 1260
 TTAATAAAG GAGGAACTG CCTTCTAAT ATTCCAAAGC CTGATGAAGC CTATAGTGCT 1320
 CCTCTCTGT GTAATAAGTT GGTGGACGCT GGGGAAGAGT GTGACTGTGG TACTCCAAAG 1380
 GAATGTGAAT TCGACCTTGG CTGCGAAGGA AGTACCTGTA AGCTTAAATC ATTTGCTGAG 1440
 TGTGCATATG GTGACTGTG TAAAGACTGT CGGTTCTTTC CAGGAGGTAC TTTATGCCGA 1500
 GGAATAACCA GTGAGTGTGA TGTTCAGAG TACTGCAATG GTTCTTCTCA GTTCTGTGAG 1560
 CCAGATGTTT TATTTCAGAA TGGATATCCT TGCCAGATA ACAAGCCTA TTGCTACAAC 1620
 GGCATGTGCC AGTATTATGA TGCTCAATGT CAAGTCACTT TTGGCTCAA AGCCAAGGCT 1680
 GCGCCCAAG ATTGTTTCT TGAAGTGAAT TCTAAAGGTG ACAGATTGG CAATTGTGGT 1740
 TTCTCTGGCA ATGAATACAA GAAGTGTGCC ACTGGGAATG CTTTGTGTGG AAAGCTTCAG 1800
 TGTGAGAATG TACAAGAGAT ACCTGTATTT GGAATTGTGC CTGCTATTAT TCAAACGCT 1860
 AGTCGAGGCA CCAATGTTG GGGTGTGGAT TTCCAGCTAG GATCAGATGT TCCAGATCCT 1920
 GGGATGTTA ACGAAGGCAC AAAATGTGGT GCTGGAAGA TCTGTAGAAA TCTCCAGTGT 1980
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 TTGAGGGACG GACTTCTGGT CTTCTTCTTC CTAATTGTTC CCCTTATTGT CTGTGCTATT 2220
 TTTATCTTCA TCAAGAGGGA TCAACTGTGG AGAAGCTACT TCAGAAAGAA GAGATCACAA 2280
 ACATATGAGT CAGATGGCAA AAATCAAGCA AACCTTCTA GACAGCCGGG GAGTGTTCCT 2340
 CGACATGTTT CTCCAGTGAC ACCTCCAGCA GAAGTTCCTA TATATGCAA CAGATTTGCA 2400
 TTACCAACCT ATGCAGCCAA GCAACCTCAG CAGTTCCTAT CAAGGCCACC TCCACCACAA 2460
 CCGAAAGTAT CATCTCAGGG AAACCTAATT CCTGCCGCTC CTGCTCCTGC ACCTCCTTTA 2520
 TATAGTTCCT TCACTTGATT TTTTAACTT TCTTTTGA AATGCTTCA GGGAACTGAG 2580
 CTAATCTTTT TTTTCTTCT TGATGTTTC TTGAAAAGCC TTTCTGTTGC AACTATGAAT 2640
 GAAACAAAAA CACCACAAA CAGACTTCAC TAACACAGAA AAACAGAAAC TGAGTGTGAG 2700
 AGTTGTGAAA TACAAGGAAA TGCAGTAAAG CCAGGGAATT TACAATAACA TTTCCGTTTC 2760
 CATCATGAAA TAAGTCTTAT TCAGTCACTG GTGAGGTTAA TGCACTAATC ATGGATTTT 2820
 TGAACATGTT ATTGAGTGA TTCTCAAAAT AACTGTATTG TGTAAGATT TTTGTCAAT 2880
 AGTGTAAAG TGTATTCTG AATTTCTAC CTTAGTTATC ATTAATGTAG TTCCTCATT 2940
 AACATGTGAT AATCTAATAC CTGTGAAAAC TGACTAATCA GCTGCCAATA ATATCTAATA 3000
 TTTTTCATCA TGTCAAGAA TATAATCAT ATACTCTAGA ATCTTGTCTG TCACTCACTA 3060
 CATGAATAAG CAAATATTGT CTTCAAAAGA ATGCACAAGA ACCACAATTA AGATGTCATA 3120
 TTATTTTGAA AGTACAAAT ATACTAAAAG AGTGTGTGTG TATTACGCA GTTACTCGCT 3180
 TCCATTTTAA TGACCTTTCA ACTATAGGTA ATAACCTCTA GAGAAATTAA TTTAATATTA 3240
 GAATTTCTAT TATGAATCAT GTGAAAGCAT GACATTCGTT CACAATAGCA CTATTTTAAA 3300
 TAAATATATA GCTTTAAGGT ACGAAGTATT TAATAGATCT AATCAATAT GTTGATTAT 3360
 GGCATAATA AGCAGGAGC AATTATAAAA TCTTCAATCA ATTGAACCTT TACAAAACCA 3420
 CTTGAGAATT TCATGAGCAC TTTAAATCT GAACCTTCAA AGCTTGTCTAT TAAATCATT 3480
 AGAATGTTA CATTTACTAA GGTGTGCTGG GTCATGTAAA ATATTAGACA CTAATATTTT 3540
 CATAGAAATT AGGCTGGAGA AAGAAGGAAG AAATGGTTT CTTAATATACC TACAAAAAAG 3600
 TTACTGTGGT ATCTATGAGT TATCATCTTA GCTGTGTAA AAATGAATTT TTAATATGGC 3660

AGATATGGTA TGGATCGTAA AATTTTAAGC ACTAAAAATT TTTTCATAAC CTTTCATAAT 3720
 AAAGTTTAAT AATAGGTTTA TTAAGTGAAT TTCATTAGTT TTTTAAAGT GTTTTGGTT 3780
 TGTGTATATA TACATATACA AATACAACAT TTACAATAAA TAAAAACTT GAAATCTCA 3840
 AAAAAAAAAA AAAAAAAAAA AAAAA

Seq ID NO: 633 Protein sequence
 Protein Accession #: NP_003807.1

1 11 21 31 41 51
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 MGSARFPSPG TLRVRWLLLL GLVGPVLGAA RPFQQTSHL SSYEIITPWR LTRERREAPR 60
 PYSKQVSYVI QAEGKEHIIH LERNKDLLPE DFVVYTYNKE GTLITDHPNI QNHCHYRGYV 120
 EGVHNSIAL SDPCFLRGLL HLENASYGIE PLQNSSHFEH IYRMDVYK EPLKCGVSNK 180
 DIEKETAKDE EEEPPSMTQL LRRRAVLPO TRYVELFIVV DKERYDMMGR NQTAVREEMI 240
 LLANYLDSMY IMLNIRIVLV GLEIWTNGL INIVGGAGDV LGNFVQWREK FLITRRRHDS 300
 AQLVLKKGFG GTAGMAFVGT VCSRSAGGI NVFGQITVET FASIVAHELG HNLGMNHDDG 360
 RDCSCGAKSC IMNSGASGR NFSSCSAEDF EKLTLNKGGL CLLNIPKPDE AYSAPSCGNK 420
 LVDAGEECDC GTPKECELD CCEGSTCKLK SFAECAYGDC CKDCRFLPGG TLCRGKTSEC 480
 DVPEYCNSS QFCQPDVFIQ NGYPCQNNKA YCYNMGCMQY DAQCQVIFGS KAKAAPKDCF 540
 IEVNSKGRDF GNCQPSGNEY KKCATGNALC GKLCENVOE IPVFGIVPAI IQTPSRGKTC 600
 WGVDFQLGSD VPDPMVNEG TKCGAGKICR NFQCVDSVL NYDCDVQKKC HGHGVCNSNK 660
 NCHCENGWAP PNCETKGVGG SVDSGPTYNE MNTALRDGLL VFFFLIVPLI VCAIFIFIKR 720
 DQLWRSYPRK KRSQTYESDG KNOANPSRQP GSVPRHVSPV TTPREVPIYA NRFAPVPTAA 780
 KQPQPPSRP PPPQPKVSSQ GNLPARPAP APPLYSSLT

Seq ID NO: 634 DNA sequence
 Nucleic Acid Accession #: NM_002091.1
 Coding sequence: 56..503

1 11 21 31 41 51
 | | | | |
 AGTCTCTGCT CTTCCAGGCC TCTCCGGCGC GCTCCAAGGG CTTCCCGTCG GGACCATGCG 60
 CGGCAGTGAG CTCCCGCTGG TCCTGCTGGC GCTGGTCTCT TGCCTAGCGC CCCGGGGGCG 120
 AGCGGTCCCG CTGCTCGCGG GCGGAGGGAC CGTGCTGACC AAGATGTACC CGCGCGGCAA 180
 CCACTGGGCG GTGGGGCACT TAATGGGGAA AAGAGCACA GGGGAGTCTT CTTCTGTTTC 240
 TGAGAGAGGG AGCCTGAAGC AGCAGCTGAG AGAGTACATC AGGTGGGAAG AAGCTGCAAG 300
 GAATTTGCTG GGTCTCATAG AAGCAAAGGA GAACAGAAAC CACCAGCCAC CTCAACCCAA 360
 GGCCTTGGCG AATCAGCAGC CTTCTGGGGA TTCAGAGGAT AGCAGCAACT TCAAAGATGT 420
 AGGTTCAAAA GGCAAGTTG GTAGACTCTC TGCTCCAGGT TCTCAACGTG AAGGAAGGAA 480
 CCCCCAGCTG AACCAAGCAT GATAATGATG GCCTCTCTCA AAAGAGAAAA ACAAAACCCC 540
 TAAGAGACTG AGTTCTGCAA GCATCAGTTC TACGGATCAT CAACAAGATT TCCTTGTCGA 600
 AAATATTTGA CTATTCTGTA TCTTTTCATC TTGACTAAAT TCGTGATTTT CAAGCAGCAT 660
 CTTCTGGTTT AAACCTGTTT GCTGTGAACA ATTGTCGAAA AGAGTCTTCC AATTAATGCT 720
 TTTTATATC TAGGCTACCT GTTGTTTAGA TTCAGGCCCC CGAGCTGTGA CCATTACACA 780
 TAAAGCTTA AACACAT

Seq ID NO: 635 Protein sequence
 Protein Accession #: NP_002082.1

1 11 21 31 41 51
 | | | | |
 MRGSELPLVL LALVLCLAPR GRAVPLPAGG GTVLTMYPR GNHWAVGHLM GKKSTGESSS 60
 VSERGSLKQQ LREYIRWEEA ARNLLGLIEA KENRNHQPPQ PKALGNQPS WDESDSSNFK 120
 DVGSKGKQVR LSAPGSQREG RNPQLNQ

Seq ID NO: 636 DNA sequence
 Nucleic Acid Accession #: NM_016522.1
 Coding sequence: 265..1299

1 11 21 31 41 51
 | | | | |
 GCGGAAGCAG CGAGGAGGGA GCCCCTTTG GCCGTCCTCC GTGGAACCGG TTTTCCGAGG 60
 CTGGCAAAAG CCGAGGCTGG ATTTGGGGGA GGAATATTAG ACTCGGAGGA GTCTGCGCGC 120
 TTTTCTCTCT CCCGCGCTCC CCGGTGCGCG CGGGTTCAAC GCTCAGTCCC CGCGCTCGCT 180
 CCGCACCCCA CCCACTTCTT GTGCTCGCCC GGGGGGCGTG TGCCGTGCGG CTGCGGAGT 240
 TCGGGGAAGT TGTGGCTGTC GAGAATGGGG GTCTGTGGGT ACCTGTTCTT GCCCTGGAAG 300
 TGCTCTGTGG TCGTGTCTCT CAGGCTGCTG TTCCTTGATC CCACAGGAGT GCCCGTGGCG 360
 AGCGGAGATG CCACCTTCCC CAAAGCTATG GACAACGTGA CGGTCCGCA GGGGAGAGC 420
 GCCACCTCA GGTGCACTAT TGACAACCGG GTCAACCGGG TGGCTGGCT AAACCGCAGC 480
 ACCATCTCT ATGCTGGGAA TGACAAGTGG TGCTTGATC CTGCGTGGT CCTTCTGAGC 540
 AACACCCAAA CGCAGTACAG CATCGAGATC CAGAACGTGG ATGTGTATGA CGAGGGCCCT 600
 TACACCTGCT CGGTGAGAC AGACAACCA CCAAGACCT CTAGGGTCCA CTTCTATGTG 660
 CAAGTATCT CCAAAATTGT AGAGATTCT TCAGATATCT CCATTAATGA AGGGAACAAT 720
 ATTAGCTCA CTGCTAGC AACTGGTAGA CCAGAGCCTA CGTTACTTG GAGACACATC 780
 TCTCCCAAAG CGGTGGCTT TGTGAGTGAA GACGAATACT TGGAAATTCA GGGCATCACC 840
 CGGGAACAGT CAGGGGACTA CGAGTGAGT GCCTCCAATG ACCTGGCCCG GCCCGTGGTA 900
 CGGAGAGTAA AGGTACCTG CACTATCCA CCATACATT CAGAAGCCAA GGTACAGGT 960
 GTCCCGTGG GACAAAAGGG GACACTGCAG TGTGAAGCCT CAGCAGTCCC CTCAGCAGAA 1020
 TTCCAGTGGT ACAAGGATGA CAAAGACTG ATTGAAGGAA AGAAAGGGGT GAAAGTGGAA 1080
 AACAGACCTT TCTCTCTCAA ACTCATCTT TCAATGTCT CTGAACATGA CTATGGGAAC 1140
 TACACTTGGG TGGCTCCAA CAAGCTGGG CACACCAATG CCAGCATCAT GCTATTGGT 1200
 CCAGGCGCGG TCAGCGAGGT GAGCAACGGC ACCTCGAGGA GGGCAGGCT CGTCTGGCTG 1260
 CTGCTCTTC TGCTTTGCA CAGCTTCTC AAATTTTGT GTGAGTGCCA CTTCCCAACC 1320
 CGGGAAGGCG TCGCGCACCC ACCACACCA ACACAACAGC AATGGCAACA CCGACAGCAA 1380
 CCAATCAGAT ATATACAAAT GAAATTAGAA GAAACACAGC CTCATGGGAC AGAAATTTGA 1440
 GGGAGGGGAA CAAAGAATAT TTTGGGGGGA AAAGAGTTT AAAAAAGAAA TTGAAAATTG 1500
 CCTTGAGAT ATTTAGGTAC AATGAGTTT TCTTTTCCA AACGGGAAGA ACACAGCACA 1560

CCCGGCTTGG ACCCACTGCA AGCTGCATCG TGCAACCTCT TTGGTGCCAG TGTGGGCAAG 1620
 GGCTCAGCCT CTCTGCCAC AGACTGCCCC CAGTGGAAC ATTCTGGAGC TGGCCATCCC 1680
 AAATTCATC AGTCCATAGA GACGAACAGA ATGAGACCTT CCGGCCCAAG CGTGGCGCTT 1740
 CCGGCCCAAG CGTGGCGCTG CCGGCACTTT GGTAGACTGT GCCACCACGG CTGTGTGTTG 1800
 GAAACGTGAA ATAAAAAGAG CAAAAAATAA AAAAAAATAA

Seq ID NO: 637 Protein sequence
 Protein Accession #: NP_057606.1

1 11 21 31 41 51
 | | | | |
 MGVCGLFLP WKCLVVVSLR LLFLVPTGVP VRSGDATFPK AMDNVTVRQG ESATLRCTID 60
 NRVTVAWLN RSTILYAGND KWCLDPRVVL LSNTQTQYSI EIQNVVDVYE GPYTCVQTD 120
 NHPKTSRVHL IVQVSPKIVE ISSDISINEG NNISLTCTAT GRPEPTVTWR HISPKAQGVF 180
 SEDEYLEIQG ITRQSGDYE CSASNDVAAP VVRVKVTVN YPPYISEAKG TGVFVQKGT 240
 LQCEASAVPS AEFQWYKDDK RLIEGKKGVK VNRPFVLSKL IFFNVSEHDY GNYTCVASNK 300
 LGHTNASIML FPGAVSEVS NGTSRRAGCV WLLPLLVLHL LLLKF

Seq ID NO: 638 DNA sequence
 Nucleic Acid Accession #: NM_012261.1
 Coding sequence: 203..1045

1 11 21 31 41 51
 | | | | |
 GATTTGCTCT GCGCAGCAGT GTCGGTGCCG CGCTCGACAC CGAGTCCTAG CTAGGCGCTC 60
 ACAGAATACG CGCTCCCTCC CTCGCCCTTC TCTGTCCCCC GCCTCTCGCT CACCCCGGCC 120
 CACTCCAGCG GCGACTTTGA GGGATTCCCT CTCTGGCGGC CTCTGCAGCA GCACAGCCGG 180
 CCTCATTCGG GGCACCTGCA GTATGGATCT CCAAGGAAGA GGGGTCCCCA GCATCGACAG 240
 ACTTCGAGTT CTCCTGATGT TGTTCATAC AATGGCTCAA ATCATGGCAG AACAAAGAAGT 300
 GGAAATCTCT TCAGGCTTTT CCACTAACCC TGAAGAGAT ATATTTGTGG TCGGGGAAAA 360
 TGGGACGACG TGTCTCATGG CAGAGTTTGC AGCCAAATTT ATTGTACCTT ATGATGTGTG 420
 GGCCAGCAAC TACGTGATC TGATCACAGA ACAGGCCGAT ATCGCATGTA CCGGGGGAGC 480
 TGAGGTGAAG GGCGCTGTG GCCACAGCCA GTCGGAGCTG CAAGTGTCTT GGGTGGATCG 540
 CGCATATGCA CTCAAAATGC TCTTTGTAAA GGAAGGCCAC AACATGTCCA AGGGACCTGA 600
 GGCGACTTGG AGGCTGAGCA AAGTGCAGTT TGTCTACGAC TCCTCGGAGA AAACCCACTT 660
 CAAAGACGCA GTCAGTGTCT GGAAGCACAC AGCCAACTCG CACCACCTCT CTGCTTGGT 720
 CACCCCGCTT GGGAGTCTCT ATGATGTGCA AGCTCAACAA ACCATTTCAC TGGCCTCTAG 780
 TGATCCGACG AAGACGCTCA CCATGATCCT GTCTGCGGTC CACATCCAAC CTTTGGACAT 840
 TATCTCAGAT TTTGTCTTCA GTGAAGAGCA TAAATGCCCA GTGGATGAGC GGGAGCAACT 900
 GGAAGAAACC TTGCCCTTGA TTTTGGGGCT CATCTTGGGC CTGTCATCA TGGTAACACT 960
 CGGATTTTAC CAGTCCACC ACAGAAATGAC TGCCAAACAG GTGCAGATCC CTCGGGACAG 1020
 ATCCAGTAT AAGCAGATGG GCTAGAGGCC GTTAGGCAGG CACCCCTTAT TCCTGCTCCC 1080
 CCAACTGGAT CAGGTAGAAC ACAAAGGCA CTTTTCATC TTGTACAGCA GATACACCAA 1140
 CATAGCTACA ATCAAACAG CCTGGGTATC TGAGGCTTGC TTGGCTTGTG TCCATGCTTA 1200
 AACCACGGA AGGGGGAGAC TCTTTCGGAT TTGTAGGGTG AAATGGCAAT TATTTCTTCC 1260
 ATGCTGGGGA GGAGGGGAGG AGGCTCTCAG ACAGCTTTCG TGCTCATGGT GGCTTGGCTT 1320
 TGACTCTCCA AAGAGCAATA AATGCCACTT GGAGCTGTAT CTGGCCCCAA AGTTTAGGGA 1380
 TTGAAACAT GCTTCTTTGA GGAGGAAACC CCTTTAGGTT CAGAAGAATA TGGGGTGTCT 1440
 TGCTCCCTTG GACACAGCTG GCTTATCCTA TACAGTTGTC AATGCACACA GAATACAAAC 1500
 TCATGCTCCC TGACGCAAG CCCCAGAAAG TGATTCATGC TTCTGGCTGG CATTCTGCAT 1560
 GTTTAGTGAT TGTCTTGGGA ATGTTTCACT GCTACCCGCA TCCAGCGACT GCAGCACCAG 1620
 AAAACGACTA ATGTAACAT GCAGAGTTGT TTGGACTTCT TCCTGTGCCA GGTCCAAGTC 1680
 GGGGACCTG AAGAATCAAT CTGTGTGAGT CTGTTTTTCA AAATGAAATA AAACACACTA 1740
 TTCTCTGGC

Seq ID NO: 639 Protein sequence
 Protein Accession #: NP_036393.1

1 11 21 31 41 51
 | | | | |
 MDLQGRGVPS IDRLRVLLML FHTMAQIMAE QEVENLSGLS TNPEKDIFVV RENGTTCLMA 60
 EFAAKFIVPY DVWASNYVDL ITEQADIALT RGAEVKGRCG HSQSELVQFW VDRAYALKML 120
 FVKESHNMKS GPEATWRLSK VQFVYDSSEK THFKDAVSAG KHTANSHHLS ALVTPAGKSY 180
 ECQAQQTISL ASSDFQKTVT MILSAVHIQF FDIISDFVFS EEHKCPVDER EQLEETLPLI 240
 LGLILGLVIM VTLAIYVHH KMTANQVQIP RDRSQYKHM

Seq ID NO: 640 DNA sequence
 Nucleic Acid Accession #: NM_002993.1
 Coding sequence: 64..408

1 11 21 31 41 51
 | | | | |
 GGCACGAGCC AGTCTCCGCG CCTCCACCCA GCTCAGGAAC CCGCGAACCC TCTCTTGACC 60
 ACTATGAGCC TCCGCTCAG CCGCGCGGCC CGTGTCCGG GTCTTCCGG CTCTTGTGC 120
 GCGCTGCTCG CGCTGCTGCT CCTGCTGACG CCGCGGGGGC CCCTCGCCAG CGCTGGTCCT 180
 GCTCTGCTG TGCTGACAGA GCTGCGTTGC ACTTGTTTAC GCGTTACGCT GAGAGTAAAC 240
 CCCAAACGA TTGGTAAACT GCAGGTGTTT CCGCAGGCC CGCAGTGCTC CAAGGTGGAA 300
 GTGGTAGCCT CCCTGAAGAA CGGGAAGCAA GTTTGTCTGG ACCCGGAAGC CCCTTTTCTA 360
 AAGAAAGTCA TCCAGAAAT TTTGGACAGT GGAACAAGA AAAACTGAGT AACAAAAAG 420
 ACCATGCATC ATAAATTGC CCACTCTTCA CGCGAGCAGT TTTCTGGAGA TCCCTGGACC 480
 CAGTAAGAAT AAGAAGGAAG GGTGGTTTTT TTTCCATTTT CTACATGGAT TCCCTACTTT 540
 GAAGAGTGTG GGGGAAAGCC TACGCTTCTC CCTGAAAGTT ACAGCTCAGC TAATGAAGTA 600
 CTAATATAGT ATTTCCACTA TTTACTGTTA TTTTACCTGA TAAGTTATTG AACCCITTGG 660
 CAATTGACCA TATTGTGAGC AAAGAATCAC TGGTTATTAG TCTTTCAATG AATATTGAAT 720
 TGAAGATAAC TATTGTATTT CTATCATACA TTCCTTAAAG TCTTACCGAA AAGGCTGTGG 780
 ATTTGATATG GAAATAATGT TTTATTAGTG TGCTGTTGAG GGAGGTATCC TGTGTGTTCT 840
 ACTCACTCTT CTCATAAAT AGGAAATATT TTAGTTCTGT TTTCTTGGGG AATATGTTAC 900

TCTTTACCT AGGATGCTAT TTAAGTTGTA CTGTATTAGA AACTGGGTG TGTCATACCG 960
 TTATCTGTGC AGAATATATT TCCTTATTCA GAATTTCTAA AAATTTAAGT TCTGTAAGGG 1020
 CTAATATATT CTCTTCCTAT GGTTTTAGAT GTTTGATGTC TTCTTAGTAT GGCATAATGT 1080
 CATGATTTAC TCATTAAACT TTGATTTTGT ATGCTATTTT TTCACTATAG GATGACTATA 1140
 ATTCTGGTCA CTAATATAC ACTTTAGATA GATGAAGAAG CCCAAAAACA GATAAATTCC 1200
 TGATTGCTAA TTTACATAGA AATGTATTCT CTGGTTTT TAAATAAAG CAAATTAAC 1260
 AATGATCTGT GCTCTGCAAA GTTTTGA AAA TATATTGAA CAATTTGAAT ATAAATTCAT 1320
 CATTAGTCC TCAAAATATA TACAGCATTG CTAAGATTTT CAGATATCTA TTGTGGATCT 1380
 TTTAAAGGTT TTGACCATTT TGTATGAGG AATTATACAT GTATCACATT CACTATATTA 1440
 AAATTGCACT TTTATTTT CCTGTGTGTC ATGTGGTTT TTGTACTTG TATTGTCATT 1500
 TGGAGAAACA ATAAAGATT TCTAAACCA AAAAAAAAAA AAAAAA

Seq ID NO: 641 Protein sequence
 Protein Accession #: NP_002984.1

1 11 21 31 41 51
 | | | | |
 MSLPSSRAAR VFGPSGSLCA LLALLLLTLP FGPLASAGPV SAVLTELRCT CLRVTLRVNP 60
 KTIGKLQVFP AGPQCSKVEV VASLRNGKQV CLDPEAPFLK KVIQKILDSG NKKN

Seq ID NO: 642 DNA sequence
 Nucleic Acid Accession #: NM_013271.1
 Coding sequence: 27..809

1 11 21 31 41 51
 | | | | |
 TCCGGAGCCA GGCTCGCTGG GGCAGCATGG CGGGGTGCGC GCTGCTCTGG GGGCCGCGGG 60
 CCGGGGGCGT CGGCCCTTTG GTGCTGTCTG TGCTCGGCCT GTTTCGGCCG CCCCCGCGCG 120
 TCTGCGCGCG GCGCGTAAAG GAACCCCGCG GCCTAAGCGC AGCGTCTCCG CCCTTGGCTG 180
 AGACTGGCGC TCCTCGCGCG TTCCGGCGGT CAGTCCCGCG AGGTGAGGCG GCGGGGCGCG 240
 TGCAGGAGCT GCGCGGGGCG CTGGCGCATC TGCTGGAGGC CGAACGTCTG GAGCGGGGCG 300
 GGGCGGAGGC GCAGGAGGCT GAGGATCAGC AGGCGCGCGT CCTGGCGCAG CTGCTGCGCG 360
 TCTGGGGCGC CCCCCGCAAC TCTGATCCGG CTCTGGGCCT GGACGACGAC CCGACGCGCG 420
 CTGACGCGCA GCTCGCTCGC GCTCTGTCTC GCGCCCGCCT TGACCTTGCC GCCCTAGCAG 480
 CCCAGCTTGT CCCCAGCGCC GTCCCGCGCG CGGCGCTCCG ACCCCGCGCC CCGGTCTACG 540
 ACGACGGCCC CGCGGGCCCG GATGCTGAGG AGGCAGGCGA CGAGACACCC GACGTGGACC 600
 CCGAGCTGTT GAGGTACTTG CTGGGACGGA TTCTTGCGGG AAGCGCGGAC TCCGAGGGGG 660
 TGGCAGCCCC GCGCGCGCTC CGCGGTGCGC CCGACCAAGA TGTGGGCTCT GAGCTGCCCC 720
 CTGAGGGCGT GCTGGGGGCG CTGCTGCGTG TGAACCGCT AGAGACCCCG GCGCCCGCAG 780
 TGCTGACGCG CGGCTCTTG CCACCTGAG CACTGCGCGG ATCCCGTGCA CCTTGGGACC 840
 CAGAAGTGCC CCGCGCATCC CGCCACGAG ACTTCTCCCC CCGACGACGT CCGAGCAAC 900
 TTACCCCGGC CAGCCAGCCC TCTACCCGGA GGATCCCTAC CCCCTGCGCC ACAATAACAT 960
 GATCTGAGC

Seq ID NO: 643 Protein sequence
 Protein Accession #: NP_037403.1

1 11 21 31 41 51
 | | | | |
 MAGSPILLWGP RAGGVLLVL LLLGLFRPPP ALCARPVKEP RGLSAASPPL AETGAPRRFR 60
 RSVPRGEAAG AVQELARALA HLEAERQER ARAEAQAEED QQARVLAQLL RVWGAPRNSD 120
 PALGLDDDDP APAAGLARAL LRAILDPAAL AAQLVPAPVP AAALRPRPPV YDDGPAGPDA 180
 EEAGDETPDV DPELLRYLLG RILAGSADSE GVAAPRRLLR AADHDVGSSEL PPEGVLGALL 240
 RVKRLPTAP QVPARRLLFP

Seq ID NO: 644 DNA sequence
 Nucleic Acid Accession #: NM_002214
 Coding sequence: 681..2990

1 11 21 31 41 51
 | | | | |
 CCCAGAGCCG CCTCCCCCTG TTGTGGCAT CCCGAGCTTC CTCCTTGCC AGCCAGGACG 60
 CTGCCGACTT GTCTTTGCCC GCTGCTCCGC AGACGGGGCT GCAAGCTGC AACTAATGGT 120
 GTTGGCTCC CTGCCACCT GTGGAAGCAA CTGCGTGAT TGATGCGCA CAGACTTTTT 180
 TCCCCTCGAC CTCGCCGCGG TACCCTCCCA CAGATCCAGC ATCACCCAGT GAATGTACAT 240
 TAGGGTGGTT TCCCCCAG CTTGGGGCTT TGTTGGGTT TGATTGTGTT TGGCTCTTCG 300
 CTAAGCTGAT TTATGCAGCA GAAGCCCGAC CGGCTGGAGA GAAACAAAAG CTCTTTTCTT 360
 TGTCCCGGAG CAGGCTGCGG AGCCCTTGCA GAGCCCTCTC TCCAGTCCGC GCCGGGCCCT 420
 TGGCCGTCGA AGGAGGTGCT TCTGCGGAG ACCGCGGGAC CCGCGTGCC GAGCCGGGAG 480
 GGCCTAGGG GCCCTGAGAT GCCGAGCGGT GCCCGGGCCC GCTTACCTGC ACCGCTTGCT 540
 CCGAGCCGCG GGGTCCGCT GCTAGGCTG CGGAAAACGT CCTAGCGACA CTCGCCGCG 600
 GGCCTGAGG TCGCCCGGGA GGCAGGCCC GCGTCCGGA GGCAGCCAGG CCGCGGGCGC 660
 GGGGGGGGCT GTTTTGCAAT ATGTGCGGCT CGGCCCTGGC TTTTITACC GCTGCATTG 720
 TCTGCTGCA AAACGACCGG CGAGGTCCCG CCTGTTCTT CTGGGCGAGC TTGGGTGTTT 780
 CACTGTGTTCT TGGACTGGGC CAAGGTGAAG ACAATAGATG TGCATCTTCA AATGCAGCAT 840
 CCTGTGCCAG GTGCCCTGCG CTGGGTCCAG AATGTGGATG GTGTGTTCAA GAGGATTTCA 900
 TTTCAAGTGG ATCAAGAAGT GAACGTTGTG ATATTGTTT CAATTTAATA AGCAAAGGCT 960
 GCTCAGTTGA TTCAATAGAA TACCCATCTG TGCATGTTAT AATACCCACT GAAATGAAA 1020
 TTAATACCCA GGTGACACCA GGAGAAGTGT CTATCCAGCT GCGTCCAGGA GCCGAAGCTA 1080
 ATTTATGCT GAAGTTTCAT CCTCTGAAGA AATATCTGT GGATCTTTAT TATCTTGTG 1140
 ATGTCTCAGC ATCAATGCAC AATAATATAG AAAAAATTA TCCGTTGGA AACGATTTAT 1200
 CTAGAAAAAT GGCATTTTTC TCCCGTACT TTCGTCTTGG ATTTGGCTCA TACGTTGATA 1260
 AAACAGTTTC ACCATACATT AGCATCCACC CCGAAAGGAT TCATAATCAA TGCAGTGACT 1320
 ACAATTTAGA CTGCATGCCT CCCCATGGAT ACATCCATGT GCTGTCTTTG ACAGAGAACA 1380
 TCACTGAGTT TGAGAAAGCA GTTCATAGAC AGAAGATCTC TGGAAACATA GATACACCAG 1440
 AAGGAGGTTT TGACGCCATG CTTAGGCGAG CTGTCTGTGA AAGTCATATC GGATGGCGAA 1500
 AAGAGGCTAA AAGATTGCTG CTGGTGATGA CAGATCAGAC GTCTCATCTC GCTCTTGATA 1560

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GCAAATTGGC AGGCATAGTG GTGCCAATG ACGGAACTG TCATCTGAAA AACAACTGCT 1620
ACGTCAAATC GACAACCATG GAACACCCCT CACTAGGCCA ACTTTCAGAG AAATTAATAG 1680
ACAACAACAT TAAATGTCATC TTTCGAGTTC AAGGAAAACA ATTTCAATGG TATAAGGATC 1740
TTCTACCCCT CTGTGCCAGG ACCATTGCTG GTGAAATAGA ATCAAAGGCT GCAAACCTCA 1800
ATAATTGGT ATTGGAAGCC TATCAGAAGC TCATTTTACA AGTGAAAGTT CAGGTGGAAA 1860
ACCAGGTACA AGGCATCTAT TTTAACATTA CCGCCATCTG TCCAGATGGG TCCAGAAAGC 1920
CAGGCATGGA AGGATGCAGA AACGTGACGA GCAATGATGA AGTTCTTTTC AATGTAACAG 1980
TTACAATGAA AAAATGTGAT GTCACAGGAG GAAAAAATA TGCAATAATC AAACCTATTG 2040
GTTTTTAATGA AACCGCTAAA ATTCATATAC ACAGAACTG CAGCTGTCTG TGTGAGGACA 2100
ACAGAGGACC TAAAGGAAAG TGTGTAGATG AAATTTTCT AGATTCCAAG TGTTTCCAGT 2160
GTGATGAGAA TAAATGTCTAT TTTGATGAAG ATCAGTTTTT TCTGAGAGT TGAAGTCAC 2220
ACAAGGATCA GCCGTGTTGC AGTGGTCCAG GAGTTTGTGT TGTGGGAAA TGTTCATGTC 2280
ACAAAATTAA GCTTGGAAAA GTGTATGGAA AATACTGTGA AAAGGATGAC TTTTCTTGTC 2340
CATATCACCA TGGAAATCTG TGTGCTGGGC ATGGAGAGTG TGAAGCAGCG AGATGCCAAT 2400
GCTTCAGTGG CTGGGAAGGT GATCGATGCC AGTGCCCTTC AGCAGCAGCC CAGCACTGTG 2460
TCAATTCAA GGGCCAAGTG TGCAGTGGAA GAGGCACGTG TGTGTGTGGA AGGTGTGAGT 2520
GCACGCATCC CAGGAGCATC GGCCTCTTCT GTGAACACTG CCCCACCTGT TATACAGCCT 2580
GCAAGGAAAA CTGGAATTGT ATGCAATGCC TTCACCTCA CAATTGTCT CAGGCTATAC 2640
TTGATCAGTG CAAAACCTCA TGTGCTCTCA TGGAAACAAC GCATTATGTC GACCAAACTT 2700
CAGAATGTTT CTCAGGCCCA AGCTACTTGA GAATATTTT CATCATTTTC ATAGTTACAT 2760
TCTTGATTGG GTTGCTTAAA GTCCTGATCA TTAGACAGGT GATACTACAA TGGAAATAGTA 2820
ATAAAATTAA GTCTCTATCA GATTACAGAG TGTGAGCCTC AAAAAAGGAT AAGTTGATT 2880
TGCAAGTGT TTGCAAGA GACATCACCT ACCGACGTGA GAAGCCTGAA GAAATAAAAA 2940
TGGATATCAG CAAATTAAT GCTCATGAAA CTTTCAGGTG CAATCTCTAA AAAAAAGATT 3000
TTAAACACTT AATGGGAAC TGGAAATGTT AATAATTGCT CCTAAAGATT ATAATTTTAA 3060
AAGTCACAGG AGGAGACAAA TTGCTCACGG TCGTCCAGT TGTGTTGTG ACACTCGAAC 3120
GAAGACTGAC AAGTATCCTC ATCATGATGT GACTCACATA GCTGCTGACT TTTTCAGAGA 3180
AAAAATGTGT TTACTACTGT TTGAGACTAG TGTGCTGTGA GCATTTTACT GTAATATATA 3240
ACTTATTTAG ATCAGCATAG AATGTAGATC CTCTGAAGAG CACTGATTAC ACTTTACAGG 3300
TACCTGTAT CCCTACGCTT CCCAGAGAGA ACAATGCTGT GAGAGAGTTT AGCATGTGT 3360
CACTACAAGG GTACAGTAA CTCTGCACTG GACATGTGAG GAAAAAATA ATCTGGCAAG 3420
TATATTTCTAA GGTTCGCAAA CACTTCAACA GTTGGTGGTT GAATAGACAA GAACAGCTAG 3480
ATGAATAAAT GATTGCTGTT TCACTCTTTC AAGAGGTGAA CAGATACAAC CTTAATCTTA 3540
AAGATTATT GCTTTTAAAA GTGTGTAGTT TTAGCATGT GTGTTTATGG TTTGCTTATT 3600
TTTGCAAGAT GGATCACTAT TCCAGCATT TCTCCTCTT GCCTTTATGT TTTGTTTCT 3660
TTTTTACAGG ATAAGTTTAT GTATGTCACA GATGACTGGA TTAATTAAGT GCTAAGTTAC 3720
TACTGCCATA AAAAATAAT AATACAATGT CAGTTTATCA GAATACTAGT TTAAAAAGCT 3780
GAATGTAA

Seq ID NO: 645 Protein sequence
Protein Accession #: NP_002205

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60

1 11 21 31 41 51
MCGSALAFFT AAFVCLQND RGPASFLWAA WVFSVLVLGL QGEDNRCASS NAASCARCLA 60
LGPECGWCVQ EDFISGGSR ERCDIVSNLI SKGCSVDSIE YPSVHVIIPT ENEINTQVTP 120
GEVSIQLRPG AEANFMLKVH PLKKYPVDLY YLVDVSASMH NNIEKLNSVG NDLSRKMAFF 180
SRDFRLGFGS YVDKTVSPYI SIHPERIHQ CSDYNLDMP PHGYIHVLSL TENITEPEKA 240
VHRQKISGNI DTPEGFPDAM LQAACVESH GWRKEAKRL LVMTDQTSHL ALDSKLAGIV 300
VPNDGNCHLK NNVYVKSTTM EHPSLGQLE KLIDNNINVI FAVQKQFHW YKDLLPLLP 360
TIAGEIESKA ANLNNLVVEA YQKLISEVKV QVENQVQGIY FNITAICPDG SRKPGMEGCR 420
NVTSNDEVLV NVVTVMKKCD VTGKNYAI KPIGFNETAK IHIHRNCSCQ CEDNRGPKGK 480
CVDETFLDSK FDEDEQFSSES CKSHKDQFVC SGRGVCVCGK CSCHKIKLGK 540
VYGKYCEKDD FSCPHYHGNL CAGHGECEAG RCQCFSGWEG DRCQCPSAAA QHCVNSKGQV 600
CSGRGTVCVG RCECTDPRSI GRFCEHPTC YTACKENWNC MQCLHPHNL QAILDQCKTS 660
CALMEQQHYV DQTSCEFPSS SYLRIFFIIF IVTFLIGLLK VLIRQVILQ WNSNRIKSSS 720
DYRVSASKND KLILQSVCTR AVTYRREKPE EIKMDISKLN AHETFRCNF

Seq ID NO: 646 DNA sequence
Nucleic Acid Accession #: NM_003318.1
Coding sequence: 1..2574

65
70
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1 11 21 31 41 51
ATGGAATCCG AGGATTTAAG TGGCAGAGAA TTGACAATTG ATTCCATAAT GAACAAAGTG 60
AGAGACATTA AAAATAAGTT TAAAAATGAA GACCTTACTG ATGAACCTAG CTGTAATAAA 120
ATTTCTGCTG ATACTACAGA TAACCTCGGA ACTGTTAACC AAATATGAT GATGGCAAA 180
AACCAGAGG ACTGGTTGAG TTTGTTGCTC AAACCTAGAGA AAAACAGTGT TCCGCTAAGT 240
GATGCTCTTT TAAATAAATT GATTGGTCTG TACAGTCAAG CAATTGAAGC GCTTCCCCCA 300
GATAAATATG GCCAAATGTA GAGTTTGTCT AGAATTCAGG TGAGATTTGC TGAATTAATA 360
GCTATTCAAG AGCCAGTGA TGACGCTGAC TACTTTTCAA TGGCCAGAGC AAACCTGCAAG 420
AAATTGCTTT TTGTTTATAT ATCTTTTGCA CAATTGGAAC TGTCACAAGG TAATGTCAAA 480
AAAAGTAAAC AACTTCTTCA AAAAGCTGTA GAACGTGGAG CAGTACCCT AGAAATGCTG 540
GAAATGCCCC TGCGGAATTT AAACCTCCAA AAAAGCAGC TGCTTTTACA GGAGGAAAAG 600
AAGAATTTAT CAGCATCTAC GGTATTAACT GCCCAAGAT CATTTTCCGG TTCCTTGGG 660
CATTTACAGA ATAGGAACAA CAGTTGTGAT TCCAGAGGAC AGACTACTAA AGCCAGGTTT 720
TTATATGGAG AGAATCATGCC ACCACAAGAT GCAGAAATAG GTTACCGGAA TTCATTGAGA 780
CAAACTAACA AAACTAACA GTCATGCCCA TTTGGAAGAG TCCAGTTAA CCTCTTAAAT 840
AGCCAGATT GTGATGTGAA GACAGATGAT TCAGTTGTAC CTGTTTAT GAAAAGACAA 900
ACCTCTAGAT CAGAATGCCG AGATTGGTT GTGCCCTGGAT CTAACCAAG TGGAAATGAT 960
TCTGTGAAT TAAGAAATTT AAAGTCTGTT CAAAATAGTC ATTTCAAGGA ACCTCTGGTG 1020
TCAGATGAAA AGAGTTCTGA ACTTATTATT ACTGATTCAA TAACCTGAA GAATAAAAACG 1080
GAATCAAGTC TTCTAGCTAA ATTAGAAGAA ACTAAAGAGT ATCAAGAACC AGAGTTTCCA 1140
GAGATTAACC AGAAGACTAG GCAATCTAAG AGAAAGTCAG AGTGATTAA CCAGAATCCT 1200
GCTGCATCTT CAATCACTG GCAGATTCCG GAGTTAGCCC GAAAAGTTAA TACAGAGCAG 1260
AAACATACCA CTTTGTAGCA ACCTGTCTTT TCAGTTTCAA AACAGTCACC ACCAATATCA 1320
ACATCTAAAT GGTTTGACCC AAAATCTATT TGTAAGACAC CAAGCAGCAA TACCTTGGAT 1380

	GATTACATGA	GCTGTTT	TAAGTCCAGTT	GTAAGAAGT	ACTTCCACC	TGCTTGT	CAG	1440
	TTGTCAACAC	CTTATGGCCA	ACCTGCCTGT	TTCCAGCAGC	AACAGCATCA	AATACTTGCC		1500
	ACTCCACTTC	AAAATTACA	GGTTTTAGCA	TCTTCTT	CAG	CAATGAATG	CATTT	1560
5	AAAGGAAGAA	TTTATTCAT	TTTAAAGCAG	ATAGGAAGT	GAGGTTC	CAAG	GATTT	1620
	CAGGTGTAA	ATGAAAGAA	ACAGATATAT	GCTATAAAAT	ATGTGAACCT	AGAAGAAGCA		1680
	GATAACCAA	CTCTTGATAG	TTACCGGAAC	GAAATAGCTT	ATTGGAATAA	ACTACAACAA		1740
	CACAGTGATA	AGATCATCCG	ACTTTATGAT	TATGAAATCA	CGGACCAGTA	CATCTACATG		1800
	GTAATGGAGT	GTGGAATAT	TGATCTTAAT	AGTTGCTTA	AAAAGAAAAA	ATCCATTGAT		1860
10	CCATGGGAAC	GCAAGAGTTA	CTGGAATAAT	ATGTTAGAGG	CAGTTCACAC	AATCCATCAA		1920
	CATGGCATTG	TTACAGATGA	TCTTAAACCA	GCTAACCTTC	TGATAGTTGA	TGGAATGCTA		1980
	AAGCTAATTG	ATTTTGGGAT	TGCAAAACCA	ATGCAACCAG	ATACAACAAG	TGTTGTATAA		2040
	GATTCTCAGG	TTGGCACAGT	TAATTATATG	CCACCAGAAG	CAATCAAAGA	TATGCTCTCC		2100
	TCCAGAGAGA	ATGGGAATC	TAAGTCAAAG	ATAAGCCCCA	AAAGTGATGT	TTGGTCTCTA		2160
	GGATGTATTT	TGTACTATAT	GACTTACGGG	AAAACACCAT	TTACAGCAGAT	AATTAATCAG		2220
15	ATTTCTAAAT	TACATGCCAT	AATTGATCCT	AATCATGAAA	TTGAATTTC	CGATATTCCA		2280
	GAGAAAGATC	TTCAAGATGT	GTTAAAGTGT	TGTTTAAAAA	GGGACCCAAA	ACAGAGGATA		2340
	TCCATTCTCTG	AGCTCTCTGG	TCATCCCTAT	GTTCAAAATC	AAACTCATCC	AGTTAACCAA		2400
	ATGGCCAAGG	GAACCACTGA	AGAAATGAAA	TATGTTCTGG	GCCAACTTGT	TGGTCTGAAT		2460
20	TCTCCTAACT	CCATTTTGAA	AGTGCTGAAA	ACTTTATATG	AACACTATAG	TGGTGGTGAA		2520
	AGTCATAAAT	CTTCATCCTC	CAAGACTTTT	GAAAAAATAA	GGGGAATAA	ATGA		

Seq ID NO: 647 Protein sequence
Protein Accession #: NP_003309.1

25	1	11	21	31	41	51	
	MESEDL	SGRE	LTIDSIM	NKV	RDINKPK	NE	DLTDELSLNK
	NPEDWLS	LLLL	KLEKNS	SVPLS	DALLNKL	LIGR	YSQAI
	AIQEPD	DARD	YFQMAR	ANCK	KPAFVH	ISFA	QFELS
30	EIALRNL	NLQ	KKQLS	EEEEK	KNLSAST	VL	AQESF
	LYGENM	PPQD	ABIGYR	NSLR	QTNKTK	QSCP	FGRVP
	TSRSECR	DLV	VPGSKP	SGND	SCELRNL	KSV	QNSHF
	ESSLLAK	LEE	TKEYQE	PEVP	ESNQKQ	WQSK	RKSEC
	KHTTFE	QPVF	SVSKQSP	PIS	TSKNFDP	KSI	CKTPSS
35	LSTPYG	OPAC	FQQQHQ	HLA	TPLQNL	QVLA	SSSAN
	QVLNEK	KQIY	AIKYVNL	EEA	DNQTL	DSYRN	EIAYL
	VMCEGN	IDLN	SWLKKK	KSID	PWERKSY	WKN	MLEAV
	KLIDFG	IANQ	MQPD	TSVVK	DSQVGT	VNYM	PPEAIK
40	GCILY	MYTYG	KTFPQ	IINQ	ISKLHAI	IDP	NHEIE
	SIPELLA	HPY	VQIQTH	PNVQ	MAKG	TTEMK	YVLQ
	SHNSSS	SKTF	EKKRGK				

Seq ID NO: 648 DNA sequence
Nucleic Acid Accession #: NM_015507
Coding sequence: 241..1902

45	1	11	21	31	41	51	
	CCGCAG	AGG	GA	GCCTCG	GC	CGG	CGCA
50	CGCCCT	CGCC	CG	CGG	CGC	CGT	CG
	CGAGTG	GAGC	GGAG	ACCG	AGCG	GCTG	AG
	GGGT	CGGG	CGCC	CGT	CG	CGG	CGG
	ATGCT	CTGC	CTG	GAG	CGT	CGT	CT
55	GGGA	ACGCG	CG	CGAG	TCA	CG	CGG
	TGTCA	CTATG	GA	CTAA	CGT	CGT	CG
	TGTGA	AGCTA	CG	GAAC	CG	CGG	CG
	AGATG	CTTTC	CAGG	ATAC	CG	GA	AAAC
	AAACCC	CGCG	CATG	CCA	CG	ATG	GTG
60	CTCAG	TGGC	ACAT	GCT	CAT	GCC	AGAT
	ATAAA	CTGTC	AGT	ACAG	CTG	TGA	AGAC
	TCAGG	ACTCC	GCCT	GGCC	CG	AAAT	GGA
	GGTAA	AGTCA	CTCT	GAG	CG	CAAT	CGA
	AAATG	TACA	TTGG	TTT	CGA	ACT	GCA
65	AATGA	ATGTA	CTAT	GGAT	AG	CCAT	ACG
	GGGT	CTCT	CA	AGT	GTA	AAAT	G
	ATCC	CTG	AA	ATT	CTG	TA	AG
	AAGA	AGT	GTG	CT	CA	AA	AG
	CCAGA	ACCA	CCAG	GA	CT	CA	AG
70	ATAG	TTT	CCA	GAG	CGG	GA	AA
	GAGG	GGCT	TTG	AGG	ATG	AG	AA
	AGCT	GCG	AG	GAG	ATG	GT	GT
	CTGG	TCC	AA	GG	AA	CG	CT
	GACT	CG	AG	CT	CA	TT	CG
75	TGGA	ATC	CTG	CTG	AT	TA	TT
	GGTC	ACA	AGA	AAG	ATT	G	AA
	AACT	TCT	GT	TG	CT	TT	GA
	TTTG	TG	AAAA	AC	AG	TA	AA
	TGGA	AG	AC	AG	CA	AA	AT
80	GAAG	CAGA	AC	AGG	CA	AA	CG
	TCAG	CT	TAT	CT	TT	AT	CT
	TTG	ACT	TT	GT	TT	TT	TT
	TTAG	AA	TT	AT	TA	TT	AT
	TCT	GT	TA	TA	AA	AT	TA
85	TTT	CT	GA	AT	CA	TT	AT
	CAG	TAT	CT	CT	TA	TA	TA
	TAG	AAAA	AA	AG	CA	AA	AG
	TAT	GAC	AT	CA	TA	TA	TA

TGTATATTAA AATTCTTTGT AATAATAATA TCCAAATCAT CAAAAAATAA AAAAAAAA

Seq ID NO: 649 Protein sequence
Protein Accession #: NP_056322

1	11	21	31	41	51	
MPLPWSLALP	LLLSWVAGGF	GNAASARHHG	LLASARQPGV	CHYGTKLACC	YGWRRNSKGV	60
CEATCEPGCK	FGECVGNPKC	RCFPGYTGKT	CSQDVNECGM	KPRPCQHRVC	NTHGSYKCF	120
LSGHMLMPDA	TCVNSRTCAM	INCQYSCEDT	EEGPQCLCPS	SGLRLAPNGR	DCLDIDECAS	180
GKVICPYNRR	CVNTFGSYYC	KCHIGFELQY	ISGRYDCIDI	NECTMDSHTC	SHHANCFTNQ	240
GSFKCKCKQG	YKGNGLRCSA	IPENSVKEVL	RAPGTIKDRI	KKLLAHKNSM	KKKAKIKNVT	300
PEPTRTPTEK	VNLQPFNYEE	IVSRGGNSHG	GKKGNBEKMK	EGLEDEKREE	KALKNDIEER	360
SLRGDVFFPK	VNEAGEFLGI	LVQRKALTSK	LEHKDLNISV	DCSFNNGICD	WKQDREDDFD	420
WNPADRDNAI	GFYMAVPALA	GHKKDIGRLK	LLLPDLQPQS	NFCLLFYRL	AGDKVGKLRV	480
FVKNSNNALA	WEKTTSEDEK	WKTGKIQLYQ	GTDATKSIIF	EAERKGKGTG	EIAVDGVLLV	540
SGLCPDSSL	VDD					

Seq ID NO: 650 DNA sequence
Nucleic Acid Accession #: NM_003506.1
Coding sequence: 259..2379

1	11	21	31	41	51	
GCAGCTCCAG	TCCCCGAGCG	AACCCCGGAG	CCGTCTCAGG	TCCCTGGGGG	GAACGGTGGG	60
TTAGACGGGG	ACGGGAAGGG	ACAGCGGCCT	TCCAGCGCCC	CCCGAGTAAT	TGACCCAGGA	120
CTCATTTTCA	GGAAAGCTTC	AAAATGAGTA	AAATAGTGAA	ATGAGGAATT	TGAACATTTT	180
ATCTTTGGAT	GGGGATCTTC	TGAGGATGCA	AAGAGTGATT	CATCCAAGCC	ATGTGGTAAA	240
ATCAGGAATT	TGAAGAAAAT	GGAGATGTTT	ACATTTTGTG	TGACGTGTAT	TTTTCTACCC	300
CTCCTAAGAG	GGCAGCTCT	CTTCACCTGT	GAACCAATTA	CTGTTCCCGA	ATGTATGAAA	360
ATGGCCTACA	ACATGACGTT	TTTCCCTAAT	CTGATGGGTC	ATTATGACCA	GAGTATTGCC	420
GCGGTGGAAA	TGGAGCATTT	TCTTCTCTCT	GCAAACTCTG	AATGTTCAAC	AAACATTGAA	480
ACTTTCCTCT	GCAAGACATT	TGTACCAACC	TGCATAGAAC	AAATTCATGT	GTTTCCACCT	540
TGTCTGTAAC	TCTTGTGAAA	AGTATATTCT	GATTGCAAAA	AATTAATTGA	CACTTTGGGG	600
ATCCGATGCG	CTGAGGAGCT	TGAATGTGAC	AGATTACAAT	ACTGTGATGA	GACTGTTCTC	660
GTAACCTTTG	ATCCACACAC	AGAATTTCTT	GGTCTCAGA	AGAAAACAGA	ACAAGTCCAA	720
AGAGACATTG	GATTTTGGTG	TCCAAGGCTT	CTTAAGACTT	CTGGGGGACA	AGGATATAAG	780
TTTCTGGGAA	TTGACCATGT	TGCGCCTCCA	TGCCCAACA	TGTATTTTAA	AAGTGATGAG	840
CTAGAGTTTG	CAAAAAGTTT	TATTGGAACA	GTTTCAATAT	TTTGTCTTTG	TGCAACTCTG	900
TTACATTCTC	TACTTTTGTG	AATTGATGTT	AGAAGATTCA	GATACCCAGA	GAGACCAATT	960
ATATATTACT	CTGTCTGTGA	CAGCATTGTA	TCTCTTATGT	ACTTCATTGG	ATTTTGTCTG	1020
GGCGATAGCA	CAGCCTGCAA	TAAGGCAGAT	GAGAAGCTAG	AACTTGGTGA	CACCTGTTGT	1080
CTAGGCTCTC	AAAATAAGGC	TTGCACCGTT	TTGTTCATGC	TTTGTGATTT	TTTCACAATG	1140
GCTGGCAGTG	TGTGTGGGTT	GATTCTTACC	ATTACTTGGT	TCTTAGCTGC	AGGAAGAAAA	1200
TGGAGTTGTG	AAGCCATCGA	GCAAAAAGCA	GTGTGGTTTC	ATGCTGTGTC	ATGGGGAACA	1260
CCAGGTTTCC	TGACTTTGTG	GCTTCTTGCT	CTGAACAAAG	TTGAAGGAGA	CAACATTAGT	1320
GGAGTTTGCT	TTGTGGGCTT	TTATGACCTG	GATGCTTCTC	GCTACTTTGT	ACTCTTGCCA	1380
CTGTGCCTTT	GTGTGTTTGT	TGGGCTCTCT	CTTCTTTTAG	CTGGCATTAT	TTCTTTAAAT	1440
CATGTTTCGAC	AAGTTCATACA	ACATGATGGC	CGGAACCAAG	AAAAACTAAA	GAAATTTATG	1500
ATTTCGAATTG	GAGTCTTCAG	CGGCTTGAT	CTTGTGCCAT	TAGTGACACT	TCTCGGATGT	1560
TACGTCTATG	AGCAAGTGAA	CAGGATTACC	TGGGAGATAA	CTTGGGTCTC	TGATCATTGT	1620
CGTCAGTACC	ATATCCCATG	TCCTTATCAG	GCAAAAAGCAA	AAGCTCGACC	AGAAATTGGT	1680
TTATTATATGA	TAAATACCTT	GATGACATTA	ATTGTTGGCA	TCTCTGCTGT	CTTCTGGGTT	1740
GGAGCAAAA	AGACATGCAC	AGAATGGGCT	GGGTTTTTTA	AACGAAATCG	CAAGAGAGAT	1800
CCAATCAGTG	AAAGTCGAA	AGTACTACAG	GAATCATGTG	AGTTTCTCTT	AAAGCACAAT	1860
TCTAAAGTTA	AACACAAAAA	GAAGCACTAT	AAACCAAGTT	CACACAGCT	GAAGGTCATT	1920
TCCAAATCCA	TGGGAACCGC	CACAGGAGCT	ACAGCAAAATC	ATGGCACTTC	TGCAGTAGCA	1980
ATTACTAGCC	ATGATTACCT	AGGACAAGAA	ACTTTGACAG	AAATCCAAAC	CTCACCAGAA	2040
ACATCAATGA	GAGAGGTGAA	AGCGGACGGA	GCTAGCACCC	CCAGGTTAAG	AGAACAGGAC	2100
TGTGGTGAAC	CTGCCTCGCC	AGCAGCATCC	ATCTCCAGAC	TCTCTGGGGA	ACAGGTCGAC	2160
GGGAAGGGCC	AGGCAGGCGA	TGTATCTGAA	AGTGCAGGGA	GTGAAGGAAG	GATTAGTCCA	2220
AAGAGTGATA	TACTTGACAC	TGGCCTGGCA	CAGAGCAACA	ATTGTCAGGT	CCCCAGTTCT	2280
TCAGAACCAA	GCAGCCTCAA	AGGTTCCACA	TCTCTGCTTG	TTCAACCCAGT	TTCAGGAGTG	2340
AGAAAAGAGC	AGGGAGGTGG	TTGTCAATTA	GATACTTGAA	GAACATTTTC	TCTCGTTACT	2400
CAGAAGCAAA	TTGTGTGTAC	ACTGGAAGTG	ACCTATGCAC	TGTTTTGTAA	GAATCACTGT	2460
TACGTTCTTC	TTTTGCACCT	AAAGTTGCAT	TGCCTACTGT	TATACTGGAA	AAAATAGAGT	2520
TCAAGAATAA	TATGACTCAT	TTCAACAAA	GGTTAATGAC	AACAATATAC	CTGAAAACAG	2580
AAATGTGCAG	GTTAATAATA	TTTTTTTAA	AGTGTGGGAG	GACAGAGTTA	GAGGAATCTT	2640
CCTTTTCTAT	TTATGAAGAT	TCTACTCTTG	GTAAGAGTAT	TTTAAGATGT	ACTATGCTAT	2700
TTTACCTTTT	TGATATAAAA	TCAAGATATT	TCTTTGCTGA	AGTATTTAAA	TCTTATCCTT	2760
GTATCTTTT	ATACATATTT	GAAAATAAGC	TTATATGTAT	TTGAACTTTT	TTGAAATCCT	2820
ATTCAAGTAT	TTTTATCATG	CTATTGTGAT	ATTTTAGCAC	TTTGGTAGCT	TTTACACTGA	2880
ATTTCTAAGA	AAATGTGAAA	ATAGTCTTCT	TTTATACTGT	AAAAAAGAT	ATACCAAAAA	2940
GTCTTATAAT	AGGAATTTAA	CTTTAAAAAC	CCACTATTTG	ATACCTTACC	ATCTAAAAATG	3000
TGTGATTTTT	ATAGTCTCGT	TTTAGGAATT	TCACAGATCT	AAATTATGTA	ACTGAAATAA	3060
GGTGTCTACT	CAAGAGATGT	CCACTATTGA	TTGTATTATG	CTGCTCACTG	ATCCTTCTGC	3120
ATATTAAAAA	TAAATGTGCC	TAAAGGGTTA	GTAGACAAAA	TGTTAGTCTT	TTGTATATTA	3180
GGCCAAGTGC	AATTGACTTC	CCTTTTTTAA	TGTTTCATGA	CCACCCATTG	ATTGTATTAT	3240
AACCACTTAC	AGTTGCTTAT	ATTTTGTGTT	TTAAGTTTGT	TTTCTTAACA	TTTAGAATAT	3300
TACATTTTGT	ATTATACAGT	ACCTTTCTCA	GACATTTTGT	AG		

Seq ID NO: 651 Protein sequence
Protein Accession #: NP_003497.1

1	11	21	31	41	51

MEMFTFLLTTC IFPLPLLRGHS LFTCEPITVP RCMKMYNMT FFPNLMGHYD QSIAAVERMEH 60
 FLPLANLECS PNIETFLCKA FVPTCIEQIH VVPPCRKLCE KVYSDCKKLI DTFGIRNPEE 120
 LECDRLOQYCD ETVPVTFDPH TEFLGPQKKT EQVQRDIGPW CPRHLKTSBG QGYKFLGIDQ 180
 CAPPCEPMYF KSDLELEFAKS FIGTVSIFCL CATLFTFLTFL LIDVRRFRYP ERPIIYYSVC 240
 5 YSIVSLMYPI GFLLDGSTAC NKADEKLELG DTVVLGSQNK ACTVLFMLLY FFTMAGTVWW 300
 VILTTITWFLA AGRKNSCEAI EQKAVWPHAV AWGTGPGFLTV MLLALNKVEG DNISGVCVFP 360
 LYDLASRYF VLLPLCLCVF VGLSLLLAGI ISLNHVRQVI QHDGRNQEKI KKFMRIGVF 420
 SGLYLVLPLVT LLGCVYVEQV NRITWEITWV SDHCRQYHIP CPYQAKAKAR PELALPMIKY 480
 10 LMTLIVGISA VEWVSGSKTTC TEWAGFPKRN RKRDPISER RVLQESCEFF LKHNSKVHKH 540
 KKHYPSSHK LKVISKSMGT STGATANHGT SAVAITSHDY LGQETLLEIQ TSPETSMREV 600
 KADGASTPRL REQDCGEPAS PAASISRLSG EQVDGKGQAG SVSESARSEG RISPKSDITD 660
 TGLAQSNLQ VPSSSEPSL KGSTSLVHP VSGVRKEGG GCHSDT

Seq ID NO: 652 DNA sequence
 Nucleic Acid Accession #: NM_014791.1
 Coding sequence: 171..2126

1 11 21 31 41 51
 20 TTGGCGGGCG GAAGCGGCCA CAACCCGGCG ATCGAAAAGA TTCTTAGGAA CGCCGTACCA 60
 GCCGGTCTCT TCAGGACAGC AGGCCCTGT CCTTCTGTCT GGGCCGCTC AGCCGTGCCC 120
 TCCGCCCTCT AGGTTCTTTT TCTAATTCCA AATAAACTTG CAAGAGGACT ATGAAAGATT 180
 ATGATGAAGT TCTCAAAATAT TATGAATTAC ATGAAACTAT TGGGACAGGT GGCTTTGCAA 240
 25 AGGTCAAATC TGCCTGCCAT ATCCTTACTG GAGAGATGGT AGCTATAAAA ATCATGGATA 300
 AAAACACACT AGGGAGTGAT TTGCCCCGGA TCAAAACGGA GATTGAGGCC TTGAAGAACC 360
 TGAGACATCA GCATATATGT CAATCTTACC ATGTGCTAGA GACAGCCAAC AAAATATTCA 420
 TGGTTCTTGA GTACTGCCCT GGAGGAGAGC TGTTTGACTA TATAATTTC CAGGATCGCC 480
 TGTCAGAAGA GGAGACCCGG GTTGCTCTTC GTCCAGATAGT ATCTGCTGTT GCTTATGTGC 540
 ACAGCCAGGG CATAGCTCAC AGGGACCTCA AGCCAGAAAA TTTGCTGTTT GATGAATATC 600
 30 ATAAATTAAA GCTGATTGAC TTTGGTCTCT GTGCAAAACC CAAGGGTAAC AAGGATTACC 660
 ATCTACAGAC ATGCTGTGGG AGTCTGGCTT ATGCGAGCACC TGAGTTAATA CAAGGCAAT 720
 CATATCTTGG ATCAGAGGGA GATGTTTGA GCATGGGCAT ACTGTTATAT GTTCTTATGT 780
 GTGGATTCTT ACCATTGATG ATGATAATG TAATGGCTTT ATACAAGAAG ATTATGAGAG 840
 35 GAAAATATGA TGTTCCTAAG TGGCTCTCTC CCAGTAGCAT TCTGCTTCTT CAACAAATGC 900
 TGCAGGTGGA CGGCAAGAAA CGGATTTCTA TGAATAATCT ATTGAACCAT CCTGTGATCA 960
 TGCAAGATTA CAATATCTCT GTTGAGTGGC AAAGCAAGAA TCCTTTTATT CACCTCGATG 1020
 ATGATTCGCT AACAGAACTT TCTGTACATC ACAGAAACAA CAGGCAACAA ATGGAGGATT 1080
 TAATTTCACT GTGGCAGTAT GATCACCTCA CGGCTACCTA TCTTCTGCTT CTAGCCAAAG 1140
 40 AGGCTCGGGG AAAACCAAGT CGTTTAAAGC TTTCTTCTTT CTCCTGTGGA CAAGCCAGTG 1200
 CTACCCCATT CACAGACATC AAGTCAAAATA ATTGGAGTCT GGAAGATGTG ACCGCAAGTG 1260
 ATAAAAATTA TGTGGCGGGA TTAATGACT ATGATTGGTG TGAAGATGAT TTATCAACAG 1320
 GTGCTGTCTAC TCCCGAACA TCACAGTTTA CCAAGTACTG GACAGAATCA AATGGGGTGG 1380
 AATCTAAATC ATTAATCTCA GCCTTATGCA GAACACCTGC AAATAAATTA AAGAACAAAG 1440
 45 AAAATGTATA TACTCTAAG TCTGCTGTAA AGAATGAAGA GTACTTTATG TTTCTGAGC 1500
 CAAAGACTCC AGTTAATAAG AACCAAGCATA AGAGAGAAAT ACTCACTACG CCAATCGTT 1560
 ACACTACACC CTCAAAAGCT AGAAACCAAGT GCCTGAAAGA AACTCCAATT AAAATACCAG 1620
 TAAATCAAC AGGAACAGAC AAGTTAATGA CAGGTGTCTA TAGCCCTGAG AGGCGGTGCC 1680
 GCTCAGTGA ATTGGATCTC AACCAAGCAC ATATGGAGGA GACTCCAAA AGAAAGGGAG 1740
 50 CCAAAGTGT TGGGAGCCTT GAAAGGGGGT TGGATAAGGT TATCACTGTG CTCACCAGGA 1800
 GCAAAAGGAA GGTGTTCTGC AGAGACGGGC CCAAGAGACT AAAGCTTAC TATAATGTGA 1860
 CTACAACATG ATTAGTGAAT CCAGATCAAC TGTGAATGA AATAATGTCT ATTCTTCAA 1920
 AGAAGCATGT TGACTTTGTA CAAAGGGTT ATACACTGAA GTGTCAAACA CAGTCAGATT 1980
 TTGGGAAAGT GACAAATGAA TTTGAATTAG AAGTGTGCCA GCTTCAAAA CCCGATGTGG 2040
 55 TGGGTATCAG GAGGCAGCG CTTAAGGGCG ATGCTGGGT TTACAAAGA TTAGTGAAG 2100
 ACATCTATC TAGCTGCAAG GTATAATTGA TGGATTCTTC CATCTGCCG GATGAGTGTG 2160
 GGTGTGATAC AGCCTACATA AAGACTGTTA TGATCGCTTT GATTTTAAAG TTCAATGGAA 2220
 CTACCAACTT GTTCTAAAG AGCTATCTTA AGACCAATAT CTCTTTGTTT TTAACAAA 2280
 GATATATATT TGTGTATGAA TCTAAATCAA GCCATCTGT CATTATGTTA CTGCTTTTT 2340
 60 TAATCATGTG GTTTGTGATA TTAATAATTG TTGACTTTCT TAGATTCACT TCCATATGTG 2400
 AATGTAAGCT CTAACTATG TCTCTTTGTA ATGTGTAATT TCTTTCTGAA ATAAACCAT 2460
 TTGTGAATAT

Seq ID NO: 653 Protein sequence
 Protein Accession #: NP_055606.1

1 11 21 31 41 51
 65 MKDYDELLKY YELHETIGTG GFAKVKLACH ILTGEMVAIK IMDKNTLGSD LPRIKTEIEA 60
 LKNLRHQHIC QLYHVLETAN KIFMVLEYCP GGELEFDYIIS QDRLSEETR VVFRQIVSAV 120
 70 AYVHSQGYAH RDLKPENLLF DEYHKLKID FGLCAKPKGN KDYLQTCCG SLAYAAPELI 180
 QGKSYLGSEA DVVSMGILLY VLMCGFLFFD DDNVMALYKK IMRGKYDVPK WLSPPSILL 240
 QQMLQVDPKK RISMKNLNLH PWIMQDYNYP VEWQSKNFFI HLDDDCVTEL SVHHRNRRQT 300
 MEDLISLWQY DHLTATYLLL LAKKARGKPV RLRLSSPFCG QASATPFTDI KSNNWSLEDV 360
 75 TASDRNYVAG LIDVDWCEDD LSTGAATPRT SQFTKYNTES NGVESKSLTP ALCRTPANKL 420
 KNKENVYTPK SAVKNEEYFM FPEKTPVKN NQHKREILT PNRYYTPSKA RNQCLKETPI 480
 KIPVNSTGTD KLMTGVISPE RRCRSVELDL NQAHMEETPK RKGAKVFGSL ERGLDKVITV 540
 LTRSKRKGSA RDGPRRLKLH YNVTTTRLVN PDQLNEIMS ILPKKHVDFV QKGYTLKQCT 600
 QSDFGKVTMQ FELEVQCLOK PDVVGIRRR LKGDWVYKR LVEDILSSCK V

Seq ID NO: 654 DNA sequence
 Nucleic Acid Accession #: NM_000582
 Coding sequence: 88..990

1 11 21 31 41 51
 85 GCAGAGCACA GCATCGTCGG GACCAGACTC GTCTCAGGCC AGTTGCAGCC TTCTCAGCCA 60
 AACGCCGACC AAGGAAACT CACTACCATG AGAATTGCAG TGATTGTCTT TTGCTCTCTA 120

	GGCATCACCT	GTGCCATACC	AGTTAAACAG	GCTGATTCTG	GAAGTTCTGA	GGAAAAAGCAG	180
	CTTTACAACA	AATACCCAGA	TGCTGTGGCC	ACATGGCTAA	ACCCTGACCC	ATCTCAGAAAG	240
	CAGAAATCTCC	TAGCCCCACA	GACCCCTCCA	AGTAAGTCCA	ACGAAAGCCA	TGACCCACATG	300
5	GATGATATGG	ATGATGAAGA	TGATGATGAC	CATGTGGACA	GCCAGGACTC	CATTGACTCG	360
	AACGACTCTG	ATGATGTAGA	TGACACTGAT	GATTCTCACC	AGTCTGATGA	GTCTCACCAT	420
	TCTGATGAAT	CTGATGAAT	GGTCACTGAT	TTTCCCACGG	ACCTGCCAGC	AAACGGAAGTT	480
	TTCACTCCAG	TGTCTCCAC	AGTAGACACA	TATGATGGCC	GAGGTGATAG	TGTGGTTTAT	540
	GGACTGAGGT	CAAAATCTAA	GAAGTTTCGC	AGACCTGACA	TCCAGTACCC	TGATGCTACA	600
10	GACGAGGACA	TACACCTACA	CATGGAAAGC	GAGGAGTTGA	ATGGTGATA	CAAGGCCATC	660
	CCCGTTGCC	AGGACCTGAA	CGCGCTTCT	GATTGGGACA	GCCGTGGGAA	GGACAGTTAT	720
	GAAACGAGTC	AGCTGGATGA	CCAGAGTGCT	GAAACCCACA	GCCACAAGCA	GTCCAGATTA	780
	TATAAGCGGA	AAGCCAAATGA	TGAGAGCAAT	GAGCATTCCG	ATGTGATTGA	TAGTCAGGAA	840
	CTTTCCAAAG	TAGCCCGTGA	ATTCCACAGC	CATGAATTTT	ACAGCCATGA	AGATATGCTG	900
15	GTGTGATAGC	CCAAAAGTAA	GGAAGAAGAT	AAACACCTGA	AATTTCTGAT	TTCTCATGAA	960
	TTAGATAGTG	CATCTTCTGA	GGTCAATTAA	AAGGAGAAAA	AATACAAATT	CTCACTTTGC	1020
	ATTTAGTCAA	AAGAAAAAAT	GCTTTATAGC	AAAATGAAAG	AGAACATGAA	ATGCTTCTTT	1080
	CTCAGTTTAT	TGGTTGAATG	TGTATCTATT	TGAGTCTGGA	AATAACTAAT	TGTTTGTATA	1140
	ATTAGTTTAG	TTTGTGGCTT	CATGGAAACT	CCCTGTAAAC	TAAAAGCTTC	AGGGTTATGT	1200
20	CTATGTTTAT	TCTATAGAAG	AAATGCAAA	TATCACTGTA	TTTTAATATT	TGTTATTCTC	1260
	TCTGAATAG	AAATTTATGT	AGAAGCAAA	AAAATACTTT	TACCCACTTA	AAAAGAGAA	1320
	ATAACATTTT	ATGTCACAT	AATCTTTTGT	TTTTTAAGTT	AGTGTATATT	TTGTGTGAT	1380
	TATCTTTTGT	TGGTGTGAAT	AAATCTTTTA	TCTTGAATGT	AATAAGAATT	TGGTGGTGT	1440
	AATTGCTTAT	TGTTTTCCT	ACGGTTGTCC	AGCAATTAAT	AAAACATAAC	CTTTTCTACT	1500
25	GCCTAAAAA	AAAAAATAA	AAAA				

Seq ID NO: 655 Protein sequence
Protein Accession #: NP_000573

	1	11	21	31	41	51	
30	MRIAVICFCL	LGITCAIPVK	QADSGSSEK	QLYNKYPDV	ATWLNPDPSQ	KQNLAPQTL	60
	PSKSNESHDL	MDDMDEDD	DHVDSDSID	SNDSDVDVDT	DDSHQSDSH	HSDEDELVT	120
	DFPTDLDPATE	VTPVPTVD	TYDGRGDSV	YGLRSKSKKF	RRPDIQVPA	TDEDITSHME	180
	SEELNGAYKA	IPVAQDLNAP	SDWDSRGKDS	YETSQLDDQS	AETHSHKQSR	LYKRKANDES	240
35	NEHSDVIDSQ	ELSKVSREEF	SHEFHSHEM	LVDVPSKEE	DKHLKFRISH	ELDSASSEVN	

Seq ID NO: 656 DNA sequence
Nucleic Acid Accession #: NM_003108.1
Coding sequence: 76..1401

	1	11	21	31	41	51	
45	GGGGTGGGAG	GGGGAGGGGG	ACCTCCGCAC	GAGACCCAGC	GGCCCGGGTT	GGAGCGTCCA	60
	GCCCTGCAAC	GGATCATGCT	GCAGCAGCG	GAGAGCTTGG	AAGCGGAGAG	CAACCTGCCC	120
	CGGGAGGGCG	TGGACACGGA	GGAGGGCGAA	TTCATGGCTT	GCAGCCCGGT	GGCCCTGGAC	180
	GAGAGCGACC	CAGACTGGTG	CAAGACGGCG	TCCGGCCACA	TCAAGCGGCC	GATGAACGCG	240
	TTATGCTAT	GGTCCAGAT	CGAACGCGAG	AAGATCATGG	AGCAGTCTCC	GGACATGCAC	300
	AACGCCGAGA	TCTCCAAGAG	GCTGGGCAAG	CGCTGGAAGA	TGCTGAAGGA	CAGCGAGAAG	360
50	ATCCCGTTCA	TCCGGGAGCG	GGAGCGGCTG	CGGCTCAAGC	ACATGGCCGA	CTACCCCGAC	420
	TACAAGTACC	GGCCCGGAA	AAAGCCCAAA	ATGACCCCTT	CGGCCAAGCC	CAGCGCCAGC	480
	CAGAGCCAG	AGAAAGAGCG	GGCCGGCGGC	GGCGGGCGGA	GCGCGGGCGG	AGGCGCGGGC	540
	GGTGCCAAAG	CTCCCAAGGG	CTCCAGCAAG	AAATGCGGCA	AGCTCAAGGC	CCCGCGGGCC	600
	GCGGGCGCCA	AGGCGGGCGC	GGGCAAGCG	GCCAGTCCG	GGGACTACGG	GGGCGGGGCG	660
55	GACGACTACG	TGCTGGGCG	CCTGCGCGTG	AGCGGCTCGG	GCGGCGGGCG	CGCGGGCAAG	720
	ACGGTCAAGT	GGGTGTTTCT	GGATGAGGAC	GACGACGACG	ACGACGACGA	CGACGAGCTG	780
	CAGCTGCAGA	TCAAACAGGA	GCCGACGAG	GAGGACGAGG	AACCAACCGA	CCAGCAGCTC	840
	CTGCAGCGCG	CGGGCAGCA	GCCGTCCGAG	CTGCTGAGAC	GCTACAACGT	CGCCAAAGTG	900
60	CCGCGCAGCC	CTCAGCTGAG	CAGCTCGGCG	GAGTCCCGCG	AGGGAGCGAG	CCTCTACGAC	960
	GAGGTGCGGG	CGGCGCGAC	CTCGGGCGCC	GGGGCGGCA	GCCGCTCTTA	CTACAGCTTC	1020
	AAGAAATCAT	CCAAGCAGCA	CCCGCCGCG	CTCGCGCAGC	CCGCGCTGTC	GCCCGCGTCC	1080
	TCCGCTCGG	CTCCACCTC	CTCGTCCAGC	AGCAGCGGCA	GCAGCAGCGG	CAGCAGCGCG	1140
	GAGGACGCG	ACGACCTGAT	GTTGACCTG	AGCTTGAATT	TCTCTCAAAG	CGGCAACAGC	1200
65	GCCAGCGAGC	AGCAGCTGGG	GGGCGGCGCG	GCGGCGGGGA	ACCTGTCCCT	GTGCTGGTGG	1260
	GATAAGGATT	TGGATTCTGT	CAGCGAGGGC	AGCCTGGGCT	CCCACTTCGA	GTTCGCCGAC	1320
	TACTGCACGC	CGGAGCTGAG	CGAGATGATC	GCGGGGAGCT	GGCTGGAGGC	GAACTTCTCC	1380
	GACCTGGTGT	TCACATATTG	AAAGGCGCCC	GCTGCTCGCT	CTTTCTCTCG	GAGGGTGCAG	1440
	AGCTGGGTTT	CTTGGGAGGA	AGTTGTAGTG	GTGATGATGA	TGATGATGAT	AATGATGATG	1500
70	ATGATGGTGG	TGTTGATGCT	GGCGGTGGTA	GGGTGGAGGG	GAGAGAAGAA	GATGCTGATG	1560
	ATATTGATAA	GATGTCTGTA	CGCAAAGAAA	TTGGAAACA	TGATGAAAT	TTTGGTGGAG	1620
	TTAAAGTGAA	ATGAGTAGTT	TTTAAACATT	TTTCTGTCTC	TTTTTTTGTG	CCCCCTCCCT	1680
	TCCTTTATCG	TGTCTCAAGG	TAGTTGCATA	CCTAGTCTGG	AGTTGTGATT	ATTTTCCCAA	1740
	AAAATGTGTT	TTTGTAAATTA	CTATTCTTTT	TTCTGTAAAT	TCGTGATTGC	AACAAAGGCA	1800
75	GAGGGGGCGG	CGCGGGCGG	GGGAGGTAGG	ACCGGCTCCG	GAAGGCGCTG	TTTGAAGCTT	1860
	GTCGGTCTTT	GAAGTCTGGA	AGACGTCTGC	AGAGGACCCT	TTTGGCAGCA	CAACTGTTAC	1920
	TCTAGGGAGT	TGGTGGAGAT	ATTTTTTTTT	CTTAAGAGAA	CTTAAAGAAC	TGTTGATTTT	1980
	TTTTTAACAA	AAAAAGGG					

Seq ID NO: 657 Protein sequence
Protein Accession #: NP_003099.1

	1	11	21	31	41	51	
85	MVQQAESLEA	ESNLPREALD	TEEGEFMACS	PVALDESDPD	WCKTASGHK	RPMNAFMVWS	60
	KIERRKIMEQ	SPDMHNAEIS	KRLGKRWKML	KDSEKIPFIR	EAERLRLKHM	ADYPDYKYRP	120
	RKKPKMDPSA	KPSASQSPK	SAAGGGGSA	GGGAGGAKTS	KGSSKKCKGL	KAPAAAGAKA	180
	GAGKAAQSGD	YGGAGDDYVL	GSLRVSGSGG	GGAGKTVKCV	FLDEDDDDDD	DDDELQLQIK	240

QEPDEEDEBP PHQQLLPFGP QPQSLLRRY NVAKVPASPT LSSSAESPEG ASLYDEVVRAG 300
 ATSGAGGGR LYYSFKNITK QHPPLAQA LSPASSRSVS TSSSSSGSS SGSSGEDADD 360
 LMFDSLNFQ QSAHSASEQQ LGGGAAGNL SLSLVKDLDD SFSEGLSGSH FEFPDYCTPE 420
 LSEMIAGDWL EANFSDLVFT Y

Seq ID NO: 658 DNA sequence
 Nucleic Acid Accession #: NM_001719
 Coding sequence: 123..1418

10 1 11 21 31 41 51
 | | | | | |
 GGGCGCAGCG GGGCCCGTCT GCAGCAAGTG ACCGACGGCC GGGACGGCCG CCTGCCCCCT 60
 CTGCCACCTG GGGCGGTGCG GGCCCGGAGC CCGGAGCCCG GGTAGCGCGT AGAGCCGGCG 120
 CGATGCACGT GCGCTCACTG CGAGCTGCGG CGCCGCACAG CTTCGTGGCG CTCTGGGCAC 180
 15 CCTCTTCTCT GCTGCGCTCC GCCCTGGCCG ACTTCAGCCT GGACAAACGAG GTGCACTCGA 240
 GCTTCATCCA CCGGCGCCTC CGCAGCCAGG AGCGGCGGGA GATGCAGCGC GAGATCCTCT 300
 CCATTTTGGG CTTGCCCCAC CGCCCGCGCC CGCACCTCCA GGGCAAGCAC AACTCGGCAC 360
 CCATGTTTAT GCTGGACCTG TACAACGCCA TGGCGGTGGA GGAGGGCGGC GGGCCCGGCG 420
 20 GCCAGGGCTT TCCTACCCG TACAAGGCGG TCCTCAGTAC CCAGGGCCCC CCTCTGGCCA 480
 GCCTGCAAGA TGCCATTTC CTCACCGACG CCGACATGGT CATGAGCTTC GTCAACCTCG 540
 TGAACATGA CAAGGAATTC TTCCACCACG GCTACACCA TCGAGAGTTC CGGTTTGATC 600
 TTTCCAAGAT CCCAGAAGGG GAAGCTGTCA CGCAGCCGA ATTCCGGATC TACAAGACT 660
 ACATCCGGGA ACGCTTCGAC AATGAGACGT TCCGGATCAG CGTTTATCAG GTGTCCAGG 720
 AGCACTTGGG CAGGGAATCG GATCTCTTCC TGCTCGACAG CCGTACCCTC TGGGCTCGG 780
 25 AGGAGGGCTG GCTGGTGTG GACATCACAG CCACAGCAA CCACTGGGTG GTCAATCCGC 840
 GGCACAACCT GGGCTGCGAG CTCTCGGTGG AGACGCTGGA TGGGCAGAGC ATCAACCCCA 900
 AGTTGGCGGG CCTGATTGGG CGGCACGGGC CCCAGAACA GCAGCCCTTC ATGGTGGCTT 960
 TCTTCAAGG CACGGAGTGC CACTTCGCGA GCATCCGGTC CACGGGGAGC AAACAGCGCA 1020
 30 GCCAGAACC CTCCAAGACG CCCAAGAACC AGGAAGCCCT GCGGATGGCC AACGTGGCAG 1080
 AGAACAGCAG CAGCGACCAG AGGCAAGCCT GTAAGAAGCA CGAGCTGTAT GTCAGCTTCC 1140
 GAGACCTGGG CTGGCAGGAC TGGATCATCG CGCCTGAAGG CTACGCGGCC TACTACTGTG 1200
 AGGGGAGTGT TGCCTTCCTT CTGAACCTCT ACATGAACGC CACCAACCA GGCATCGTGC 1260
 AGACGCTGCT CCACTTCATC AACCGGAAA CGGTGCCCAA GCCCTGCTGT GCGCCACGCG 1320
 35 AGCTCAATGC CATCTCCGTC CTCTACTTCG ATGACAGCTC CAACGTCATC CTGAAGAAAT 1380
 ACAGAAACAT GGTGGTCCGG GCCTGTGGCT GCCACTAGCT CCTCCGAGAA TTCAGACCTT 1440
 TTGGGGCCAA GTTTTCTGG ATCTCTCATT GCTCGCCTTG GCCAGGAACC AGCAGACCAA 1500
 CTGCTTTTGG TGAGACCTTC CCTTCCCTAT CCCCACTTT AAAGGTGTGA GAGTATTAGG 1560
 40 AAACATGAGC RISVYQLQGE TTTTGTACAG TTTTGTACAG GCAGCATCCA ATGAACAAGA 1620
 TCTTACAAGC TGTGCGAGCA AAACCTAGCA GGAAGAAAAA ACAACGCATA AAGAAAAATG 1680
 GCCGGGCCAG GTCATTGGCT GGGAGTCTC AGCCATGCAC GGACTCGTTT CCAGAGGTAA 1740
 TTATGAGCGC CTACACGCAA GGCAACCCAG CCGTGGGAGG AAGGGGGCGT GCAAGGGGT 1800
 GGGCACATTG GTGTCTGTGC GAAAGGAAAA TTGACCCGGA AGTTCCTGTA ATAAATGTCA 1860
 CAATAAACG AATGAATG

Seq ID NO: 659 Protein sequence
 Protein Accession #: NP_001710

1 11 21 31 41 51
 | | | | | |
 50 MHVRSRLAAA PHSFVALWAP LFLRLSALAD FSLDNEVHSS FIHRLRSQE RREMQRILS 60
 ILGLPHRPRP HLQGHNSAP MFMLDLNAM AVEEGGGPGG QGSYSPYKAV FSTQGPPLAS 120
 LQDSHFLTDA DMVMSFVNLV EHDKEFFHPR YHREPRFDL SKIPEGEAVT AAEFRYKYD 180
 IRERFDNETF RISVYQLQGE TTTTGTACAG TTTTGTACAG GCAGCATCCA ATGAACAAGA 1620
 55 HNLGLQLSVE TLDGQSINPK LAGLIGRHGP QNKOPFMVAF FKATEVHFRS IRSTGSKQRS 300
 QNRSTPKNQ BALRMANVAE NSSSDQRQAC KKHLYVSFR DLGWQDWIIA PEGYAAYYCE 360
 GECAFPLNSY MNATNHAIVQ TLVHFINPET VPKPCCAPTQ LNAISVLYFD DSSNVILKKY 420
 RNMVVRACGC H

Seq ID NO: 660 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 211..1895

1 11 21 31 41 51
 | | | | | |
 65 GGATCTGAGG GGGCGCCAGT CACTTCTCC ACCTTCTCGT GCTGGGCGGG AGGAGCGGAT 60
 GGGGCTTGGG AGGAGCCTG CTCTCCAGTC CCTATCCACC CACAGGTTT TTTGGTGGGA 120
 GAGGAATTAT CTGATAAAT TCCTGGGTGA ATATTTTAA AAACGAGAG TTTTAAAAA 180
 TGATTTTTT CCCTCGAAAA TGACCTTTT ATGCTTCGAA GCAGTTTGT CACACAGATA 240
 70 GTGCTTTTTC TTTTCTCTTC TTTTCTACG ATAAATGAAA GCATTCTTC AAGAAAAAGG 300
 CACAGGTTC TTGAACAGCT GATTTCTGAT GGCACCATTA CTATAGAGGA GCAGATTGTC 360
 CTTGTGCTGA AAGCGAAAGT ACATGTGAA CTCAACATCA CAGCTCAACT CCAGGAGGGA 420
 GAAGTAATT GTTCCCTGA ATGGGATGGA CTCATTGTG GGGCCAGAGG AACAGTGGG 480
 AAAATATCGG CTGTTCCATG CCCTCCTTAT ATTTATGACT TCAACCATAA AGGAGTTGCT 540
 75 TTCCGACACT GTAACCCCAA TGGAACATGG GATTTATGC ACAGCTTAAA TAAACATGG 600
 GCCAATTATT CAGACTGCCT TCGCTTCTG CAGCCAGATA TCAGCATAGG AAAGCAAGAA 660
 TTCTTTGAAC GCCTCTATGT AAGTATACC GTTGGCTACT CCATCTCTT TGGTTCTTGG 720
 GCTGTGGCTA TTCTCATCAT TGTCTACTTC AGACGATTGC ATTGCACTAG GAACTATATC 780
 CACATGCACT TATTTGTGTC TTTTATGCTG AGAGCTACAA GCATCTTGT CAAAGACAGA 840
 80 GTAGTCCATG CTCACATAGG AGTAAAGGAG CTGGAGTCCC TAATAATGCA GGATGACCCA 900
 CAAAATCCA TTGAGGCAAC TTCTGTGAC AAATCAAT ATATCGGGT CAAGATTGCT 960
 GTGTGATGT TTATTTACTT CCTGGCTACA AATTATTATT GGATCTGGT GGAAGGTCTC 1020
 TACCTGCATA ATCTCATCTT TGTGGCTTTC TTTTGGGACA CCAATACCT GTGGGGCTTC 1080
 85 ATCTTGATAG GTCGGGGTTC TCCAGCAGCA TTTGTTGCAG CATGGGCTGT GGCACGAGCA 1140
 ACTCTGGCTG ATGCGAGGTG CTGGGAACCT AGTGTGAGG ACATCAAGTG GATTTATCAA 1200
 GCACCGATCT TAGCAGCTAT TGGGCTGAAT TTTATCTGT TTCTGAATAC GGTTAGAGTT 1260
 CTAGCTACCA AAATCTGGGA GACCAATGCA GTTGGGCATG ACACAGGAA GCAATACAGG 1320
 AAATGGCCA AATCGACACT GGTCTGGTC CTAGTCTTTG GAGTGCATTA CATCTGTTC 1380

GTATGCCTGC CTCCTCTCTT CACTGGGCTC GGGTGGGAGA TCCGCATGCA CTGTGAGCTC 1440
 TTCTTCAACT CCTTTCAGGG TTTCTTTGTG TCTATCATCT ACTGCTACTG CAATGGAGAG 1500
 GTTCAGGCAG AGGTGAAGAA GATGTGGAGT CGGTGGAATC TCTCCGTGGA CTGGAAAAGG 1560
 ACACCGCCAT GTGGCAGCCG CAGATGCGGC TCAGTGCTCA CCACCGTGAC GCACAGCACC 1620
 AGCAGCCAGT CACAGGTGGC GGCCAGCACA CGCATGGTGC TTATCTCTGG CAAAGCTGCC 1680
 AAGATCGCCA GCAGACAGCC TGACAGCCAC ATCACTTTAC CTGGCTATGT CTGGAGTAAC 1740
 TCAGAGCAGG ACTGCCTGCC ACACCTTTTC CACGAGGAGA CCAAGGAAGA TAGTGGGAGG 1800
 CAGGAGATG ATATTCTAAT GGAGAAACCT TCCAGGCCTA TGGATCTAA CCCAGACACT 1860
 GAAGGATGCC AAGGAGAAAC TGAGGATGTT CTCTGA

Seq ID NO: 661 Protein sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 MLRSSLSSTSI VLFLFPSPST INESSISRKR HRFLEQLDSD GTITIEEQIV LVLKAKVQCE 60
 LNIITAQLQEG EGNCFPEWDG LICWPRGTVG KISAVPCPPY IYDFNHKGVA FRHCNPNGTW 120
 DFMHSLNKTW ANYSDCLRFL QPDISIGKQE FFERLYVMTY VGSISFSGSL AVAILLIQYF 180
 RRLHCTRNYY VMHFLVFSFML RATSIFVKDR VVHAHIGVKE LESLIMQDDP QNSIEATSV 240
 KSOYIGCKIA VMPFIYFLAT NYWILVEGL YLHNLIFVAF FSDTKYLWGF ILIGWGFPA 300
 FVAWAVARA TLADARCWEL SAGDIKWIYQ APILAAIGLN FILFLNTVRV LATKIWETNA 360
 VGHDTRKQYR KLAKESTLVLV LVFVGHYIVF VCLPHSFTGL GWEIRMHCEL FFNSFQGFV 420
 SIIYCYCNGE VQAEEVKKWS RNWLSVDWKR TPCCGSRRCG SVLTTVTHST SSQSQAAS 480
 RMVLISGKAA KIASRQPSH ITPGYVWSN SEQDCLPHSF HEETKEDSGR QGDDILMEKP 540
 SRPMESNPDT EGCQGETEDV L

Seq ID NO: 662 DNA sequence
 Nucleic Acid Accession #: NM_005048
 Coding sequence: 143..1795

1 11 21 31 41 51
 GGCCGGTGGC CGGGGCCCGA CCACCCAGC TGCGCGTCTG TACTGGCCAC AAGTTTGCTC 60
 TGGGCCAGCC AAGTTGGCAA CTGGGAAGCT TCTCCCGGGC TCTGGAGGAG GGTCCCTGCT 120
 TCTTCTTACA GCGGTTCGGG GCATGGCCGG GCTGGGGCGG TCGCTCCACG TCTGGGGTTG 180
 GCTAATGCTC GGCAGCTGCC TCCTGGCCAG AGCCAGCTG GATTCTGATG GCACCATTAC 240
 TATAGAGGAG CAGATTGTCC TTGTGCTGAA AGCGAAAGTA CAATGTGAAC TCAACATCAC 300
 AGCTCAACTC CAGGAGGGAG AAGGTAATTG TTTCCCTGAA TGGGATGGAC TCATTGTGTT 360
 GCCCAGAGGA ACAGTGGGGA AAATATCGGC TGTTCATGTC CCTCCTTATA TTTATGACTT 420
 CAACCATAAA GGAGTTGCTT TCCGACACTG TAACCCCAAT GGAACATGGG ATTTTATGCA 480
 CAGCTTAAAT AAAACATGGG CCAATTATTC AGACTGCCTT CGCTTCTGCG AGCCAGATAT 540
 CAGCATAGGA AAGCAAGAAT TCTTTGAACG CCTCTATGTA ATGTATACCG TTGGCTACTC 600
 CATCTCTTTT GGTTCCTTGG CTGTGGCTAT TCTCATCATT GGTACTTCA GAGGATTGCA 660
 TTGCACTAGG AACTATATCC ACATGCACCT ATTTGTGTCT TTCATGCTGA GAGCTACAAG 720
 CATCTTTGTC AAAGACAGAG TAGTCCATGC TCACATAGGA GTAAAGGAGC TGGAGTCCCT 780
 AATAATGACG GATGACCCAC AAAATTCCAT TGAGGCAACT TCTGTGGACA AATCACAATA 840
 TATCGGGTGC AAGATTGCTG TTGTGATGTT TATTACTTTC CTGGCTACAA ATTATTATTG 900
 GATCCTGGTG GAAGGTCTCT ACCTGCATAA TCTCATCTTT GTGGCTTCTT TTTCCGACAC 960
 CAAATACCTG TGGGCTTCA TCTTGATAGG CTGGGGGTTT CCAGCAGCAT TTGTGTCAGC 1020
 ATGGGCTGTG CACACGACAA CTCTGGCTGA TGCGAGGTGC TGGGAACCTA GTGCTGAGA 1080
 CATCAAGTGG ATTTATCAAG CACCGATCTT AGCAGCTATT GGGCTGAATT TTATTCTGTT 1140
 TCTGAATACG GTTAGAGTTC TAGCTACCAA AATCTGGGAG ACCAATGCAG TTGGGCATGA 1200
 CACAAGGAAG CAATACAGGA AACTGGCCAA ATCGACACTG GTCTCTGGTCC TAGTCTTTGG 1260
 AGTGCAATTAC ATCGTGTTCG TATGCCTGCC TCACTCCTTC ACTGGGCTCG GGTGGGAGAT 1320
 CCGCATGCAC TGTGAGCTCT TCTTCAATC CTTCAGGGT TTCTTTGTGT CTATCATCTA 1380
 CTGCTACTGC AATGAGAGAG TTCAGGCAGA GGTGAAGAAG ATGTGGAGTC GGTGGAATCT 1440
 CTCCGTGGAC TGGAAAAGGA CACCGCCATG TGGCAGCGCG AGATGCGGCT CAGTGTCTAC 1500
 CACCGTGACG CACAGCACC ACGAGCCATC ACAGGTGGCG GCCAGCACAC GCATGGTGCT 1560
 TATCTCTGGC AAAGCTGCCA AGATCGCCAG CAGACAGCCT GACAGCCACA TCACTTTACC 1620
 TGGCTATGTC TGGAGTAAT CAGAGCAGGA CTGCCCTGCC CACTCTTTCC ACGAGGAGAC 1680
 CAGGAAGAT AGTGGGAGTG AGGGAGATGA TATTCTAATG GAGAAGCCTT CCAGGCCTAT 1740
 GGAATCTAAC CACAGCAGTG AAGGATGCCA AGGAGAACT GAGGATGTT TCTGAATGGA 1800
 CATTTGTGGC TGACTTTTAT GGGCTGGTCC AATGGCTGGT TGTGTGAGAG GGCTTGGCTG 1860
 ATACTCCTAT GCTTGAGTTC AAAGGCTGAA AATTCAGTTA AGGTGTTACT TAATAATAGT 1920
 TTTTAGGCTC CATGAATTGG CTCCTGTAAA TACTAACGAC ATGAAAATGC AAGTGTCAAT 1980
 GGAGTAGTTT ATTACCTTCT ATTGGCATCA AGTTTTCCTC TAAATTAATG TATGGTATT 2040
 GCTCTGTGAT TGTTCATTTT TTTCTGTAC TTTTGGGTAG AAAAAAGATT CAATTGCTTG 2100
 GCTGTAGCTT TCTCTCATAT ATATCACCTT AAATATAATG AAGATCTTTT AGTGTGTATC 2160
 ATTTCTCTTT TAGAACTAG TATTCTCTTA TTTCTTACTT TAATGTACTT CTATCACTGC 2220
 ATTTATTTTG CTGTGTCATA GGAGCAATTA GGATCTAAAA AAATATATGG GAAGATAAAA 2280
 GATCTAAGAA CAAGTACTTG CTGGAAAATT AGTTGGCTGG ACATTGATAA AATAATGCAT 2340
 TTATAACAAT TACATGTGTT TTTGGGAACA AGGAAAATTT CTCAAAAAAG AATATTTTAC 2400
 ACATCCCTTC TTTTGAATGG CCTCTTTGTG ACCAGCCAGA CCTCAGGTCT TCACTCTTTC 2460
 TTCTTTGTAA ACCATGTGAT GTGGAAAAGT TTCCTCAGTT AGTGAGCTTG TGTCTGCAAA 2520
 TTGATTTTGT TTGTAATGTA TTTTGATAGC AAATCATGCT GCATCTATAT CTTTCTCTTG 2580
 TTTGAGCTGT TACTACATG TACATGGCAT GTGGGATCAA TTAATAATTT GTTTAAAAAA 2640
 T

Seq ID NO: 663 Protein sequence
 Protein Accession #: NP_005039

1 11 21 31 41 51
 MAGLGASLHV NGWMLGSL LARAQLSDG TITIEEQIVL VLKAKVQCEL NITAQLQEGE 60
 GNCPEWDGL ICWPRGTGK ISAVPCPPYI YDFNHKGVA FRHCNPNGTW FMSHSLNKTW 120
 NYSDCLRLFL QPDISIGKQE FERLYVMTY GYSISFSGSL VAILLIQYFR RLHCTRNYYH 180
 MHLFVSFMLR ATSIFVKDRV VHAHIGVKEL ESLIMQDDPQ NSIEATSVDK SQYIGCKIAV 240

VMPIYFLATN YYWILVEGLY LHNLI FVAFV SDTKYLWGFPI LIGWGFPAAF VAAWAVARAT 300
 LADARCWELS AGDIKWIYQA PILAAIGLNF ILFLNTRVRL ATKIWETNAV GHDTRKQYRK 360
 LAKSTLVVLV VFGVHYIVFV CLPHSFTGLG WEIRMHCELF FNSFQGFVVS ILYCYCNGEV 420
 QAEVKKMWSR WNLSDWKRTP PCGSRRCGS VLTIVTHSTS SQSQVAASR MVLISGKAAK 480
 IASRQPDSHI TLPGVVWSNS EQDCLPHSFH EETKEDSGRQ GDDILMEKPS RPMESNPDTB 540
 GCQGETEDVL

Seq ID NO: 664 DNA sequence
 Nucleic Acid Accession #: NM_012152
 Coding sequence: 43..1104

1 11 21 31 41 51
 | | | | | |
 15 CTCTTTTAAA TTCTTTTCTA GGATGTTTCC TTCTTCTCCA CAATGAATGA GTGTCACTAT 60
 GACAAGCACA TGGACTTTTT TTATAATAGG AGCAACACTG ATACTGTGGA TGACTGGACA 120
 GGAACAAAGC TTGTGATTGT TTTGTGTGTT GGGACGTTTT TCTGCCTGTT TATTTTTTTT 180
 TCTAATTCTC TGGTCATCGC GGCAGTGATC AAAAACAGAA AATTTCATTT CCCCTTCTAC 240
 TACCTGTTGG CTAATTTAGC TGCTGCCGAT TTCTTGCTG GAATTGCCTA TGTATCTCTG 300
 ATGTTTAAAC CAGGCCCACT TTCAAAAACT TTGACTGTCA ACCGCTGGTT TCTCCGTGAG 360
 20 GGGCTTCTGG ACAGTAGCTT GACTGCTTCC CTCACCAACT TGCTGGTTAT CGCCGTGGAG 420
 AGGCACATGT CAATCATGAG GATCGGGTTC CATAGCAACC TGACCAAAAA GAGGGTGACA 480
 CTGCTCATTT TGCTTGTCTG GGCATCGGCC ATTTTATATG GGGCGGTCCC CACACTGGGC 540
 TGGAAATTGC TCTGCAACAT CTCTGCCCTG TCTTCCCTGG CCCCATTATA CAGCAGGAGT 600
 TACCTTGTTT TCTGACAGT GTCCAACCTC ATGGCCTTCC TCATCATGGT TGTGGTGTAC 660
 25 CTGCGGATCT ACGTGTAGCT CAAGAGGAAA ACCAACGTCT TGTCTCCGCA TACAAGTGGG 720
 TCCATCAGCC CGCGGAGGAC ACCCATGAAG CTAATGAAGA CGGTGATGAC TGTCTTAGGG 780
 GCGTTTGTGG TATGCTGGAC CCCGGGCTGT GTGGTCTGTC TCCTCGACGG CCTGAAGTGC 840
 AGGCAGTGTG GCGTCGACCA TGTGAAAAGG TGGTTCCTGC TGCTGGCGCT GCTCAACTCC 900
 30 GTCGTGAACC CCGTACTCTA CTCCTACAAG GACGAGGACA TGTATGGCAC CATGAAGAAG 960
 ATGATCTGCT GCTTCTCTCA GGAGAACCCA GAGAGGCGTC CCTCTCGCAT CCCCTCCACA 1020
 GTCTCAGCA GAGGTGACAC AGGCAGCCAG TACATAGAGG ATAGTATTAG CCAAGGTGCA 1080
 GTCTGCAATA AAAGCACTTC CTAACCTCTG GATGCCTCTC GGCCCAACCA GGTGATGACT 1140
 GTCTTAGG

Seq ID NO: 665 Protein sequence
 Protein Accession #: NP_036284

1 11 21 31 41 51
 | | | | | |
 40 MNECHYDKHM DFFYNRSNTD TVDDWTGTKL VIVLCVGTFF CLFIFFSNLS VIAAVIKNRK 60
 FHFPFYLLA NLAAADFFAG IAYVFLMNT GPVSKTLTVN RWFLRQGLLD SSLTASLTNL 120
 LVIAVERHMS IMRMVHNSL TKKRVTLIL LVWAIATPMG AVPTLGNWCL CNISACSSLA 180
 PYRSRYLFT WTVSNLMAPL IMVVVYLRIY VYVKRKTNVL SPHTSGSISR RRTPMKLMKT 240
 45 VMTVLGAFVV CMTPLGLVLL LDGLNCRQCG VQHVKNWFL LALLNSVNP IYYSKDEDM 300
 YGTMKMICC FSQENPERRP SRIPSTVLSR SDTGSQYIED SISQGAVCNK STS

Seq ID NO: 666 DNA sequence
 Nucleic Acid Accession #: NM_002821
 Coding sequence: 150..3362

1 11 21 31 41 51
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 55 AACTCCCGCC TCGGGACGCC TCGGGGTCCG GCTCCGGCTG CGGCTGCTGC TCGCGCGCCC 60
 GCGCTCCGGT GCGTCCGCTT CCTGTGCCCG CCGCGGAGCA GTCTGCCGCC CGCGTGCGC 120
 CCTCAGCTCC TTTTCTGAG CCCGCCGCGA TGGGAGCTGC GCGGGGATCC CCGGCCAGAC 180
 CCGCGCGGTT GCGCTGTGCT AGCGTCTGCT TGCTGCCGCT GCTGGGCGGT ACCCAGACAG 240
 CCATTGTCTT CATCAAGCAG CCGTCTCTCC AGGATGCACT GCAGGGGCGC CGGGCGCTGC 300
 TTCGTGTGA GGTGAGGCT CCGGGCCCGG TACATGTGTA CTGGCTGCTC GATGGGGCCC 360
 60 CTGTCCAGGA CAGCGAGCGG CGTTTCGCC AGGGCAGCAG CCTGAGCTTT CGAGCTGTGG 420
 ACGGGCTGCA GGAATCTGGC ACCTTCCAGT GTGTGGCTCG GGATGATGTC ACTGGAGAAG 480
 AAGCCCGCAG TGCCACAGCC TCCTTCAACA TCAATGGAT TGAGGCAGGT CCTGTGGTCC 540
 TGAAGCATCC AGCCCTGGAA GCTGAGATCC AGCCACAGAC CCAGGTCACT CTTCGTGTGC 600
 ACATTGATGG GCACCTCGG CCCACCTACC AATGGTCCG AGATGGGACC CCCCTTCTG 660
 65 ATGGTCAGAG CAACACACA GTACGAGCA AGGAGCGGAA CCTGACGCTC CGGCCAGCTG 720
 GTCTGAGCA TAGTGGCTG TATTCTGCT GCGCCACAG TGCTTTTGGC CAGGCTTGCA 780
 GCAGCCAGAA CTTCACCTTG AGCATTGCTG ATGAAAGCTT TGCCAGGGTG GTGCTGGCAC 840
 CCCAGGACGT GGTAGTAGCG AGGTATGAGG AGGCCATGTT CCATTGCCAG TTCTCAGCCC 900
 AGCCACCCCG GAGCCTGCAG TGGCTCTTTG AGGATGAGAC TCCATCACTT AACCGCAGTC 960
 GCGCCCCACA CCTCCGCGA GCCACAGTGT TTGCCAACGG GTCTCTGCTG CTGACCCAGG 1020
 70 TCCGGCCAGC CAATGAGGG ATCTACCGCT GCATTGGCCA GGGGCGAGAG GGGCCACCCA 1080
 TCATCTGGA AGCCACACT CACCTAGCAG AGATTGAAGA CATGCCGCTA TTTGAGCCAC 1140
 GGGTGTTTAC AGCTGGCAGC GAGGAGCGTG TGACCTGCCT TCCCCCAAG GGTCTGCCAG 1200
 AGCCAGCGT GTGGTGGGAG CACGCGGAG TCCGGCTGCC CACCCATGGC AGGGTCTACC 1260
 75 AGAAGGGCCA CGAGCTGGTG TTGGCCAATA TTGCTGAAAG TGATGCTGGT GTCTACACT 1320
 GCCACGCGCG CAACCTGGCT GGTACGCGA GACAGGATGT CAACATCACT GTGGCCACTG 1380
 TTCCCTCCTG GCTGAAGAAG CCCCAAGACA GCCAGCTGGA GGAGGGCAAA CCGGCTACT 1440
 TGGATTGCTT GAGCCAGGCC ACACCAAAAC CTACAGTTGT CTGGTACAGA AACCATGATC 1500
 TCATCTCAGA GGAATCAGG TTCGAGGTCT TCAAGAATGG GACCTTGCCT ATCAACAGCG 1560
 TGGAGGTGTA TGATGGGACA TGGTACCGTT GTATGAGCAG CACCCAGGCC GGCAGCATCG 1620
 80 AGGCGCAAGC CGGTGTCAA GTGCTGGAAG AGCTCAAGTT CACACACCA CCGCAGCCAC 1680
 AGCAGTGCAT GGAGTTTGAC AAGGAGGCCA CGGTGCCCTG TTCAGCCACA GGCAGAGAGA 1740
 AGCCCACTAT TAAGTGGGAA CGGGCAGATG GGAGCAGCCT CCCAGAGTGG GTGACAGACA 1800
 ACCTGCGGAC CTGCTATTTT GCGCGGGTGA CTCGAGATGA CGTGGCAAC TACACTTGCA 1860
 85 TTGCTCCAA CGGGCGCAG GGCCAGATTC GTGCCCATGT CCAGCTCACT GTGGCAGTTT 1920
 TTATCACCTT CAAAGTGGAA CCAGAGCGTA CGACTGTGTA CCAGGGCCAC ACAGCCCTAC 1980
 TGCAGTGCAG GGGCCAGGGG GACCCCAAGC CGCTGATTCA GTGAAAAGGC AAGGACCGCA 2040
 TCCTGAGACC CACCAAGCTG GGACCCAGGA TGCACATCTT CCAGAATGGC TCCTGCTGTA 2100

	TCCATGACGT	GGCCCTCTGAG	GACTCAGGCC	GCTACACCTG	CATTGCAGGC	AACAGCTGCA	2160
	ACATCAAGCA	CACGGAGGCC	CCCCTCTATG	TCGTGGACAA	GCCTGTGCCG	GAGGAGTCGG	2220
	AGGGCCCTTG	CAGCCCTCCC	CCCTACAAGA	TGATCCAGAC	CATTGGGTTG	TCGGTGGGTTG	2280
5	CGCTGTGGC	CTACATCAT	GCCGTGCTGG	GCCTCATGTT	CTACTGCAAG	AAGCGCTGCA	2340
	AAGCCAAGCG	GCTGCAGAG	CAGCCCGAGG	GCGAGGAGCC	AGAGATGGAA	TGCCTCAACG	2400
	GAGGGCCTTT	GCAGAACGGG	CAGCCCTCAG	CAGAGATCCA	AGAAGAAGTG	GCCTTGACCA	2460
	GCTTGGGCTC	CGGCCCCCGC	GCCACCAACA	AACGCCACAG	CACAAGTGAT	AAGATGCACT	2520
	TCCCACGGTC	TAGCCTGCAG	CCCATCACCA	CGCTGGGGAA	GAGTGAGTTT	GGGGAGGTGT	2580
10	TCCTGGCAA	GGCTCAGGGC	TTGGAGGAGG	GAGTGGCAGA	GACCCCTGTA	CTTGTAAGA	2640
	GCCTGCAGAC	GAAGGATGAG	CAGCAGCAGC	TGGACTTCCG	GAGGGAGTTG	GAGATGTTTG	2700
	GGAAGCTGAA	CCACGCCAAC	GTGTTGCGGC	TCCTGGGGCT	GTGCCGGGAG	GCTGAGCCCC	2760
	ACTACATGGT	GCTGGAATAT	GTGGATCTGG	GAGACCTCAA	GCAGTTCCTG	AGGATTTCCT	2820
	AGAGCAAGGA	TGAAAAATTG	AAGTCACAGC	CCCTCAGCAC	CAAGCAGAAG	GTGGCCCTAT	2880
15	GCACCCAGGT	AGCCCTGGGC	ATGGAGCACC	TGTCCAACAA	CCGCTTTGTG	CATAAGGACT	2940
	TGGTGC CGG	TAACTGCCTG	GTCACTGCCC	AGAGACAAGT	GAAGGTGTCT	GCCCTGGGCC	3000
	TCAGCAAGGA	TGCTGACAA	AGTGAGTACT	ACCACTTCCG	CCAGGCCTGG	GTGCCGCTGC	3060
	GCTGGATGTC	CCCCGAGGCC	ATCCTGGAGG	GTGACTTCTC	TACCAAGTCT	GATGTCTGGG	3120
	CCTTCGGTGT	GCTGATGTGG	GAAGTGTTTA	CACATGGAGA	GATGCCCAT	GGTGGGCAGG	3180
20	CAGATGATGA	AGTACTGCGC	GATTTCAGG	CTGGGAAGGC	TAGACTTCCT	CAGCCGAGG	3240
	GCTGCCCTTC	CAAACTCTAT	CGGCTGATGC	AGCGCTGCTG	GGCCCTCAGC	CCCAAGGACC	3300
	GGCCCTCCTT	CAGTGAGATT	GCCAGCGCCC	TGGGAGACAG	CACCGTGGAC	AGCAAGCCGT	3360
	GAGGAGGGAG	CCCGCTCAGG	ATGGCTGGG	CAGGGGAGGA	CATCTCTAGA	GGAAGCTCA	3420
	CAGCATGATG	GGCAAGATCC	CTGTCTCTCT	GGGCCCTGAG	GTGCCCTAGT	GCAACAGGCA	3480
25	TTGCTGAGGT	CTGAGCAGGG	CCTGGCCTTT	CCTCCTCTTC	CTCACCTCA	TCCTTTGGGA	3540
	GGCTGACTTG	GACCCTCAGT	GGGCGACTAG	GGCTTTGAGC	TGGGCAGTTT	CCCTTGCCAC	3600
	CTCTCTCTCT	ATCAGGGACA	GTGTGGGTGC	CACAGGTAAC	CCCAATTTCT	GGCCTTCAAC	3660
	TTCTCCCTCT	GACCGGGTCC	AACTCTGCCA	CTCATCTGCC	AACTTTGCCT	GGGGAGGGCT	3720
	AGGCTTGGGA	TAGCTGTGGT	TTGTGGGGAG	TTCTTAAATA	TTCTCAAGTT	CTGGGCACAC	3780
30	AGGGTTAATG	AGTCTCTTGC	CCACTGGTCC	ACTTGGGGGT	CTAGACCAGG	ATTATAGAGG	3840
	ACACAGCAAG	TGAGTCCCTC	CCACTCTGGG	CTTGTGCACA	CTGACCAGA	CCCACGTCTT	3900
	CCCCACCTTT	CTCTCCTTTC	CTCATCTTAA	GTGCTTGCCA	GATGAAGGAG	TTTTCAGGAG	3960
	CTTTTGACAC	TATATAAACC	GCCCTTTTTG	TATGCACCAC	GGGCGGCTTT	TATATGTAAT	4020
	TGCAGCGTGG	GGTGGGTGGG	CATGGGAGGT	AGGGGTGGGC	CCTGGAGATG	AGGAGGGTGG	4080
35	GCCATCCTTA	CCCCACACTT	TTATGTTGT	CGTTTTTGT	TTGTTTTGTT	TTTTTGT	4140
	TGTTTTTGT	TTTACACTCG	CTGCTCTCAA	TAAATAAGCC	TTTTTTA		

Seq ID NO: 667 Protein sequence

Protein Accession #: NP_002812

40	1	11	21	31	41	51	
	MGAARGSPAR	PRRLPLLSVL	LLPLLGTTQT	AIVFIKQPSS	QDALQGRRAL	LRCEVEAPGP	60
	VHVVYLLDGA	PVQDTERRFA	QSSLSFAAV	DRLQDSGTFQ	CVARDDVTGE	EARSANASFN	120
45	IKWIEAGPVV	LKHPASEAEI	QPQTQVTLRC	HIDGHPRTY	QWFRDGTPLS	DQSNHTVSS	180
	KERNLTLRPA	GPEHSGLYSC	CAHSAFGQAC	SSQNFTLSIA	DESFAFVFLA	PQDVVVARYE	240
	EAMFHCQFSA	QPPSLQLWLF	EDETPITNRS	RPHLRRAATV	FANGSLLLTQ	VRPRNAGIYR	300
	CIGQGQRGPP	IILEATLHLA	EIEDMPLFEP	RVFTAGSEER	VTCLPPKGLP	EPSVWWEHAG	360
	VRLPHTGRVY	QKGHELVLAN	IAESDAGVYT	CHAANLAGQR	RQDVNITVAT	VPSWLKKPQD	420
50	SQLLEGKPGY	LDCLTQATPK	PTVVVYRNQM	LISEDSRFEV	FKNGTLRINS	VEVYDGTWYR	480
	CMSSTPAGSI	EAQARVQVLE	KLKFTPPQPQ	QQCFEFDKEA	TVPCSATGRE	KPTIKWERAD	540
	GSSLPEWVTD	NAGTLHFARV	TRDDAGNYTC	IASNGPQGGI	RAHVQLTVAV	FITPKVEPER	600
	TTVYQGHATL	LQCEAQGDPK	PLIQWKGKDR	ILDPTKLGRP	MHIFQNGSLV	IHDVAPEDSG	660
	RYTCIAGNSC	NIKHTEAPLY	VVDKPVPEES	EGPGSPPPYK	MIQTIGLSVG	AAVAYIIAVL	720
55	GLMFYCKKRC	KAKRLQKQPE	GEEPEMECLN	GGPLQNGQPS	AEIQEEVALT	SLGSGPAATN	780
	KRHSTSDKMH	PPRSLQIPIT	TLGSEFGEV	FLAKAQGLEE	GVAETLVVLK	SLQTKDEQQQ	840
	LDFFRELEMF	GKLNHANVVR	LLGLCREAEP	HYMVLEYVDL	GDLKQFLRIS	KSKDEKLKSK	900
	PLSTKQKVAL	CTQVALGMEH	LSNRRFVHKD	LAARNCLVSA	QRQVKVSALG	LSKDVIYNSEY	960
	YHFRQAWVPL	RWMSPEALE	GDFSTKSDVW	AFGLVMNEVF	THGEMPHGGQ	ADDEVLDLQ	1020
60	AGKARLPQPE	GCPSKLYLRM	QRNALSPKD	RPSFSEIASA	LGDSTVDSKP		

Seq ID NO: 668 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 1..1389

65	1	11	21	31	41	51	
	ATGGGCTACC	AGAGGCGAGG	GCCTGTCACT	CCGCCGCGAG	GAGATTTAGA	TGACAGAGAA	60
	ACCCCTGTTT	CTGAACATGA	GTATAAAGAG	AAAACCTGTC	AGTCTGCTGC	TCTTTTAAAT	120
70	GTGTGCAACT	CGATTATAGG	ATCTGGTATA	ATAGGATTGC	CTTATTCAAT	GAAGCAAGCT	180
	GGGTTTCTCT	TGGGAATATT	GCTTTTATTC	TGGGTTTCAT	ATGTTACGGA	CTTTCCCTTT	240
	GTTTTATTGA	TAAAAGGAGG	GGCCCTCTCT	GGAACAGATA	CCTACCAGTC	TTTGGTCAAT	300
	AAAACTTTTG	GCTTTCCAGG	GTATCTGCTC	CTCTCTGTTT	TTCAAGTTT	GTATCCTTTT	360
	ATAGCAATGA	TAAGTTACAA	TATAATAGCT	GGAGATACTT	TGAGCAAAGT	TTTTCAAGA	420
75	ATCCCAGGAG	TTGATCTCTG	AAAGTGTTT	ATTGGTGGCC	ACTTCATTAT	TGGACTTTCC	480
	ACAGTTACCT	TTACTCTGCC	TTTATCCTTG	TACCGAAATA	TAGCAAAGCT	TGGAAAGGTC	540
	TCCCTCATCT	CTACAGGTTT	AACAACCTG	ATTCTTGGAA	TTGTAATGGC	AAGGGCAATT	600
	TCACTGGGTC	CACACATACC	AAAAACAGAA	GACGCTTGGG	TATTTGCAAA	GCCCAATGCC	660
	ATTCAAGCGG	TGGGGTTTAT	GTCTTTTGCA	TTTATTGGCC	ACCATAACTC	CTTCTTAGTT	720
80	TACAGTTCTG	TAGAAGAACC	CACAGTAGCT	AAGTGGTCCC	GCCTTATCCA	TATGTCCATC	780
	GTGATTCTCT	TATTTATCTG	TATATTCTTT	GCTACATGTG	GATACTTGAC	ATTACTGGC	840
	TTCAACCAAG	GGGACTTATT	TGAAAATTAC	TGCAGAAATG	ATGACCTGGT	AACATTTGGA	900
	AGATTTTGTT	ATGGTGTATC	TGTCATTTTG	ACATACCCTA	TGGAAATGCT	TGTGACAAGA	960
	GAGGTAATTG	CCAATGTGTT	TTTTGGTGGG	AATCTTTTCAT	CGGTTTTCCA	CATTGTTGTA	1020
85	ACAGTGATGG	TCATCACTGT	AGCCACGCTT	GTGTCTATGC	TGATTGATTG	CCTCGGGATA	1080
	GTTCTAGAAC	TCAATGGTGT	GCTCTGTGCA	ACTCCCTCA	TTTTTATCAT	TCCATCAGCC	1140
	TGTTATCTGA	AACTGTCTGA	AGAACCAAGG	ACACACTCCG	ATAAGATTAT	GTCTTGTGTC	1200
	ATGCTTCCCA	TTGGTGTGTT	GGTGATGTTT	TTTGGATTCT	TCATGGCTAT	TACAAATACT	1260

CAAGACTGCA CCCATGGGCA GGAAATGTTC TACTGCTTTC CTGACAATTT CTCTCTCACA 1320
 AATACCTCAG AGTCTCATGT TCAGCAGACA ACACAACITTT CTACTTTAAA TATTAGTATC 1380
 TTTCATGA

5 Seq ID NO: 669 Protein sequence
 Protein Accession #: Eos sequence

	1	11	21	31	41	51	
10	MGYQRQEPVI	PPQRDLDDRE	TLVSEHEYKE	KTCQSAALFN	VVNSIIGSGI	IGLPYSMKQA	60
	GFPLGILLLF	WVSIVTDFSL	VLLIKGGALS	GTDTYQSLVN	KTFGPPGYLL	LSVLQFLYPF	120
	IAMISYNIIA	GDTLSKVQFR	IPGVDPENVF	IGRHFIIGLS	TVPTPLPLSL	YRNIKLGKV	180
	SLISTGLTTL	ILGIVMARAI	SLGPHIPKTE	DAWVFAKPN	IQAVGVMSFA	FICHNSFLV	240
15	YSSLEPTVA	KWSRLIHMSI	VISVFICIFP	ATCGYLTFTG	FTQGDLPENY	CRNDDLVTFG	300
	RFCYGVTVIL	TYPMECFVTR	EVIANVFFGG	NLSSVPHIVV	TVMVITVATL	VSLIDCLGI	360
	VLELNGVICA	TPLIPIIPSA	CYLKLSSEPR	THSDKIMSCV	MLPIGAVVMV	FGFVMAITNT	420
	QDCTHQEMF	YCFPDNFSLT	NTSESHVQQT	TQLSTLNISI	FQ		

20 Seq ID NO: 670 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..1284

	1	11	21	31	41	51	
25	ATGGGCTACC	AGAGGCAGGA	GCCTGTCATC	CCGCCGCAGA	GAGGATTGCC	TTATTCAATG	60
	AAGCAAGCTG	GGTTTCCTTT	GGGAATATTG	CTTTTATTCT	GGGTTTCATA	TGTTACAGAC	120
	TTTTCCCTTG	TTTTATTGAT	AAAAGGAGGG	GCCCTCTCTG	GAACAGATAC	CTACCACTCT	180
	TTGGTCAATA	AAACITTCGG	CTTCCAGGG	TATCTGCTCC	TCTCTGTCT	TCAGTTTITG	240
30	TATCCTTTTA	TAGCAATGAT	AAGTTACAAT	ATAATAGCTG	GAGATACTTT	GAGCAAAGTT	300
	TTTCAAAGAA	TCCCAGGAGT	TGATCCTGAA	AACGTGTTTA	TTGGTCGCCA	CTTCATTATT	360
	GGACTTTCCA	CAGTTACCTT	TACTCTGCCT	TTATCCTTGT	ACCGAAATAT	AGCAAAGCTT	420
	GGAAAGGTCT	CCCTCATCTC	TACAGGTTTA	ACAACCTCTG	TTCTTGGAAT	TGTAATGGCA	480
	AGGGCAATTT	CACTGGGTCC	ACACATACCA	AAAACAGAAG	ACGCTTGGGT	ATTGCAAAAG	540
35	CCCAATGCCA	TTCAAGCGGT	CGGGGTTATG	TCTTTTGCT	TTATTTGCCA	CCATAACTCC	600
	TTCTTAGTTT	ACAGTCTCT	AGAAGAACC	ACAGTAGCTA	AGTGGTCCCG	CCTTATCCAT	660
	ATGTCCATCG	TGATTCTGT	ATTATCTGT	ATATCTTTG	CTACATGTGG	ATACTTGACA	720
	TTTACTGGCT	TCACCAAGG	GGACTTATTT	GAAAATTACT	GCAGAAATGA	TGACCTGGTA	780
	ACATTTGGAA	GATTTTGTTA	TGGTGTCACT	GTCATTTTGA	CATACCTTAT	GGAATGCTTT	840
40	GTGACAAGAG	AGGTAATGTC	CAATGTGTTT	TTTGGTGGGA	ATCTTTCATC	GGTTTTCCAC	900
	ATTGTTGTAA	CAGTGATGGT	CATCACTGTA	GCCACGCTTG	TGTCATTGCT	GATTGATTGC	960
	CTCGGGATAG	TTCTAGAACT	CAATGGTGTG	CTCTGTGCAA	CTCCCTCAT	TTTTATCATT	1020
	CCATCAGCCT	GTTATCTGAA	ACTGTCTGAA	GAACCAAGGA	CACACTCCGA	TAAGATTATG	1080
	CTCTGTGTCA	TGCTTCCCAT	TGGTGTGTG	GTGATGGTTT	TTGGATTGCT	CATGGCTATT	1140
45	ACAAATATCT	AAGACTGCAC	CCATGGGCAG	GAAATGTTCT	ACTGCTTTCC	TGACAAATTC	1200
	TCTCTACAA	ATACCTCAGA	GTCTCATGTT	CAGCAGACAA	CACAACTTTC	TACTTTAAAT	1260
	ATTAGTATCT	TTCAACTCGA	GTAA				

50 Seq ID NO: 671 Protein sequence
 Protein Accession #: Eos sequence

	1	11	21	31	41	51	
55	MGYQRQEPVI	PPQRGLPYSM	KQAGFPLGIL	LLFWVSIVTD	PSLVLLIKGG	ALSGTDTYQS	60
	LVNKTGFPFG	YLLLSVLQPL	YPFIAMISYN	IIAGDTLSKV	FORIPGVDP	NVPIGRHFII	120
	GLSTVTFTLP	LSLYRNIAKL	GKVSILSTGL	TTLLILGIUMA	RAISLGHPIH	KTEDAWVFAK	180
	PNAIQAVGVM	SFAFICHNS	FLVYSLEEP	TVAKWSRLIH	MSIVISVFIC	IFFATCGYLT	240
	FTGFTQGDLE	ENYCRNDLIV	TGFRFCYVTV	VILTYPMECF	VTREIVANVF	FGNLSVVFH	300
	IVVTVMVITV	ATLVSLILDC	LGIVLELNGV	LCATPLIFII	PSACYLKLSE	EPRTHSDKIM	360
60	SCVMLPIGAV	VMVFGFVMAI	TNTQDCTHQ	EMFYCFPDNF	SLTNTSESHV	QQTQLSTLN	420
	ISIFQLE						

65 Seq ID NO: 672 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..1203

	1	11	21	31	41	51	
70	ATGGGCTACC	AGAGGCAGGA	GCCTGTCATC	CCGCCGCAGT	TTTCCCTTGT	TTTATTGATA	60
	AAAGGAGGGG	CCCTCTCTGG	AACAGATACC	TACCAGTCTT	TGGTCAATAA	AACTTTCGGC	120
	TTTCCAGGGT	ATCTGCTCCT	CTCTGTTCTT	CAGTTTITGT	ATCCTTTTAT	AGCAATGATA	180
	AGTTACAATA	TAATAGCTGG	AGATACTTTG	AGCAAAGTTT	TTCAAAGAAT	CCCAGGAGTT	240
	GATCCTGAAA	ACGTGTTTAT	TGGTCGCCAC	TTCAATTATG	GACTTTCAC	AGTTACCTTT	300
	ACTCTGCCTT	TATCCTTGTA	CCGAATATA	GCAAAGCTTG	GAAAGGTCTC	CCTCATCTCT	360
75	ACAGGTTTAA	CAACTCTGAT	TCTTGGAATT	GTAATGGCAA	GGGCAATTTC	ACTGGGTCCA	420
	CACATACCAA	AAACAGAAGA	CGCTTGGGTA	TTTGCAAAAG	CCAATGCCAT	TCAAGCGGTC	480
	GGGGTTATGT	CTTTTGCAAT	TATTTGCCAC	CATAACTCCT	TCTTAGTTTA	CAGTTCTCTA	540
	GAAGAACCCA	CAGTAGCTAA	GTGGTCCCGC	CTTATCCATA	TGTCCATCGT	GATTTCTGTA	600
	TTTATCTGTA	TATCTTTTGC	TACATGTGGA	TACTTGACAT	TTACTGGCTT	CACCCAGGGG	660
	GACTTATTTG	AAAATTACTG	CAGAAATGAT	GACCTGGTAA	CAITTTGGAAG	ATTTTGTAT	720
80	GGTGTCACTG	TCATTTTGAC	ATACCCTATG	GAATGCTTTG	TGACAAGAGA	GGTAATTGCC	780
	AATGTGTTTT	TTGGTGGGAA	TCTTTTCATG	GTTTTCACCA	TTGTTGTAAC	AGTGATGGTC	840
	ATCACTGTAG	CCACGCTTGT	GTCAATTGCTG	ATTGATTGCC	TGGGATAGT	TCTAGAACTC	900
	AATGGTGTGC	TCTGTGCAAC	TTCCCTCAT	TTTATCATTC	CATCAGCTG	TTATCTGAAA	960
85	CTGTCTGAAG	AACCAAGGAC	ACACTCCGAT	AAGATTATGT	CTTGTGTCAT	GCTTCCCAAT	1020
	GGTGTGTGG	TGATGGTTTT	TGGATTCTG	ATGGCTATTA	CAAATACTCA	AGACTGCACC	1080
	CATGGGCAGG	AAATGTTCTA	CTGCTTTCCT	GACAAATTCT	CTCTCACAAA	TACCTCAGAG	1140
	TCTCATGTTT	AGCAGACAAC	ACAACCTTCT	ACTTTAAATA	TAGTATCTT	TCAACTCGAG	1200

TAA

Seq ID NO: 673 Protein sequence
Protein Accession #: Eos sequence

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1      11      21      31      41      51
|      |      |      |      |      |
MGYQRQEPVI PPQFSLVLLI KGGALSGTDT YQSLVNKTFG FPGYLLLSVL QPLYPFIAMI 60
SYNIIAGDTL SKVFQRIPIV DPENVFIGRH FIIGLSTVTF TLPLSLYRNI AKLGKVSLSIS 120
TGLTTLILGI VMARAIISLG HIPKTEDAWV FAKPNAIQAV GVMSFAPICH HNSPLVYSSL 180
EPTVAKWSR LIHMSIVISV PICFFATCG YLTFTGTQG DLFENYCRND DLVTFGRFCY 240
GVTIVLTYPM ECFVTREIV NVFPFNNLSS VFHIVVTVMV ITVATLVSL LDCLGIVLEL 300
NGVLCATPLI FIIPSACYLK LSEEPRTSD KIMSCVMLPI GAVVMVFGFV MAITNTQDCT 360
HGQEMFYCFP DNFSLTNTSE SHVQQTQLS TLNISIFQLE

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Seq ID NO: 674 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..1140

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1      11      21      31      41      51
|      |      |      |      |      |
ATGGGCTACC AGAGGCAGGA GCCTGTCATC CCGCCGAGG TCAATAAAAC TTTCGGCTTT 60
CCAGGGTATC TGCTCCTCTC TGTCTTCAG TTTTGTATC CTTTATAGC AATGATAAGT 120
TACAAATATA TAGCTGGAGA TACTTTGAGC AAAGTTTTTC AAAGAATCCC AGGAGTTGAT 180
CCTGAAAACG TGTTTATGG TCGCCACTTC ATTATTGGAC TTCCACAGT TACCTTTACT 240
CTGCCTTTAT CCTGTACCG AAATATAGCA AAGCTTGAA AGGTCTCCCT CATCTCTACA 300
GGTTTAAACA CTCTGATTC TGGAAATGTA ATGGCAAGGG CAATTTCACT GGGTCCACAC 360
ATACCAAAAG CAGAAGACG TTGGGTATT GCAAAGCCCA ATGCCATTCA AGCGGTGCGG 420
GTTATGCTCT TTGCATTAT TTGCCACCAT AACTCCTTCT TAGTTTACAG TTCTCTAGAA 480
GAACCCACAG TACCTAAGTG GTCCCGCCTT ATCCATATGT CCATCGTGAT TTCTGTATT 540
ATCTGTATAT CTCTTGCTAC ATGTGGATAC TTGACATTTA CTGGCTTCAC CCAAGGGGAC 600
TTATTTGAAA ATTACTGCAG AAATGATGAC CTGGTAACAT TTGGAAGATT TTGTTATGGT 660
GTCACTGTCA TTTTGACATA CCCTATGGAA TGCTTTGTGA CAAGAGAGGT AATTGCCAAT 720
GTGTTTTTGG GTGGGAATCT TTCATCGGT TTCCACATTG TTGTAACAGT GATGGTCATC 780
ACTGTAGCCA CGCTGTGTGC ATTGCTGATT GATTGCCTCG GGATAGTTCT AGAACTCAAT 840
GGTGTGCTCT GTGCAACTCC CCTCATTTT ATCATTCCAT CAGCCTGTTA TCTGAAACTG 900
TCTGAAGAAC CAAGGACACA CTCGATAAG ATTATGTCT GTGTCTGCT TCCCATGGT 960
GCTGTGGTGA TGGTTTTTGG ATTGCTCATG GCTATTACAA ATACTCAAGA CTGCACCCAT 1020
GGGCAGGAAA TGTCTACTG CTTTCTGAC AATTCTCTC TCACAAATAC CTCAGAGTCT 1080
CATGTCAGC AGACAACACA ACTTCTACT TAAATATTA GTATCTTCA ACTCGAGTAA

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Seq ID NO: 675 Protein sequence
Protein Accession #: Eos sequence

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1      11      21      31      41      51
|      |      |      |      |      |
MGYQRQEPVI PPQVKNKTFG PGYLLLSVLQ FLYPFIAMIS YNIIAGDTLS KVFQRIPIVD 60
PENVFIRRH IIGLSTVFT LPLSLYRNI KLGKVSLSIS GLTTLILGIV MARAISLGP 120
IPKTEDAWV AKPNAIQAV VMSFAPICH NSFLVYSSLE EPTVAKWSRL IHMSIVISV 180
ICIFFATCGY LTFTGFTQGD LFENYCRND LVTFGRCYV VTVILTYPME CFVTREIVAN 240
VFPGNNLSSV FHVIVTVMVI TVATLVSLLI DCLGIVLELN GVLCATPLIF IIPSACYLKL 300
SEEPRTSDK IMSCVMLPIG AVVMVFGFVM AITNTQDCTH GQEMFYCFPD NFSLTNTSES 360
HVQQTQLST LNISIFQLE

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Seq ID NO: 676 DNA sequence
Nucleic Acid Accession #: NM_006853.1
Coding sequence: 26..874

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1      11      21      31      41      51
|      |      |      |      |      |
AGGAATCTGC GCTCGGGTTC CGCAGATGCA GAGGTTGAGG TGGCTGCGGG ACTGGAAGTC 60
ATCGGGCAGA GGTCTCAGAG CAGCCAAGGA ACCTGGGGCC CGCTCCTCCC CCTCCAGGC 120
CATGAGGATT CTGCAGTTAA TCCTGCTTGC TCTGGCAACA GGGCTTGTAG GGGGAGAGAC 180
CAGGATCATC AAGGGGTTCG AGTCAAGCC TCACTCCAG CCCTGGCAGG CAGCCTGTT 240
CGAGAAGACG CGGCTACTCT GTGGGGCGAC GCTCATCGCC CCCAGATGGC TCCTGACAGC 300
AGCCCACTGC CTCAGCCCC GCTACATAGT TCACCTGGGG CAGCAACAAC TCCAGAAGGA 360
GGAGGGCTGT GAGCAGACCC GGACAGCCAC TGAGTCCTTC CCCCACCCG GCTTCAACAA 420
CAGCCTCCCC AACAAAGACC ACCGCAATGA CATCATGCTG GTGAAGATGG CATCGCCAGT 480
CTCCATCACC TGGGCTGTGC GACCCCTCAC CCTCTCTCA CGCTGTGTC CTGCTGGCAC 540
CAGCTGCCTC ATTTCCGGCT GGGGCAGCAC GTCCAGCCCC CAGTTACGCC TGCTCACAC 600
CTTGGCATGC GCCAATATCA CCATCATTTA GCACCAGAAG TGTGAGAAGC CCTACCCCGG 660
CAACATCACA GACACCATGG TGTGTGCCAG CGTGCAGGAA GGGGGCAAG ACTCTGGCA 720
GGGTGACTCC GGGGGCCTC TGGTCTGTAA CCAGTCTCTT CAAGGCATTA TCTCTGGGG 780
CCAGGATCCG TGTGCGATCA CCCGAAAGCC TGGTGTCTAC ACGAAAGTCT GCAAAATATG 840
GGACTGGATC CAGGAGACGA TGAAGAACAA TTAGACTGGA CCCACCCACC ACAGCCCATC 900
ACCTCCATT TCCATTGGT GTTTGGTTCC TGTCTACTCT GTTAATAAGA AACCTAAGC 960
CAAGACCTTC TACGAACATT CTTTGGGCTT CCTGGACTAC AGGAGATGCT GTCATTAAAT 1020
AATCAACCTG GGGTTCGAAA TCAGTGAGAC CTGGATTCAA ATTCTGCCTT GAAATATTGT 1080
GACTCTGGGA ATGACAACAC CTGTTTGTG CTCTGTTGTA TCCCCAGCCC CAAAGACAGC 1140
TCCTGGCCAT ATATCAAGGT TTCAATAAAT ATTTGCTAAA TGAGTG

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Seq ID NO: 677 Protein sequence
Protein Accession #: NP_006844.1

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1      11      21      31      41      51
|      |      |      |      |      |
MRILQLILLA LATGLVGGET RIIGFCECKP HSQPWQAALF EKTRLLCGAT LIAPRWLLTA 60

```

AHCLKPRYIV HLGQHNLOKE EGCEQTRTAT ESFPHPGFNN SLPNKDHRND IMLVKMASPV 120
 SITWAVRPLT LSSRCVTAQT SCLISGWGST SSPQLRLPHT LRCANITIE HQKCENAYPG 180
 NITDTMVCAS VQEGGKDSQ GDSGGPLVCN QSLQGIISWG QDPCAITRKP GVTYKVCKYV 240
 DWIQETMKNN

Seq ID NO: 678 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..933

10 1 11 21 31 41 51
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 TTCGACAAGA GTGATGAGAA GGAGTGCCCC AAGGCTAAGT CGAAATGTGG CCCGACCTTC 120
 TTCCCGCTGTG CCAGCGGCAT CCATTGCATC ATTGGTCGCT TCCGGTGCAA TGGGTTTGAG 180
 15 GACTGTCCCG ATGGCAGCGA TGAAGAGAAC TGCACAGCAA ACCCTCTGCT TTGCTCCACC 240
 GCCCGCTACC ACTGCAAGAA CGGCCTCTGT ATTGACAAGA GCTTCATCTG CGATGGACAG 300
 AATAACTGTC AAGACAACAG TGATGAGGAA AGCTGTGAAA GTTCTCAAGA ACCCGGCAGT 360
 GGGCAGGTGT TTGTGACTTC AGAGAACCAA CTGTGTATT ACCCCAGCAT CACCTATGCC 420
 20 ATCATCGGCA GCTCCGTCAT TTTTGTGCTG GTGGTGGCCC TGCTGGCACT GGTCTTGAC 480
 CACCAGCGGA AGCGGAACAA CCTCATGACG CTGCCCGTGC ACCGGCTGCA GCACCCTGTG 540
 CTGCTGTCCC GCCTGGTGGT CCTGGACCAC CCCCACCACT GCAACGTCAC CTACAACGTC 600
 AATAATGGCA TCCAGTAGT GGCACGCCAG GCGGAGCAGA ATGCGTCGGA AGTAGGCTCC 660
 CCACCCTCCT ACTCCGAGGC CTGTGCTGAC CAGAGGCCTG CGTGGTATGA CCTTCCTCCA 720
 25 CCGCCCTACT CTTCTGACAC GGAATCTCTG AACCAAGCCG ACCTGCCCCC CTACCGCTCC 780
 CGGTCCGGGA GTGCCAACAG TGCCAGCTCC CAGGCAGCCA GCAGCCTCCT GAGCGTGGAA 840
 GACACCAGCC ACAGCCCGGG GCAGCCTGGC CCCCAGGAGG GCACTGCTGA GCCCAGGGAC 900
 TCTGAGCCCA GCCAGGGCAC TGAAGAAGTA TAA

Seq ID NO: 679 Protein sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 | | | | | |
 MCSNGRCIPG AWQCDGLPDC FDKSDEKECP KAKSKCGPTF FPCASGIHCI IGRFRNGFE 60
 35 DCPDGSDEEN CTANPLLCST ARYHCKNGLC IDKSFICDQG NNQDNDSEDE SCESSQEPGS 120
 GQVFTVSENQ LVVYPSITYA IIGSSVIFVL VVALLALVLH HQRKRNLMT LPVHRLQHPV 180
 LLSRLVLDH PHHCNVTVNV NNGIQYVASQ AEQNASEVGS PPSYSEALD QRPAYWDLPP 240
 PPYSSTESL NQADLPYRS RSGSANSASS QAASSLLSVE DTSHPGQPG PQEGTAEPRD 300
 SEPSQGTVEV

Seq ID NO: 680 DNA sequence
 Nucleic Acid Accession #: S78203.1
 Coding sequence: 1..2190

45 1 11 21 31 41 51
 | | | | | |
 ATGAATCCTT TCCAGAAAAA TGAGTCCAAG GAAACTCTTT TTTACACCTGT CTCCATTGAA 60
 GAGGTACCAC CTCGACCACC TAGCCCTCCA AAGAAGCCAT CTCGACAAT CTGTGGCTCC 120
 50 AACTATCCAC TGAGCATTGC CTTCAATTGT GTGAATGAAT TCTGCGAGCG CTTTTCCTAT 180
 TATGGAATGA AAGCTGTGCT GATCCTGTAT TTCTGTATT TCCTGCAGTG GAATGAAGAT 240
 ACCTCCACAT CTATATACCA TGCCTTCAGC AGCCTCTGTT ATTTTACTCC CATCTGGGA 300
 GCAGCCATTG CTGACTCGTG GTTGGGAAAA TTCAAGACAA TCATCTATCT CTCCTTGGTG 360
 TATGTGCTTG GCCATGTGAT CAAGTCCTTG GGTGCCTTAC CAATACTGGG AGGACAAGTG 420
 55 GTACACACAG TCCTATCATT GATCGGCCTG AGTCTAATAG CTTTGGGGAC AGGAGGCATC 480
 AAACCCCTGTG TGGCAGCTTT TGGTGGAGAC CAGTTTGAAG AAAAACATGC AGAGGAACGG 540
 ACTAGATACT TCTCAGTCTT CTACCTGTCC ATCAATGCAG GGAGCTTGAT TTCTACATT 600
 ATCACACCCA TGCTGAGAGG AGATGTGCAA TGTTTTGGAG AAGACTGCTA TGCATTGGCT 660
 TTTGGAGTTC CAGGACTGCT CATGGTAATT GCACCTGTGT TGTTTGCAAT GGAAGCAAA 720
 60 ATATACAATA AACCAACCCC TGAAGGAAAC ATAGTGGCTC AAGTTTTCAA ATGTATCTGG 780
 TTTGCTATTT CCAATCGTTT CAAGAACCGT TCTGGAGACA TTCCAAGCG ACAGCACTGG 840
 CTAGACTGGG CAGCTGAGAA ATATCCAAG CAGCTCATT TGGATGTAAA GGCAGTACC 900
 AGGGTACTAT TCCTTATAT CCCATTGCC ATGTCTCGGG CTCTTTTGA TCAGCAGGGT 960
 TCAGATGGA CTTTGAAGC CATCAGGATG AATAGGAATT TGGGTTTIT TGTGCTTCAG 1020
 65 CCGGACCAGA TGCAGTTCTT AAATCCCTTT CTGGTTCTTA TCTTCATCCC GTTGTGTGAC 1080
 TTTGTCAATT ATCGTCTGGT CTCCAAGTGT GGAATTAAT TCTCATCACT TAGGAAAAATG 1140
 GCTGTTGGTA TGATCTTAGC GTGCCCTGGCA TTTGCAGTTG CGGCAGCTGT AGAGATAAAA 1200
 ATAAATGAAA TGGCCCCAGC CCAGTCAGGT CCCCAGGAGG TTTTCTTACA AGTCTTGAAT 1260
 CTGGCAGATG ATGAGGTGAA GGTGACAGTG GTGGGAAATG AAAACAATTC TCTGTTGATA 1320
 70 GAGTCCATCA AATCCTTTCA GAAAAACCA CACTATTCCA AACTGCACCT GAAAAACAAA 1380
 AGCCAGGATT TTCATTCCA CCTGAAATAT CACAATTTGT CTCTCTACAC TGAGCATTTCT 1440
 GTGCAGGAGA AGAAGTGGTA CAGTCTGTG ATTCGTGAAG ATGGGAACAG TATCTCCAGC 1500
 ATGATGGTAA AGGATACAGA AAGCAAAACA ACCAATGGGA TGACAACCGT GAGGTTTGT 1560
 AACACTTTGC ATAAAGATGT CAACATCTCC CTGAGTACAG ATACCTCTCT CAATGTTGGT 1620
 75 GAAGACTATG GTGTGCTGCT TTATAGAACT GTGCAAGAG GAGAATACCC TGCAGTGCAC 1680
 TGTAGAACAG AAGATAAGAA CTTTCTCTG AATTGGGCT TCTAGACTT TGGTGCAGCA 1740
 TATCTGTTG TTATTACTAA TAACACCAAT CAGGGTCTTC AGGCCTGGAA GATTGAAGAC 1800
 ATTCACGCCA ACAAATGTC CATTGGGTGG CAGCTACCAC AATATGCCCT GGTACAGCT 1860
 GGGGAGGTCA TGTCTCTGT CACAGTCTT GAGTTTCTT ATTCTCAGGC TCCCTTAGC 1920
 80 ATGAAATCTG TGCTCCAGGC AGCTTGGCTA TTGACAATTG CAGTTGGGAA TATCATCGTG 1980
 CTTGTGTGG CACAGTTCAG TGGCCTGGTA CAGTGGGCG AATTCAATTT GTTTTCTGTC 2040
 CTCCTGCTGG TGATCTGCCT GATCTTCTCC ATCATGGCT ACTACTATGT TCCTGTAAG 2100
 ACAGAGGATA TGGGGGTCC AGCAGATAAG CACATTCCTC ACATCCAGGG GAACATGATC 2160
 AAAGTAGAGA CCAAGAAGAC AAAACTCTGA

Seq ID NO: 681 Protein sequence
 Protein Accession #: AAB34388.1

1 11 21 31 41 51
| | | | |
MNPFQKNESE ETLFSPVSIE EVPPRPSPS KKPSPITCGS NYPLSIAPIV VNEFCERFSY 60
YGMKAVLILY FLYFLHWNED TSTSIYHAFS SLCYPTPIIG AAIADSWLKG FKTIYILSLV 120
5 YVLGHVILKSL GALPILGGQV VHTVLSLIGL SLIALGTGGI KPCVAAFQGD QFEKHAEER 180
TRYFSVPYLS INAGSLISTP ITPLMRGDVQ CFGECDYALA FGVPGLLMVI ALVVFAMGSK 240
IYNKPPPEGN IVAQVFKCIW FAISNRFKNR SGDIPKRQHW LDWAAEKYKP QLIMDVKALT 300
RVLFYIPLP MFWALLDQGG SRWTLQAI RM NLGPFVQL PDQMQLNPF LVLIFIPFLD 360
10 FVIYRLVSKC GINFSSLRKM AVGMILACLA FAVAAVEIK INEMAPAQSG PQEVFLQVLN 420
LADDEVKVTV VGNENNSLLI ESIKSFQKTP HYSKLHLKTK SQDFHFLKY HNLSLYTEHS 480
VQEKWYSLV IREDGNSISS MMVKDTESKT TNGMTTVRFV NTLHKDVNIS LSTDTSLNVG 540
EDYGVSAVRT VQGEYPAVH CRTEDKNFSL NLGLLDFGAA YLFVITNNTN QGLQAWKIED 600
IPANKMSIAW QLPQYALVTA GEVMSVTGL EFSYSQAPSS MKSVLQAAWL LTIAGVNIIV 660
15 LVVAQFSGLV QWAEFILFSC LLLVICLIFS IMGYVYPVK TEDMRGPADK HIPHIQGNMI 720
KLETKTKL

Seq ID NO: 682 DNA sequence
Nucleic Acid Accession #: NM_016077.1
Coding sequence: 128..667

1 11 21 31 41 51
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25 ACTGTAGATG CCTCCAAAT CCTTGGTTAT GGAATATTTG GCTCATCCCA GTACACTCGG 180
CTTGGCTGTT GGAGTTGCTT GTGGCATGTG CCTGGGCTGG AGCCTTCGAG TATGCTTTGG 240
GATGCTCCCC AAAAGCAAGA CGAGCAAGAC ACACACAGAT ACTGAAAGTG AAGCAAGCAT 300
CTTGGGAGAC AGCGGGGAGT ACAAGATGAT TCTTGTGGTT CGAAATGACT TAAAGATGGG 360
30 AAAAGGGAAG ATGGCTGCC AGTGCTCTCA TGCTGCTGTT TCAGCCTACA AGCAGATTCA 420
AAGAAGAAAT CCTGAAATGC TCAACAATG GGAATACTGT GGCCAGCCCA AGGTGGTGGT 480
CAAAGCTCCT GATGAAGAAA CCCTGATTGC ATTATTGGCC CATGCAAAAA TGCTGGGACT 540
GACTGTAAGT TTAATTCAAG ATGCTGGACG TACTCAGATT GCACCAGGCT CTCAACTGT 600
CCTAGGGATT GGGCCAGGAC CAGCAGACCT AATTGACAAA GTCAGTGGTC ACCTAAACT 660
35 TTACTAGGTG GACTTTGATA TGACAACAAC CCCTCCATCA CAAGTGTGTTG AAGCCTGTCA 720
GATTCTAACA ACAAAAGCTG AATTCTTCA CCAACTTAA ATGTCTCTGA GATGAAATA 780
AAACCTATTC CCATGTTCTA AAAAAA

Seq ID NO: 683 Protein sequence
Protein Accession #: NP_057161.1

1 11 21 31 41 51
| | | | |
MPSKSLVMEY LAHPSTLGLA VGVACGMCLG WSLRVCFGML PKSKTSKTHT DTESEASILG 60
DSGEYKMLV VRNDLKMKG KVAACQSHAA VSAYKQIQR NPMLKQWEY CGQPKVVVKA 120
45 PDEETLIALL AHAKMLGLTV SLIQDAGRTQ IAPGSQTVLG IGPSPADLID KVTGHLKLY

Seq ID NO: 684 DNA sequence
Nucleic Acid Accession #: NM_004864.1
Coding sequence: 26..952

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55 GGCCGAGGCG AGCCGCGCAA GTTCCCGGG ACCCTCAGAG TTGCACTCCG AAGACTCCAG 180
ATTCCGAGAG TTGCGGAAAC GCTACGAGGA CCTGCTAACC AGGCTGCGGG CCAACCAGAG 240
CTGGGAAGAT TCGAACACCG ACCTCGTCCC GGCCCTGCA GTCCGGATAC TCACGCCAGA 300
AGTGGCGCTG GGATCCGCGC GCCACCTGCA CCTGCGTATC TCTCGGGCCG CCCTTCCCGA 360
60 GGGGCTCCCC GAGGCTCCCC GCCTTCACCG GGCTCTGTTT CGGCTGTCCC CGACGGCGTC 420
AAGGTGCTGG GACGTGACAC GACCGCTGCG GCGTCAGCTC AGCCTTGCAA GACCCCAAGC 480
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CATGCACGCG CAGATCAAGA CGAGCCTGCA CCGCCTGAAG CCCGACACGG AGCCAGCGCC 840
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GTCGCTCCAG ACCTATGATG ACTTGTAGC CAAAGACTGC CACTGCATAT GAGCAGTCCT 960
70 GGTCCCTTCCA CTGTGCACCT GCGCGGGGGA GCGGACCTCA GTTGCTCTGC CCTGTGGAAT 1020
GGGCTCAAGG TTCCTGAGAC ACCCGATTCC TGCCCAACA GCTGTATTTA TATAAGTCTG 1080
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AAAA

Seq ID NO: 685 Protein sequence
Protein Accession #: NP_004855.1

1 11 21 31 41 51
| | | | |
MPGQELRTVN GSQMLLVLLV LSWLPHGGAL SLAEASRAS PGPSELHSED SRPRELRKRY 60
80 EDLLTRLRAN QSWEDSNTDL VPAPAVRILT PEVRLGSGGH LHLRISRAAL PEGLPASRL 120
HRALFRLSPT ASRSWDVTRP LRRQLSLARP QAPALHLRLS PPSPSQDQLL AESSSARPL 180
ELHLRPQAR GRRRARANG DDCLPGRC CRLHTRASL EDLGWADWVL SPREVQVTCM 240
85 IGACPSQFRA ANMHAQIKTS LHLRKPDEP APCCVPASYN PMVLIQKTDV GVSQTYDDL 300
LAKDCHCI

Seq ID NO: 686 DNA sequence

Nucleic Acid Accession #: NM_002423.2
Coding sequence: 48..851

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5      1      11      21      31      41      51
      |      |      |      |      |      |
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      TGTGTGTGTC TGTGTGCTCG CTGCCTGGCA GCCTGGCCCT GCCGCTGCCT CAGGAGGCGG 120
      GAGGCATGAG TGAGCTACAG TGGGAACAGG CTCAGGACTA TCTCAAGAGA TTTTATCTCT 180
      ATGACTCAGA AACAAAAAAT GCCAACAGTT TAGAAGCCAA ACTCAAGGAG ATGCAAAAAAT 240
      TCTTTGSCCT ACCTATAACT GGAATGTTAA ACTCCCGCGT CATAGAAATA ATGCAGAAGC 300
      CCAGATGTGG AGTGCCAGAT GTTGCAGAAT ACTCACTATT TCCAAATAGC CCAAAATGGA 360
      CTTCCAAAGT GGTACCTAC AGGATCGTAT CATATACTCG AGACTTACCG CATATTACAG 420
      TGGATCGATT AGTGTCAAAG GCTTTAAACA TGTGGGGCAA AGAGATCCCC CTGCATTCA 480
      GGAAGTTTGT ATGGGGAACT GCTGACATCA TGATTGGCTT TCGCGAGGA GCTCATGGGG 540
      15 ACTCTACCCC ATTTGATGGG CCAGGAAACA CGCTGGCTCA TGCCTTTGCG CCTGGGACAG 600
      GTCTCGGAGG AGATGCTCAC TTCGATGAGG ATGAACGCTG GACGGATGGT AGCAGTCTAG 660
      GGATTAACCT CTGTATGCT GCAACTCATG AACTTGGCCA TTCTTGGGT ATGGGACATT 720
      CCTCTGATCC TAATGCAGTG ATGTATCCAA CCTATGGAAA TGGAGATCCC CAAAATTTTA 780
      20 AACTTTCCCA GGATGATATT AAAGGCATTG AGAACTATA TGGAAAGAGA AGTAATTCAA 840
      GAAAGAAATA GAACTTCAG GCAGAACATC CATTCAATCA TTCATTGGAT TGATATCAT 900
      TGTGACAA TCAGAAATGA TAAGCACTGT TCCTCCACTC CATTAGCAA TTATGTCACC 960
      CTTTTTATT GCAGTTGGTT TTGAATGTC TTCACTCCT TTTATTGGTT AAACCTCTTT 1020
      ATGGTGTGAC TGTGCTTAT TCCATCTATG AGCTTTGTCA GTGCGGTAG ATGTCAATAA 1080
      25 ATGTTACATA CACAATAAA TAAATGTTT ATTCCATGTT AAATTTA
```

Seq ID NO: 687 Protein sequence
Protein Accession #: NP_002414.1

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30      1      11      21      31      41      51
      |      |      |      |      |      |
      MRLTVLCAVC LLPGLALPL PQEAGGMSEL QWEQAQDYLK RPYLYDSETK NANSLEAKLK 60
      EMQKFFGLPI TGMINSRVIE IMQKPRCGVP DVAEYSLFPN SPKWTISKVVT YRIVSYTRDL 120
      PHITVDRLV KALNMWGKEI PLHFRKVWVG TADIMIGFAR GAHGDSPFPD GPGNTLAHAF 180
      35 APGTGLGGDA HFDEDERWTD GSSLGINFLY AATHELGHSL GMGHSSDPNA VMYPTYNGND 240
      PQNFKLSQDD IKGIQKLYGK RSNRKK
```

Seq ID NO: 688 DNA sequence
Nucleic Acid Accession #: NM_005221.3
Coding sequence: 1..870

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      ATGACAGGAG TGTTTGACAG AAGGGTCCCC AGCATCCGAT CCGGCGACTT CCAAGCTCCG 60
      45 TTCCAGACGT CCGCAGCTAT GCACCATCCG TCTCAGGAAT CGCCAACCTT GCCCGAGTCT 120
      TCAGCTACCG ATTCTGACTA CTACAGCCCT ACGGGGGAG CCCCGCACGG CTACTGCTCT 180
      CCTACCTCGG CTTCCTATGG CAAAGCTCTC AACCCTACC AGTATCAGTA TCACGGCGTG 240
      AACGGCTCCG CCGGGAGCTA CCCAGCCAAA GCTTATGCCG ACTATAGCTA CGCTAGCTCC 300
      TACCACCACT ACGGCGGCGC CTACAACCGC GTCCCAAGCG CCACCAACCA GCCAGAGAAA 360
      50 GAAGTGACCG AGCCCGAGGT GAGAATGGTG AATGGCAAAC CAAAGAAAGT TCGTAACCCC 420
      AGGACTATTT ATTCCAGCTT TCAGCTGGCC GCATTACAGA GAAGGTTTCA GAAGACTCAG 480
      TACCTCGCCT TGCCGGAACG CGCCGAGCTG GCCGCCTCGC TGGGATTGAC ACAAAACAG 540
      GTGAAAATCT GGTTCAGAA CAAAAGATCC AAGATCAAGA AGATCATGAA AACCGGGAG 600
      ATGCCCCCGG AGCACAGTCC CAGCTCCAGC GACCCAATGG CGTGTAACTC GCCGAGTCT 660
      CCAGCGGTGT GGGAGCCCCA GGGCTCGTCC CGCTCGCTCA GCCACCACCC TCATGCCAC 720
      55 CCTCCGACCT CCAACCAATC CCCAGCGTCC AGCTACCTGG AGAACTCTGC ATCCTGGTAC 780
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      CTGGCGCTGG CCTCCGGGAC ACTCTATTAG
```

Seq ID NO: 689 Protein sequence
Protein Accession #: NP_005212.1

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60      1      11      21      31      41      51
      |      |      |      |      |      |
      MTGVFDRRVP SIRSGDFQAP FQTSAMHHP SQESPTLPES SATDSDYSP TGGAPHGYCS 60
      65 PTSASYGKAL NPYQYQYHGV NGSAGSYPK AYADYSYASS YHQYGGAYNR VPSATNQPEK 120
      EVTEPEVRMV NGPKPKVRKP RTIYSSPQLA ALQRRFQKTQ YLALPERAEL AASLGLTQTQ 180
      VKIWFQNKRS KIKKIMNGE MPPEHSPSSS DPMACNSPOS PAVWEPQSSS RSLSHHPHAH 240
      PPTSNQSPAS SYLENSASWY TSAASSINSH LPPPGSLQHP LALASGTLV
```

It is understood that the examples described above in no way serve to limit the true scope of this invention, but rather are presented for illustrative purposes. All publications, sequences of accession numbers, and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference.

WHAT IS CLAIMED IS:

- 1 1. A method of detecting a lung cancer-associated transcript in a cell
2 from a patient, the method comprising contacting a biological sample from the patient with a
3 polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence
4 as shown in Tables 1A-16.
- 1 2. The method of claim 1, wherein the polynucleotide selectively
2 hybridizes to a sequence at least 95% identical to a sequence as shown in Tables 1A-16.
- 1 3. The method of claim 1, wherein the biological sample is a tissue
2 sample.
- 1 4. The method of claim 1, wherein the biological sample comprises
2 isolated nucleic acids.
- 1 5. The method of claim 4, wherein the nucleic acids are mRNA.
- 1 6. The method of claim 4, further comprising the step of amplifying
2 nucleic acids before the step of contacting the biological sample with the polynucleotide.
- 1 7. The method of claim 1, wherein the polynucleotide comprises a
2 sequence as shown in Tables 1A-16.
- 1 8. The method of claim 1, wherein the polynucleotide is labeled.
- 1 9. The method of claim 8, wherein the label is a fluorescent label.
- 1 10. The method of claim 1, wherein the polynucleotide is immobilized on
2 a solid surface.
- 1 11. The method of claim 1, wherein the patient is undergoing a therapeutic
2 regimen to treat lung cancer.
- 1 12. The method of claim 1, wherein the patient is suspected of having lung
2 cancer.
- 1 13. A method of monitoring the efficacy of a therapeutic treatment of lung
2 cancer, the method comprising the steps of:

3 (i) providing a biological sample from a patient undergoing the therapeutic
4 treatment; and
5 (ii) determining the level of a lung cancer-associated transcript in the
6 biological sample by contacting the biological sample with a polynucleotide that selectively
7 hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16,
8 thereby monitoring the efficacy of the therapy.

1 14. The method of claim 13, further comprising the step of: (iii) comparing
2 the level of the lung cancer-associated transcript to a level of the lung cancer-associated
3 transcript in a biological sample from the patient prior to, or earlier in, the therapeutic
4 treatment.

1 15. The method of claim 13, wherein the patient is a human.

1 16. A method of monitoring the efficacy of a therapeutic treatment of lung
2 cancer, the method comprising the steps of:

3 (i) providing a biological sample from a patient undergoing the therapeutic
4 treatment; and

5 (ii) determining the level of a lung cancer-associated antibody in the biological
6 sample by contacting the biological sample with a polypeptide encoded by a polynucleotide
7 that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in
8 Tables 1A-16, wherein the polypeptide specifically binds to the lung cancer-associated
9 antibody, thereby monitoring the efficacy of the therapy.

1 17. The method of claim 16, further comprising the step of: (iii) comparing
2 the level of the lung cancer-associated antibody to a level of the lung cancer-associated
3 antibody in a biological sample from the patient prior to, or earlier in, the therapeutic
4 treatment.

1 18. The method of claim 16, wherein the patient is a human.

1 19. A method of monitoring the efficacy of a therapeutic treatment of lung
2 cancer, the method comprising the steps of:

3 (i) providing a biological sample from a patient undergoing the therapeutic
4 treatment; and

5 (ii) determining the level of a lung cancer-associated polypeptide in the
6 biological sample by contacting the biological sample with an antibody, wherein the antibody
7 specifically binds to a polypeptide encoded by a polynucleotide that selectively hybridizes to
8 a sequence at least 80% identical to a sequence as shown in Tables 1A-16, thereby
9 monitoring the efficacy of the therapy.

1 20. The method of claim 19, further comprising the step of: (iii) comparing
2 the level of the lung cancer-associated polypeptide to a level of the lung cancer-associated
3 polypeptide in a biological sample from the patient prior to, or earlier in, the therapeutic
4 treatment.

1 21. The method of claim 19, wherein the patient is a human.

1 22. An isolated nucleic acid molecule consisting of a polynucleotide
2 sequence as shown in Tables 1A-16.

1 23. The nucleic acid molecule of claim 22, which is labeled.

1 24. The nucleic acid of claim 23, wherein the label is a fluorescent label

1 25. An expression vector comprising the nucleic acid of claim 22.

1 26. A host cell comprising the expression vector of claim 25.

1 27. An isolated polypeptide which is encoded by a nucleic acid molecule
2 having polynucleotide sequence as shown in Tables 1A-16.

1 28. An antibody that specifically binds a polypeptide of claim 27.

1 29. The antibody of claim 28, further conjugated to an effector component.

1 30. The antibody of claim 29, wherein the effector component is a
2 fluorescent label.

1 31. The antibody of claim 29, wherein the effector component is a
2 radioisotope or a cytotoxic chemical.

1 32. The antibody of claim 29, which is an antibody fragment.

- 1 33. The antibody of claim 29, which is a humanized antibody
- 1 34. A method of detecting a lung cancer cell in a biological sample from a
2 patient, the method comprising contacting the biological sample with an antibody of claim
3 28.
- 1 35. The method of claim 34, wherein the antibody is further conjugated to
2 an effector component.
- 1 36. The method of claim 35, wherein the effector component is a
2 fluorescent label.
- 1 37. A method of detecting antibodies specific to lung cancer in a patient,
2 the method comprising contacting a biological sample from the patient with a polypeptide
3 encoded by a nucleic acid comprises a sequence from Tables 1A-16.
- 1 38. A method for identifying a compound that modulates a lung cancer-
2 associated polypeptide, the method comprising the steps of:
3 (i) contacting the compound with a lung cancer-associated polypeptide, the
4 polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least
5 80% identical to a sequence as shown in Tables 1A-16; and
6 (ii) determining the functional effect of the compound upon the polypeptide.
- 1 39. The method of claim 38, wherein the functional effect is a physical
2 effect.
- 1 40. The method of claim 38, wherein the functional effect is a chemical
2 effect.
- 1 41. The method of claim 38, wherein the polypeptide is expressed in a
2 eukaryotic host cell or cell membrane.
- 1 42. The method of claim 38, wherein the functional effect is determined by
2 measuring ligand binding to the polypeptide.
- 1 43. The method of claim 38, wherein the polypeptide is recombinant.

1 44. A method of inhibiting proliferation of a lung cancer-associated cell to
2 treat lung cancer in a patient, the method comprising the step of administering to the subject a
3 therapeutically effective amount of a compound identified using the method of claim 38.

1 45. The method of claim 44, wherein the compound is an antibody.

1 46. The method of claim 45, wherein the patient is a human.

1 47. A drug screening assay comprising the steps of
2 (i) administering a test compound to a mammal having lung cancer or a cell
3 isolated therefrom;
4 (ii) comparing the level of gene expression of a polynucleotide that selectively
5 hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16 in a
6 treated cell or mammal with the level of gene expression of the polynucleotide in a control
7 cell or mammal, wherein a test compound that modulates the level of expression of the
8 polynucleotide is a candidate for the treatment of lung cancer.

1 48. The assay of claim 47, wherein the control is a mammal with lung
2 cancer or a cell therefrom that has not been treated with the test compound.

1 49. The assay of claim 47, wherein the control is a normal cell or mammal.

1 50. A method for treating a mammal having lung cancer comprising
2 administering a compound identified by the assay of claim 47.

1 51. A pharmaceutical composition for treating a mammal having lung
2 cancer, the composition comprising a compound identified by the assay of claim 47 and a
3 physiologically acceptable excipient.